	FIGURE 1: Down	in Mild OA C	nly	-	· ·	1	<u>l</u>	<u> </u>
—		Gene	Ref		Protein			
SEQ	Description of	Accession	Accession		Accession			
ID No	Sequence	Number	Number	UniGene	Number	normal	mild	severe
						1 (0.725 to	1	0.556 (0.504
l 1	FCR1090;Novel;					1.275)		to 0.608)
	, , , , , , , , , , , , , , , , , , , ,						01.00	
ļ	MIOA2900;ALU							
	SUBFAMILY J]					
	SEQUENCE		ŀ				ļ	
	CONTAMINATIO							
	N WARNING					1 (0.686 to		1.53 (1.205
	ENTRY ;P39188	BC035122.1		Hs.382273		1.314)	0.497	to 1.854)
	seob7176;U50'							
	snoRNA and U50							
	snoRNA					1 (0.837 to		0.651 (0.572
	;AB017710.1	AB017710.1				1.163)	0.497	to 0.731)
	miob0185;DNA							
	sequence (clone					İ		
	RP11-38M8 from					1.000		
	7q31)					(0.696 to		0.585 (0.568
2	;AC009275.5	AC009275.8				1.304)	0.497	to 0.601)
	seoa5479;EST(a							
	a89a04.r1					İ		
	Stratagene fetal							
	retina 937202							
	clone 838446 5') ;AA457594	A A 457504	NIM COACAO	11- 24207	ND 070440	1 (0.977 to		0.832 (0.561
<u> </u>	,AA437394	AA457594	NM_024843	HS.31297	NP_079119	1.023)	0.495	to 1.102)
	seob3694;hypoth							
	etical protein							
	FLJ10147			·				
	(FLJ10147)(ORF	NM 018010			Į.	1 (0.927 to		0.934 (0.808
);NM_018010.1	1	NM 018010	Hs 170318	NP 060480	1.073)		to 1.060)
	MIOA1763;MHC					1.07.07	0.700	1.000)
	class 1 region					1 (0.523 to		0.88 (0.815
3	;AF055066	AF055066			AAC24825.	1.477)		to 0.945)
						<u> </u>		
	ncrc1999;INTER							
	FERON-							
	INDUCED							
	TRANSMEMBRA							
	NE PROTEIN 3							
	(INTERFERON-	i						
	INDUCIBLE					1.000		
		NM_021034.	NM_021034.		NP_066362.	`		0.711 (0.638
	;Q01628	1	1	Hs.433414	1	1.471)	0.492	to 0.784)

Fig	jure	1	Cont'd	
		_		=

<u></u>	gure 1 Cont'd.							
	MIOA6236;EST(I					
	qr24f06.x1							
	NCI_CGAP_GC6							
	clone							
	IMAGE:1941827					1 (0.716 to		0.61 (0.567
	3') ;Al203343	AI203343	NM 016586	Hs 16755	NP 057670	1.284)		to 0.653)
	SEOA6643a;DN	7112000-10	1111_010000	113.10700	141 _007070	1.204)	0.432	10 0.000)
	A sequence		J					
	(chromosome 16		l					
	cloneRPCI-							
	11_567P19,						ł	
	WORKING							
	DRAFT							
	SEQUENCE, 63							
	unordered							
1	pieces)					1 (0.794 to		0.774 (0.611
4	;AC009152.1	AC009152.7			<u> </u>	1.206)	0.491	to 0.938)
	fcrb5788;H19,							
	imprinted			1				
	maternally							
	expressed			}				
	untranslated					1 (0.848 to		1.191 (1.007
	;Hs.334822	AF087017.1				1.152)	l .	to 1.375)
⊢ –	113.004022	A 007017.1		}		1.102)	0.431	10 1.373)
	SEOA3908;elong							
	ation factor-1-					4 (0 000 +-		0.740 (0.000
		744504	NINA 004404	050404	ND 004005	1 (0.833 to		0.742 (0.683
	gamma ;Z11531	Z11531	NM_001404	HS.256184	NP_001395	1.167)	0.49	to 0.802)
	FCR6188;hypoth							
	etical protein							
	(KIAA0121)					1 (0.846 to		0.704 (0.580
	;D50911	D50911	XM_052386	Hs.155584		1.154)	0.49	to 0.827)
	MIOB2691;HRIH							
	FB2072							
	(=AF115778							
	M.musculus							
	short coiled coil							
	protein SCOCO							
	(Scoc))					1 (0.686 to		1.157 (1.108
	;AB015335.1	AB015335.1	NM_032547	Hs 286013	NP 115936		1	to 1.207)
	seoa3242;EST	50 10000.1	7.111_0020-77	1.10.200010	111 _110000	1.017)	0.700	1.201)
	zp96a07.r1							
	Stratagene							
	muscle 937209							
]	}			
	cDNA clone			•				
	628020 5'			l		1 (0.85 to	_	
	;AA196423	AA196423		Hs.374621		1.150)	0.486	0.885
	SEOA5977a;hyp							
	othetical protein					1.000		
	(KIAA0569)					(0.959 to		0.960 (0.88
	;AB011141	AB011141	NM_014795	Hs.34871	NP_055610	1.041)	0.485	to 1.041)

Application of: Liew, et. al. Our Docket #: 4231/2042 Figure 1 Cont'd.

- 10	gure 1 Conta.							
<u> </u>	ncrb7403;EST			_				
	(EST390300							
	MAGE							
	resequences,							
	MAGO cDNA)					1 (0.831 to		0.613 (0.61
	;AW978191.1	AW978191.1		Hs.117927		1.169)	0.485	to 0.616)
	seob6836;hXBP-							
	1 transcription							
	factor DNA							
	(=TREB protein)					1 (0.933 to	i	0.616 (0.554
	;L13850.1	L13850.1				1.067)	0.485	to 0.678)
	miob3968;gamm							
	a-aminobutyric							
	•							
	acid (GABA) A							
	receptor, alpha 4		:					
	(GABRA4)	NM_000809.				1 (0.747 to		0.926 (0.898
	;NM_000809.1	1	NM 000809	Hs.248112	NP 000800	1.253)	0.484	to 0.954)
 	SEOA2970a;maj							,
	or]			
İ	T .				1			
1	histocompatibility							
	class II antigen							
	gamma chain					1 (0.615 to		1.777 (1.256
	;K01144	K01144	NM 004355	Hs.84298	NP 004346	1.385)	0.48	to 2.297)
	,		_		-	, , , , , , , , , , , , , , , , , , ,		,
	05040057.54							
	SEOA9357;hypot		 					
	hetical protein,							1
	estradiol-induced							
1	(E2IG5), (ORF)	NM_014367.				1 (0.783 to		0.658 (0.528
	;NM 014367.1	1	NM 014367	He 5243	NP_055182	· `		to 0.788)
-			14141_0 14307	113.0240	141 _000102			0.635 (0.529
İ	MIOA8338;HepG			l., ,,,,,		1 (0.525 to		
	2 ;D17039	D17039	NM_004048	Hs.48516	NP_004039	1.475)	0.48	to 0.742)
	SEOB1273;CGI-				1			
	129 protein				1	1 (0.963 to		0.909 (0.823
	;AF151887.1	AF151887.1	NM 016098	Hs.108725	NP 057182			to 0.995)
-	,					,		
	SEO 40422:55							
	SEOA9433;fibron							
	ectin leucine rich				1			
	transmembrane				1			
	protein 2			İ	1			
	(FLRT2), mRNA	NM 013231				1 (0.910 to		0.598 (0.489
	;NM_013231.1	11	NM 013231	Hs ARGOR	NP 037363	1.09)	l .	to 0.707)
 		'	11111 0 10201	113.70330	141 _007 003	1.03)	0.413	0.707
	seoa1431;EST				1			
	(wg57e08.x1		ł		1			
	Soares_NSF_F8				1			
	_9W_OT_PA_P_				1			
	S1 clone			1	1			
	IMAGE:2369222	İ	İ		1	1 (0.569 to		0.866 (0.862
	I II VI/NOL. EUUUELE	i	•	I	I	1 (0.000 10	ı	10.000 (0.002
	1	AI760043.1	NM_019000	LL 00070	NP_061873	1.431)	0.470	to 0.870)

_ 	gure 1 Conta.					·	 ·
	ncr0238;EST tt13f10.x1 NCI_CGAP_GC6 IMAGE:2240683 3' similar to TR:P97434 P97434 P116RIP. ;contains element A3R repetitive element					1 (0.639 to	0.968 (0.778
	;Al655514	AI655514	NM_007032	Hs 40342	NP_619538	1.361)	to 1.158)
	SEOB1513;T-cell receptor alpha chain-c6.1A fusion protein (c6.1A-TCRC) gene ;S72931.1	S72931.1			AAB30469	1 (0.81 to 1.190)	0.567 (0.483 to 0.651)
	seob7039;high- risk human papilloma viruses E6 oncoproteins targeted protein E6TP1 alpha (=AB007900 KIAA0440) ;AF090989.1		NM_015556	Hs 172180	NP 056371	1 (0.735 to 1.265)	0.702 (0.665 to 0.738)
	ncrc6072;testis specific ankyrin- like protein 1 (LOC51281) ;NM_016552.1	NM_016552.			NP_060314	1 (0.846 to	0.846 (0.748 to 0.944)
	ncrb0045;chitina se 3-like 1(cartilage glycoprotein-39) (CHI3L1) ;NM_001276.1	NM_001276. 1	NM_001276		NP_001267	1 (0.764 to 1.236)	0.644 (0.608 to 0.681)
	miob4752;EST(a a17g07.r1 Soares_NhHMPu _S1 clone IMAGE:813564	AA455459.1		Hs.445247		1 (0.905 to 1.095)	0.77 (0.511 to 1.029)

	gure 1 Contid.							
	seob5203;microv							
	ascular							
	endothelial							
,	differentiation							
1	gene 1 product							0.525 (0.374
1	;AB026908.1	AB026908.1	NM_012328	He 6790	NP 036460	1	0.451	to 0.675)
	SEOB1411;KIAA	AB020300.1	14141_012320	113.0730		<u>'</u>	0.431	10 0.070)
1								
	0879 protein							
	(KIAA0879)	NM_014936.				1 (0.706 to		0.614 (0.558
	;NM_014936.1	1	NM_014936	Hs.54037	NP_055751	1.294)	0.449	to 0.669)
	MIOA6207;EST(
	an41g01.s1							
	Gessler Wilms							
	tumor clone							
	IMAGE:1701264					1 (0.537 to		0.517 (0.467
	3') ;AI174629	AI174629		Hs.6634		1.463)		to 0.567)
 	7 -1							10 0.00. /
	miob4692;dJ93K							
	22.1 (novel							
	protein (contains							
	DKFZP564B116)					1 (0 215 +		0.500 (0.406
١ ,		A1 050000				1 (0.315 to		0.588 (0.426
<u> </u>) ;AL050333	AL050333				1.685)	0.447	to 0.749)
	ncrc4864;fibrobla							
	st activation							
	protein,							
	alpha;seprase							
	(RefSeq aa 6e-							
	91)	NM 004460.	NM 004460.		NP_004451.	1 (0.353 to		0.738 (0.515
	;NP_004451.1	2	2	Hs.418	11	1.647)	0.446	to 0.960)
<u> </u>	SEOB2750;PGK					, ,		,
	1=phosphoglycer							
	ate kinase 1					1 (0.994 to		1.370 (1.174
	;S75476.1	S75476.1				1.006)		to 1.567)
—	miob5780;DNA	57 5 7 7 5. 1			1	1.000)	0.440	1.501)
	sequence (clone					·		
		AC007274 4				1 (0 706 4-		0 500 (0 400
_	/	AC007371.1				1 (0.796 to		0.522 (0.498
		6				1.204)	0.443	to 0.547)
	fcrb1731;NDUFV							
	3 gene for							
	mitochondrial							
	NADH-							
	Ubiquinone							
	oxidoreductase					1 (0.975 to		1.555 (0.334
	;AB038163.1	AB038163.1			BAB13732	1.025)		to 2.775)
	·		L	<u> </u>	, ::=:-:			··· =··· • /

 gure i Conta.							
seob5880;EST zx48b06.r1 Soares_testis_N HT cDNA clone IMAGE:795443 5' similar to contains Alu repetitive element;contains element MER13 repetitive element; ;AA454038.1		NM_017925	Hs 29032	NP 060395	1 (0.676 to 1.324)		0.740 (0.646 to 0.834)
 ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	77434030. I	14141_017925	115.23032	NF_000393	1.324)	0.420	10 0.634)
miob2355;NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3 (12kD, B12) (NDUFB3)	NM_002491.				1 (0.865 to		0.739 (0.669
 ;NM_002491.1	1	NM_002491	Hs.109760	NP_002482	1.135)	0.428	to 0.808)
ncr0644;EST(AV 724328 HTB cDNA clone HTBAYE08 5') ;AV724328.1	AV724328.1	NM_007111	He 70353	NP_009042	1 (0.664 to 1.336)		0.549 (0.546 to 0.553)
fcrb5537;slug (chicken homolog), zinc finger protein, clone MGC:10182 IMAGE:3908245, mRNA, complete cds /cds=(152,958) /gb=BC014890 /gi=15928855 /ug=Hs.93005	N / 24320.	NW_00/111	115.78333	14F_009042			
/len=2010 ;Hs.93005	BC014890	NM_003068	Hs.93005	NP_003059	1 (0.329 to 1.671)		0.52 (0.482 to 0.558)

- 110	ure 1 Cont'd.							
1	f							
Ì	fcrb3691;FLJ220							
	66 fis, clone				ļ			
	HEP10611				İ		Į	
	/cds=UNKNOWN							
	/gb=AK025719							
	/gi=10438328	į	1					
}	/ug=Hs.251664							
1	/len=2281				l	1 (0.582 to		1.101 (0.419
	;Hs.251664	AK025719		Hs.251664		1.418)		to 1.783)
	MIOA4076a;ARP							
	2/3 COMPLEX							
	20 KD SUBUNIT				ĺ			
	(P20-ARC),	į.						
	putative	NM_020154.	NIM 020154		NP_064539.	1 (0 383 to		2.909 (2.011
	;Q18491	1	14141_020104.	Hs.4245	1	1.617)		to 3.806)
	SEOB1449;C-	'		115.4245	· ·	1.017)	0.410	10 3.600)
	type lectin	no significant				1 (0 022 4-		0 572 (0 547
	• •	_			1	1 (0.833 to		0.572 (0.517
8	;BAA95671.1	match				1.167)	0.393	to 0.626)
	ncrb4957;WNT1							
	inducible							
	signalling							
	pathway protein							
	2 (WISP2)	NM_003881.				1 (0.769 to		0.722 (0.646
	;NM_003881.1	1	NM_003881	Hs.194679	NP_003872	1.231)	0.387	to 0.798)
1	SEOB3360;dual							
	specificity							
	phosphatase 1							
	(DUSP1)	NM_004417.				1 (0.821 to		0.646 (0.573
	;NM_004417.2	2	NM_004417	Hs.171695	NP_004408	1.179)	0.386	to 0.719)
	seob1967;hypoth							
	etical protein							•
	(FLJ11041 fis,	-						
	clone							
	PLACE1004405)					1 (0.217 to		2.451 (1.884
	;AK001903.1	AK001903.1		Hs.28792		1.783)		to 3.019)
	SEOB1385;hypot		*- <u></u>		_	55)	0.004	.5 5.5 10)
	hetical protein							
	(KIAA0907)	[1 (0.749 to	,	0.601 (0.527
	;AB020714.1	AB020714.1	NM 014949	He 24656	NP 055764	1.251)		to 0.676)
-	mioa4318;embry	10020114.1	14141_014343	113.24000		1.201)	V.311	0.070)
	onic lung protein							
	• •					1 (0 004 1-		0 604 (0 500
}	(HUEL)	A E 0.06 C 0.4 .4	NINA 000045	11- 070050	ND 000000	1 (0.924 to		0.601 (0.536
	;AF006621.1	AF006621.1	NM_006345	HS.270956	INP_006336	1.076)	0.377	to 0.667)
	aaab 47001:45			:				
	seob4726;differe							
	ntiation-related							
	gene 1 (nickel-				-			
	specific induction							
	, , , ,	NM_006096.				1 (0.637 to		0.710 (0.479
	;NM_006096.1	1	NM_006096	Hs.75789	NP_006087	1.363)	0.359	to 0.941)

	garo i Oonta.							
	SEOA8195a;SO					1 (0.386 to		0.516 (0.381
	X9 ;Z46629	Z46629	NM_000346	Hs.2316	NP_000337	1.614)	0.356	to 0.651)
	ncrc0981;EST							
	(cDNA clone							
	HEMBA1000915							
	3' HEMBA1)					1 (0.976 to		1.322 (0.621
	;AU144114.1	AU144114.1		Hs.453087		1.024)	0.35	to 2.022)
	miob2375;H3							
	histone, family							
	3B (H3.3B)							
	(H3F3B)	NM_005324.		<u> </u>		1 (0.850 to		0.632 (0.580
	;NM_005324.1	1	NM_005324	Hs.393660	NP_005315	1.15)	0.339	to 0.684)
	SEOB1322;fos							
	proto-oncogene							
	(c-fos)	1				1 (0.688 to		0.643 (0.622
	;K00650.1	K00650.1			AAA52471	1.312)	0.289	to 0.665)
	SEOA1079a;chiti						·	
	nase			İ				
	(HUMTCHIT)					1 (0.172 to		2.606 (2.244
	;U58515	U58515	NM_004000	Hs.154138	NP_003991	1.828)	0.282	to 2.969)
	ncrc2705;EST(wr							
	53g02.x1							
	NCI_CGAP_Ut1							
	cDNA clone							
	IMAGE:2491442	1				1 (0.261 to	•	0.748 (0.252
	3') ;AI973251.1	Al973251.1	NM_031461	Hs.182364	NP_113649	1.739)	0.269	to 1.243)
	MIOA7395a;SOD	1						
	2 manganese							
	superoxide							
	dismutase	l				1 (0.218 to		0.595 (0.273
l	;X65965	X65965		1		1.782)	0.232	to 0.916)

	FIGURE 2: Down	n in Severe OA	Only					
SEQ		Gene	Ref		Protein			
ID	Description of	Accession	Accession		Accession			
NO	Sequence	Number	Number	UniGene	Number	normal	mild	severe
	FCR1566;EST							
	(np83a06.s1				ļ			
	NCI_CGAP_Thy							
	1 clone					ŀ	į	
	IMAGE:1132882					ļ		
ļ	gb:L06505 60S					İ		
	RIBOSOMAL							0.42
	PROTEIN					1 (0.401		(0.341 to
	L12);AA632687	AA632687	NM_000976	Hs.378011	NP_000967	to 1.599)	0.694	0.499)
	fcrb1690;EST							
	(7n15h06.x1							
	NCI_CGAP_Brn							
	23 DNA clone							0.412
	IMAGE:3564899	DE405450 4		11 454070		1 (0.667		(0.328 to
	3') ;BF195152.1	BF195152.1		Hs.451373		to 1.333)	0.523	0.497)
	ncrc3541;EST(x n38h02.x1							
	NCI_CGAP_Kid							
	11 cDNA clone							
	IMAGE:2696019							0.489
	3')					1 (0.943		(0.489 to
	;AW195479.1	AW195479.1	NM 005398	Hs 303090	NP 005389	to 1.057)	0.832	0.489)
	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	744100110.1		110.000000		1.007)	0.002	0.400)
	ncrb8425;EST(6							
	01463665F1							
	NIH_MGC_67							
	cDNA clone							0.48
	IMAGE:3866801					1 (0.806		(0.474 to
	5') ;BE777895.1	BE777895.1	NM_021639	Hs.169854	NP_067652	to 1.194)	0.554	0.485)
	ncrb8303;Hypoth							
	etical							
	protein(cDNA	;						
	FLJ11339 fis,							
	clone						ŀ	
	PLACE1010743,							
	weakly similar to							
	myosin-IXb]		
	splice variant							0.394
	mRNA)	A14000004 4	NINA OCAAAS	11- 450000	ND 004400	1 (0.319	0	(0.305 to
L	;AK002201.1	AK002201.1	NM_004145	HS.159629	NP_004136	to 1.681)	<u> </u> 0.528	0.482)

Figure	2 (Cor	nt'd.
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 guic 2 Conta.		· · · · ·						
ncr1204;promyel ocytic leukemia zinc finger protein (PLZF) gene, complete cds ;AF060568	AF060568				AAD03619	1	0.824	0.402 (0.324 to 0.48)
MIOA0090;EST (wh87a08.x1 NCI_CGAP_CLL 1 clone IMAGE:2387702 3' WP:B0035.2 CE05160 DNAJ PROTEIN LIKE) ;AI760344.1	AI760344.1	NM	_004125	Hs.433898	NP_004116	1 (0.606 to 1.394)	0.6	0.442 (0.425 to 0.459)
seoa8384;EST(t h76e02.x1 Soares_NhHMP u_S1 clone IMAGE:2124602 3') ;AI434978.1	Al434978.1			Hs.164315		1	NO DATA	0.424 (0.418 to 0.431)
MIOA3760a;zinc finger transCRiption factor GKLF ;AF105036.1 FCR1580;EST	AF105036.1	NM_	_004235	Hs.356370	NP_004226		NO DATA	0.384 (0.367 to 0.402)
(zs83g12.s1 NCI_CGAP_GC B1 clone IMAGE:704134 3');AA279281	AA279281	NM_	_004089	Hs.75450	NP_004080	1 (0.288 to 1.712)	0.676	0.336 (0.272 to 0.399)
 miob4857;EST(DKFZp434O157 2 clone DKFZp434O157 2) ;AL137333.1 miob6713;zinc	AL137333.1	XM	_042234	Hs.194478		1 (0.918 to 1.082)	0.659	0.411 (0.391 to 0.432)
finger protein (ZNF-U69274) ;NM_014415.1	NM_014415.1	NM_	014415	Hs.301956	NP_055230	1 (0.892 to 1.108)	0.539	0.41 (0.373 to 0.447)
seoa3815;EST(o j25g11.s1 NCI_CGAP_Kid 5 clone IMAGE:1493252 3') ;AA886870	AA886870	NM_	_018359	Hs.107381	NP_060829	1 (0.642 to 1.358)	NO DATA	0.359 (0.345 to 0.373)

Application of: Liew, et. al. Our Docket #4231/2042 Figure 2 Cont'd.

FIG	gure 2 Cont'd.							
	ncrc9528;nuclea r factor of kappa lightpolypeptide gene enhancer in B-cells inhibitor, alpha;Nuclear factor of kappa light chain gene enhancer inB- cells (RefSeq aa 4e-38) ;NP_065390.1	NM_020529			NP_065390.	1 (0.458 to 1.542)		0.38 (0.356 to 0.403)
	ncrb8237;TSC- 22-like Protein mRNA, ;AF183393.1	AF183393.1	NM_004089	Hs.75450	NP_004080	1 (0.286 to 1.714)	0.707	0.326 (0.297 to 0.355)
9	miob2933;DNA sequence PAC clone RP5- 1060B11 from 7q11.23-q21.1, complete sequence ;AC006322.2	AC006322.2				1 (0.714 to 1.286)	1.088	0.388 (0.352 to 0.424)
	MIOA1025;myle oid differentiation primary response protein MyD88 ;U70451		NM_002468	Hs.82116	NP_002459	1 (0.912 to 1.088)		0.366 (0.331 to 0.401)
	miob0762;EST(t c01c04.x1 NCI_CGAP_Co1 6 cDNA clone IMAGE:2062566 3') ;AI343957.1	Al343957.1				1	NO DATA	0.325 (0.320 to 0.33)
	FCR6730;DNA sequence (Xq13 3' end of PAC 92E23 containing the X inactivation transcipt (XIST)) ;U80460	U80460				1 (0.331 to 1.669)	1.621	0.329 (0.320 to 0.337)

	miob4228;DNA				T			
l	sequence (PAC							
	121G13							
ł	chromosome 6)					1 (0.969	NO	0.398 (0.3
	;Z86062.1	Z86062.1				to 1.031)		to 0.497)
	ncr6316;seleniu							
	m binding							
	protein 1				ł			
	(RefSeq aa 8e-							0.202
	40)		NM_003944.		NP_003935.	1 (0.454		(0.189 to
	;NP_003935.1	NM_003944.2	2	Hs.334841	1	to 1.546)	0.519	0.214)

	FIGURE 3: Up in Mild OA Only			<u> </u>			T	
		Gene	Ref		Protein			
SEQ ID		Accession	Accession		Accession			
NO	Description of Sequence	Number	Number	UniGene	Number	normal	mild	severe
	MIOA8106;DNA							
	sequence(HS_5573_B1_E05_SP			l				
	6 RPCI-11 Male BAC Library							1.018
	genomic clone Plate=1149 Col=9					1 (0.871 to		(0.964 to
	Row=J) ;AQ750872.1	AQ750872.1				1.129)	3.168	1.072)
	FCR4376;EST (ol15b11.s1							0.901
	Soares_NFL_T_GBC_S1 clone					1 (0.871 to	ŀ	(0.798 to
	IMAGE:1523517 3') ;AA904355	AA904355	NM_032682	Hs.274344	NP_116071	1.129)	3.047	1.005)
								1.791
						1 (0.823 to		(1.729 to
11	hfcr8691;No significant match;					1.177)	2.727	1.852)
								1.151
	SEOA0824;alpha-tubulin					1 (0.728 to	1	(1.051 to
	;K00557	K00557	NM_006009	Hs.433394	NP_006000	1.272)	2.688	1.252)
	EODOOG DNA	!						
	FCR6361;DNA sequence					F		
	(12p13.3 BAC RPCI11-500M8							<u></u> .
40	(Roswell Park Cancer Institute	4 0005000				1 (0.977 to		1.3 (1.254
12	Human BAC Library) ;AC005832	AC005832				1.023)	2.625	to 1.345)
						4 (0 000 4		1.784
	hfor2000:Novol:	1149606 4				1 (0.808 to		(1.553 to
	hfcr3990;Novel;	U48696.1		ļ		1.192)	2.614	2.015)
						1 (0 740 +	ļ	1.125 (0.872 to
	SEOA0114;MacMarcks ;X70326	Y70226	NM 023009	Un 75061	NP_075385	1 (0.742 to		1,
	ncrb4428;Ras association	X70320	14141_023009	HS.75061	INF_0/5365	1.200)	2.556	1.378)
	(RalGDS/AF-6) domain family 2			į				1.304
	(RASSF2)(= KIAA0168)	NM_014737				1 (0.635 to		(1.298 to
	;NM_014737.1	1.1	NM_014737	Hs 80905	NP_739580	1.365)		1.309)
	<u>,,</u>	- 1	14141_014707	113.00000	141 _700000	1.500)	2.307	1.386
	ncrb4154;glucosamine-6-					1 (0.609 to		(0.950 to
	phosphate ;AJ002231.1	AJ002231.1	NM_005471	Hs 278500	NP 005462			1.823)
	ncr0679;membrane protein,							
	palmitoylated 3 (MAGUK p55							
	subfamily member 3)							0.871
]	(MPP3), mRNA	NM 001932	NM_001932.		NP_001923.	1 (0.935 to		(0.840 to
		.2	2	Hs.423809		1.065)		0.901)
	fcrb1982;hypothetical protein					 		1.714
	MGC3047 (MGC3047)					1 (0.547 to		(1.584 to
	;XM_027710.1	NM_032348	NM_032348	Hs.59384		1.453)	1	1.844)
	MIOA8952;erythrocyte membrane				. "	<u> </u>		1.793
	protein band 4.1-like 2 (EPB41L2)	NM_001431				1 (0.627 to	.]	(1.761 to
	;NM_001431.1	.1	NM_001431	Hs.7857	NP_001422		i .	1.826)
	bfcn0190n;Homo sapiens							1.309
	chromosome 15, clone CTD1-					1 (0.987 to		(1.124 to
13	2291N1, complete sequence	AC107908.3				1.013)	2.248	1.494)

<u>'</u>	Igure 3 Contu.			т	,		**	
	fcr3730;EST xb22e11.x1							1.33
	NCI_CGAP_Kid13 cDNA clone			1		1 (0.999 to		(0.973 to
	IMAGE:2577068 3' ;AW075553	AW075553		Hs.243278		1.001)	2.241	1.687)
	fcrb5705;kinesin-like 5 (mitotic							
	kinesin-like protein 1) (KNSL5),							
	mRNA /cds=(117,2687)			:				
	/gb=NM_004856 /gi=13699831							1.190
	/ug=Hs.270845 /len=3323					1 (0.911 to		(1.054 to
i	I;Hs.270845	NIM OOMOES	NM_138555	Un 270045	ND 612565			١,
——	1,119.270043	14141_004650	14M_136333	IDS.270045	NP_012303	1.089)	2.203	1.326)
	and a constant of the second of							1.174
	seoa0387;matrix Gla protein	1455070				1 (0.775 to		(0.889 to
	(MGP) ;M55270	M55270			AAB53765	1.225)	2.202	1.458)
	l				į			1.028
	hfcr0439;alpha-1-antitrypsin					1 (0.945 to		(0.879 to
	mRNA, complete cds ;K01396.1	K01396.1	NM_000295	Hs.297681	NP_000286	1.055)	2.192	1.178)
	miob1269;EST (an12d12.s1							1.813
	Stratagene schizo brain S11							(1.454 to
	IMAGE:1685399 3') ;AI003217.1	AI003217.1				l 1	2.187	2.173)
					<u> </u>			
	miob3252;CILP gene for cartilage							0.993
	intermediate layer protein,				ļ	1 (0.901 to		(0.958 to
	complete cds ;AB022430.1	AB022430.1			BAA76692	1.099)	2 18	,
	ncrb4477;Homo sapiens serine	AD022430.1		<u> </u>	DAA10092	1.099)	2.10	1.028)
	(or cysteine) proteinase inhibitor,							
	clade A							
	l I							
	(alpha-1 antiproteinase,							1.224
	antitrypsin), member 1		NM_000295.		NP_000286.			(0.773 to
	(SERPINA1), mRNA	.2	2	Hs.297681	2	1.244)	2.179	1.674)
i	cr0517;Homo sapiens 12 BAC							
	RP13-820C6 (Roswell Park			ĺ				1.082
	Cancer Institute Human BAC							(1.035 to
14	Library) complete sequence	AC137590.2				1	2.178	1.128)
	FCR2743;EST (qa21e02.x1							1.231
	NCI_CGAP_Brn23 clone	·				1 (0.961 to		(1.213 to
	<u> </u>	AI088910	NM_017714	Hs 88367	NP 060184		2 175	1.249)
	fcr6308;EST df54g09.y1 Morton					1.000/		1.332
	Fetal Cochlea cDNA clone					1 (0.871 to		(1.179 to
		AW023432		Hs.188375			2.450	
	100/ CL.240/ 303 3 ,/XVV023432	~VVUZ343Z		115.1003/5		1.129)	∠.159	1.486)
	norb4942:ranlination protain A4	NIM 000045						1.158
	ncrb4843;replication protein A1	NM_002945	NINA 000045	04040	ND COCCE			(1.098 to
	(70kD) (RPA1) ;NM_002945.1	.1	NM_002945	Hs.84318	NP_002936	1	2.154	1.218)
1	seob4891;DNA sequence (BAC				;	ļ l		1.27
	clone RP11-15J24 chromosome					1 (0.729 to		(1.145 to
15	2) ;AC007736.3	AC007736.3				1.271)	<u>2.1</u> 47	1.394)
	MIOB2566; DNA sequence							
	(chromosome 4 clone RP11-							
	340K9 map 4, WORKING							1.082
	DRAFT SEQUENCE, 24							(0.827 to
16	-	AC012205.3				1	2.145	1.338)
			<u> </u>	L	L	<u> </u>	=. 1∓0	

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Figure 3 Cont'd.

	gure 3 Cont a.					· · · · · · · · · · · · · · · · · · ·		
1	FCR0620;EST (oe35b11.s1				•			0.849
1 1	NCI_CGAP_Pr25 clone					1 (0.946 to		(0.828 to
	IMAGE:1410525 3');AA857238	AA857238		Hs.4248		1.054)	2.13	0.869)
	FCR6069;EST (zf01g11.s1							1.418
	Soares fetal heart NbHH19W					1 (0.908 to		(1.396 to
	clone 375716 3') ;AA033743	AA033743	XM_087386	Hs.433452		1.092)	2.119	1.441)
	miob4693;DNA sequence							
	(chromosome 6 clone RP11-		İ					
1 1	780P12, WORKING DRAFT							1.812
	SEQUENCE, 4 unordered pieces)			 		1 (0.767 to		(1.559 to
	;AC022218.4	AC022218.5				1.233)	2.096	2.066)
	hfcr7667;EST (yr10e10.s1							
	Soares fetal liver spleen 1NFLS							
	clone IMAGE:204906 3')(contains							
	Alu repetitive element)							
	;H57324.1	H57324.1				1	2.087	
	cr0503;EST (PM4-NN0090-							1.001
	230400-001-d11 NN0090)	AW899788.				1 (0.882 to		(0.908 to
<u> </u>	;AW899788.1	1				1.118)	2.085	1.093)
	:							1.408
	FCR5665;EST (yd33h08.r1 clone					1 (0.880 to		(1.393 to
	, .	T85246		Hs.452509		1.12)	2.081	1.423)
1 1	ncr7382;protease inhibitor 1 (anti-							
	elastase),alpha-1-antitrypsin							0.893
1 1	(RefSeq aa 3e-43)				NP_000286.	1 (0.783 to		(0.68 to
	;NP_000286.1	NM_000295			1	1.217)	2.076	1.105)
4 1	fcr4642;EST (integral membrane							
	protein 2A, clone		ł					1.172
	IMAGE:4149910,					1 (0.764 to		(1.144 to
r	mRNA);BC010511	BC010511	NM_004867	Hs.17109	NP_004858	1.236)	2.068	1.200)
								1.718
	SEOA4017a;retinoic acid-induced					1 (0.882 to		(1.634 to
Ir	protein (RAI2) ;AF136587.1	AF136587.1			AAD33688	1.118)	2.059	1.801)
								1.294
						1 (0.933 to		(1.100 to
	hfcr1438;No significant match;					1.067)	2.052	1.489)
	hfcr0263;paired basic amino acid		1					
1	cleaving enzyme (furin,							0.884
		NM_002569	1	,		1 (0.975 to		(0.882 to
	protein) (PACE) ;NM_002569.1	.1	NM_002569	Hs.59242	NP_002560	1.025)	2.049	0.885)
	ncr7477;cDNA sequence (cDNA							1.602
	sequence FLJ11736 fis, clone		ĺ					(1.422 to
		AK021798.1			BAB13899	1	2.045	1.783)
	ncr2015;G protein-coupled					_		1.973
		NM_005296				1 (0.765 to		(1.816 to
	;NM_005296.1	.1	NM_005296	Hs.27812	NP_005287	1.235)	2.044	2.131)
	mioa9984;EST wm09d08.x1							
	NCI_CGAP_ cDNA clone							
] [1	IMAGE:2435439 3' similar to							
	contains Alu repetitive							1.245
								4
	element;contains element THR					1 (0.722 to		(1.202 to

clone IMAGE:2979544 3' ;AW665381.1	AW665381.			Hs.445324			1 (0.889 to 1.111)		(1.19 to 1.519)
Soares_NFL_T_GBC_S1 cDNA									1.354
 hfcr6052;EST hi90a09.x1					 ``		<u> </u>	2.007	0.701
beta-tubulin cofactor D ;NM_005993.2	NM_005993 .2	NM	005993	Hs.12570	NP	005984	1	2.004	0.781
chaperone d (TBCD)= AJ006417	NIM COECOO								
fcrb1183;tubulin-specific									
/len=456 ;Hs.337337	AW009305			Hs.337337			1.059)		1.432)
/clone_end=3' /gb=AW009305 /gi=5858083 /ug=Hs.337337							1 (0.941 to		1.217 (1.002 to
/clone=IMAGE:2504281									4 047
fcrb3863;cDNA, 3' end									
23698) ;AF052094.1	AF052094.1	NM	001430	Hs.8136	NP.	_001421	1.389)		1.777)
miob1165;DNA sequence (clone							1 (0.611 to		(1.745 to
 ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	110430	IAIAI	_000402	113.173133	INP.	_000473	1.134)	2.02	1.761
FCR6039;protein kinase Dyrk2 ;Y13493	Y13493	NIM	006483	Hs.173135	ND	006472	1 (0.868 to 1.132)		(1.157 to 1.197)
									1.177
(low match) ;AA915413	AA915413						1.14)		2.514)
Soares 2NbMT clone 1327939 5')							1 (0.860 to		(1.462 to
 MIOA2551;EST(vz29h10.r1	AA393410	IAIAI	_0 14335	ITS.301137	INP.	_055150_	1.042)	2.023	0.977) 1.988
Soares testis NHT clone 728206 5');AA393418	AA393418	NINA	014225	Hs.381137	ND	055150	1 (0.958 to		(0.852 to
FCR1427;EST (zt75e12.r1									0.914

	FIGURE 4: Up in S	evere OA On	lv		ľ			Γ		
SEQ		Gene	Ref			Pro	tein			
ID	Description of	Accession	Acc	ession		Acc	ession			
NO	Sequence	Number	Nun	nber	UniGene	Nur	nber	normal	mild	severe
							·	<u> </u>		
•	FCR1346;receptor									
	of retinoic acid									
}	(=M73779 PML-									2.651
	RAR protein (PML-							1 (0.804		(2.19 to
	RAR));X06614	X06614	NM_	000964	Hs.361071	NP_	000955	to 1.196)	1.577	3.113)
	MIOA5404a;actin-									
	like 6									
	(ACTL6)=AF04147									
	4 =BAF53a									2.975
	(BAF53a)(ORF)	NM_004301.								(2.785 to
	;NM_004301.1	1	NM	178042	Hs.274350	NP_	829888	1	1.011	3.165)
	SEOA6743;EST(z					1				
	e26h09.r1 Soares									
	retina N2b4HR									2.349
	clone 360161 5')							1 (0.953		(2.297 to
	;AA013461	AA013461			Hs.161598	<u> </u>		to 1.047)	1.442	2.401)
	FCR5026;6-									
	phosphofructo-2-									
	kinase/fructose-2,6									
	bisphosphatase									
	(PF2K)							Ì		
	(=AB007902									2.289
	KIAA0442)							1 (0.944		(2.269 to
	;AF041832	AF041832				1		to 1.056)	1 46	2.309)
<u> </u>	miob4484;hypothet							1.000)	1.70	2.000)
	ical protein									3.424
	(KIAA0584)									(2.207 to
	;AB011156.1	AB011156.1	NM	015101	Hs.106794	NP	055916	1 1	1.547	4.641)
	seob7571;EST			 		 				
	(qh03a05.x1									
	Soares_NFL_T_G									
	BC_S1									2.080
	IMAGE:1843568							1 (0.945		(2.041 to
	3') ;Al222189.1	Al222189.1	NM	002556	Hs.24734	NP	002547	to 1.055)	1.615	2.12)

	FIGURE 5: Down	n in Mild OA I	Up in Severe C)A				
SEQ ID NO	Description of Sequence	Gene Accession Number	Ref Accession Number	UniGene	Protein Accession Number	normal	mild	severe
	MIOA4076a;AR P2/3 COMPLEX 20 KD SUBUNIT (P20-ARC), putative ;Q18491	NM_020154. 1	NM 020154.1	Hs.4245	NP_064539.	1 (0.383 to 1.617)	0.418	2.909 (2.011 to 3.806)
	seob1967;hypot hetical protein (FLJ11041 fis, clone PLACE1004405) ;AK001903.1	AK001903.1		Hs.28792		1 (0.217 to 1.783)	0.384	2.451 (1.884 to 3.019)

	FIGURE 6a:	OA stage specific markers for mild OA only		· · · · · · · · · · · · · · · · · · ·	
Common					
name	Genbank	Description	RefSeq	UniGene	Rep_Prot
		mRNA for KIAA0447 protein, partial cds.			
2025		/cds=(234,1634) /gb=AB007916 /gi=6683704		l	
ncrc6905	AB007916	/ug=Hs.214646 /len=5932		Hs.214646	NP_878258
seoa9924	AB007960	chromosome 1 specific transcript KIAA0491	NM 016009	Hs.136309	NP_057093
	AB011110	mRNA for KIAA0538 protein, partial cds	NM 006989	Hs.184367	NP_008920
110102101	7.50	mRNA for KIAA0640 protein, partial cds.	1111_00000	110.104007	
		/cds=(1,1813) /gb=AB014540 /gi=3327093			
seoc4468	AB014540	/ug=Hs.153026 /len=4824		Hs.153026	NP_055870
00001.00	7.201.1010	mRNA for heat shock protein apg-2,		110.100020	141 _000070
		complete cds. /cds=(279,2801)			
		/gb=AB023420 /gi=4579908 /ug=Hs.90093			
senh7030	AB023420	//en=2839		Hs.90093	NP 002145
30007000	715020420	7611-2000		113.30033	141 _002 143
seoa8696	AB037754	mRNA for KIAA1333 protein, partial cds	NM_017769	Hs.79828	NP_060239
		mRNA for KIAA1367 protein, partial cds.			
		/cds=(1,1741) /gb=AB037788 /gi=7243114			
miob8583	AB037788	/ug=Hs.224961 /len=4196		Hs.224961	NP_059133
		mRNA for KIAA1367 protein, partial cds.			
		/cds=(1,1741) /gb=AB037788 /gi=7243114			
miob8583	AB037788	/ug=Hs.224961 /len=4196		Hs.224961	NP_059133
seob4263	AB040894	mRNA for KIAA1461 protein, partial cds	NM_018328	Hs.94125	NP_060798
seoh4263	AB040894	mRNA for KIAA1461 protein, partial cds	NM 018328	Hs.94125	NP 060798
0000 1200	7.8010004	mRNA for KIAA1754 protein, partial cds.	14141_010020	113.04120	141 _000730
	_	/cds=(32,1816) /gb=AB051541 /gi=12698052			
miob2503	AB051541	/ug=Hs.28501 /len=4088	NM_033397	Hs.28501	NP 203755
	7.2001011	mRNA for KIAA1913 protein, partial cds.	11111_000007	110.20001	141 _200700
		/cds=(818,2347) /gb=AB067500			
mioc2385	AB067500	/gi=15620884 /ug=Hs.172870 /len=3512	NM_052913	Hs.172870	NP 443145
1111002000	712007000	191 10020004749 110.117207071011 0012	1411_002510	113.172070	141 _440140
mioc7513	AF279370	DZIP3 mRNA, partial cds	NM_014648	Hs.165662	NP_055463
i7540	A F070270	DZIDO seDNA sestial ada	044040	105000	ND 055400
mioc7513	AF279370	DZIP3 mRNA, partial cds	NM_014648	Hs.165662	NP_055463
mioc7513	AF279370	DZIP3 mRNA, partial cds	NM_014648	Hs.165662	NP_055463
		•	_		
			NM_002481;	1	NP_002472;
		myosin phosphatase target subunit 2	NM_032103;		NP_115286;
		(MYPT2) gene, exons 11 through 24, and	NM_032104;		NP_115287;
fcrb6309	AF324892	complete cds	NM_032105		NP_115288
		chemokine-like factor super family member 8 (CKLFSF8) mRNA, complete cds /cds=(295,816) /gb=AF474370 /gi=25167350		, ., .	
fcrc6564	AF474370	/ug=Hs.154986 /len=1185		Hs.154986	NP_849199

rigure	oa Conta.				
		chemokine-like factor super family member 8 (CKLFSF8) mRNA, complete cds			
1		/cds=(295,816) /gb=AF474370 /gi=25167350			
foreSEG4	AF474370	/ug=Hs.154986 /len=1185		Hs.154986	NP_849199
fcrc6564	AF474370	/ug=Hs. 154966 /lell=1165		115.154900	141 _049199
		sulfatase SULF1 precursor, mRNA, complete			
		cds /cds=(707,3322) /gb=AF545571	;		
ncrc0075	AF545571	/gi=28191289 /ug=Hs.70823 /len=5699	NM_015170	Hs.70823	NP 055985
ncr1522	AJ000052	gene encoding splicing factor SF1, exons 2-8	NM_004630		NP_004621
miod7007	AJ251973	partial steerin-1 gene	NM_020443		NP_065176
		mRNA full length insert cDNA clone			
miod1528	AJ420597	EUROIMAGE881791		Hs.34665	NP_775945
	AK001419	cDNA FLJ10557 fis, clone NT2RP2002537	NM_014053	Hs.270594	NP_054772
ncr3785	AK001911	cDNA FLJ11049 fis, clone PLACE1004548	NM_020819	Hs.107287	NP_065870
			NM_002788;		
seoc3640	AK021499	cDNA FLJ11437 fis, clone HEMBA1001226	NM 152132		NP_002779
36000040	711021433	CDIVITED THOS IIS, CIONE TIEMDS (TO 1220	14.0102102		NF_002113
miob0007	AK024433	mRNA for FLJ00023 protein, partial cds	NM 022497	Hs.23450	NP_071942
1111009007	AKU24433	IIIRNA for FE300023 protein, partial cus	14141_022497	115.25450	07 1342
 miod6848	AK026850	cDNA: FLJ23197 fis, clone REC00917	NM 005402	Hs.6906	NP 005393
1111000040	7 11 10 20000	cDNA FLJ31353 fis, clone MESAN2000264.			
		/gb=AK055915 /gi=16550762 /ug=Hs.352554			
mioc9655	AK055915	/len=2192	ļ	Hs.352554	NP_006440
	Ì	cDNA FLJ25195 fis, clone REC04480, highly			
miob8096	AK057924	similar to Mus musculus exportin 4 mRNA	NM_022459	Hs.117102	NP_071904
seob1782	AK074172	mRNA for FLJ00245 protein		Hs.244343	NP_443068
	<u> </u>	-DNA EL 100545 5- clore OVADC1000410			
coob7524	AK075026	cDNA FLJ90545 fis, clone OVARC1000410, weakly similar to angiopoietin Y1 mRNA		Hs.8025	NP_036230
Se007534	AKU/3026	weakly similar to angiopoletin 11 mknx		115.0023	14F_030230
		cDNA FLJ33555 fis, clone BRAMY2009349,			
		moderately similar to Mus musculus ubiquitin-			
seob5621	AK090874	protein ligase E3-alpha (Ubr1) mRNA		Hs.15303	NP 056070
		cDNA FLJ40887 fis, clone UTERU2000696,		-	
		moderately similar to Endoplasmic reticulum		1	
seoc6732	AK098206	resident protein 58	1	Hs.83286	NP_714916
		mRNA; cDNA DKFZp434J214 (from clone			
		DKFZp434J214); partial cds /cds=(1,1082)	1		
		/gb=AL080156 /gi=5262614 /ug=Hs.12813			
ncrc1765	AL080156	/len=2749		Hs.12813	NP_056323
		mRNA; cDNA DKFZp434M011 (from clone		11- 004004	ND 440040
miod7095	AL096734	DKFZp434M011)	NM_030980	Hs.301904	NP_112242
foreC 400	AL 440450	mRNA; cDNA DKFZp586E0524 (from clone	NIM OOOOOO	He 226240	ND 000074
fcrc6486	AL110153	DKFZp586E0524)	NM_000983	[ITS.320249	NP_000974

Figure	ba Contd.				
		mRNA; cDNA DKFZp434M2216 (from clone			
mioc2507	AL137295	DKFZp434M2216)	NM_004641	Hs.199429	NP_004632
		mRNA; cDNA DKFZp586C2117 (from clone			
seoa3357	AL162009	DKFZp586C2117)		Hs.356386	NP_004628
		mRNA; cDNA DKFZp451D084 (from clone			
miod2065	AL832012	DKFZp451D084); complete cds	NM_006827	Hs.74137	NP_006818
		mRNA; cDNA DKFZp547F222 (from clone			
miob8803	AL833934	DKFZp547F222)	NM_022458	Hs.107537	NP 071903
		mRNA; cDNA DKFZp434J1323 (from clone			
ncrc7173	AL834204	DKFZp434J1323)	NM_015208		NP_056023
		mRNA; cDNA DKFZp586M1819 (from clone			
		DKFZp586M1819) /cds=(1,795)			
		/gb=AL834255 /gi=21739805 /ug=Hs.355753			
fcrc2573	AL834255	/len=1723		Hs.355753	NP_848934
10102070	AL004200	xj42g07.x1 Soares_NFL_T_GBC_S1 cDNA		110.000700	111 _010001
		clone IMAGE:2659932 3', mRNA sequence			
		/clone=IMAGE:2659932 /clone end=3'			
		/gb=AW182493 /gi=6450953 /ug=Hs.176245			
norb0113	A)A/402402	//len=432		Hs.176245	NP 060046
	AW182493		ļ		NP 006577
fcr3932	BC011767	clone IMAGE:3609644, mRNA	<u> </u>	Hs.56828	INP_000577
			NINA 004004.		
			NM_001894;	70050	110 000407
ncr7284	BC013088	clone IMAGE:3452986, mRNA	NM_152221	Hs.79658	NP_689407
mioc8879	BC017107	clone IMAGE:3537687, mRNA		Hs.16577	NP_208385
		l	1		1
		clone MGC:24133 IMAGE:4693393, mRNA,			
		complete cds /cds=(61,528) /gb=BC017973			
fcrb9161	BC017973	/gi=22450811 /ug=Hs.288010 /len=946	NM_174896	Hs.288010	NP_777556
miod0057	BC020167	clone IMAGE:3529287, mRNA	NM_152740	Hs.284170	NP_689953
			ŧ		
		Vpr-binding protein, mRNA (cDNA clone		ł	
seoc4785	BC022792	MGC:23092 IMAGE:4853730), complete cds	NM_014703	Hs.118738	NP_055518
ncrc2382	BC032405	clone IMAGE:5209850, mRNA		Hs.146428	NP_000084
		clone IMAGE:4432159, mRNA		-	
		/gb=BC032437 /gi=21595543 /ug=Hs.249247			1
seob0220	BC032437	/len=2309		Hs.249247	
· · · -		Similar to NS1-associated protein 1, clone			
		MGC:45213 IMAGE:5495201, mRNA,		ļ	
mioa8580	BC032643	complete cds		Hs.373499	NP 006363
·	· · · · · · · · · · · · · · · · · · ·	Indian hedgehog (Drosophila), clone			†
		MGC:34815 IMAGE:5182642, mRNA,			
		complete cds /cds=(74,955) /gb=BC034757	,		
fcrb8094	BC034757	/gi=21961329 /ug=Hs.115274 /len=1760	[Hs.115274	1
.5.55554	2000-1101	clone MGC:21662 IMAGE:4747440, mRNA,	 	1.10.1.1027	1
ncrc3706	BC035312	complete cds		Hs.145010	NP_115965
10103700	100000012	Sec23 A (S. cerevisiae), clone MGC:26267	-	113.143010	111 _ 110300
noro2000	BC036640		NIM DOESEA	He 272027	ND ODESEE
ncrc3089	BC036649	IMAGE:4821858, mRNA, complete cds	NM_006364	Hs.272927	NP_006355

riguie	oa Conto.				
		Similar to CD47 antigen (Rh-related antigen,			
		integrin-associated signal transducer), clone			1
		MGC:33903 IMAGE:5260986, mRNA,			
miob0681	BC037306	complete cds	NM_001777	Hs.313342	NP_001768
ncr3803	BC037492	clone IMAGE:5260578, mRNA		Hs.5518	NP_689971
		Similar to RIKEN cDNA 3110032G18 gene,			
		clone IMAGE:4472603, mRNA		1	
		/gb=BC042102 /gi=27695553 /ug=Hs.432901			
fcrb4479	BC042102	/len=2132		Hs.432901	NP 859060
1012 1 17 0					
		Similar to adducin 1 (alpha), clone			
i		MGC:44427 IMAGE:5297337, mRNA,	NM 001119;		
		complete cds /cds=(869,2857)	NM_014189;		
		/gb=BC042998 /gi=28175763 /ug=Hs.183706			
foroCC11	BC042998	//en=4761	NM_176801	Hs.183706	NP 789771
fcrc6611	BC042996 BC044258	clone IMAGE:6068796, mRNA	170001	Hs.11861	NP 005112
fcr3593	BC044256	602507208F1 NIH_MGC_79 cDNA clone		П5.11001	NP_005112
		IMAGE:4604760 5', mRNA sequence	<u> </u>		
		/clone=IMAGE:4604760 /clone end=5'			
		· · · · · · · · · · · · · · · · · · ·			
	DC 424047	/gb=BG434947 /gi=13341453 /ug=Hs.382990		 	ND 00012E
seocoodo	BG434947	/len=677 AGENCOURT_8493271 NIH_MGC_100		Hs.382990	NP_060135
		cDNA clone IMAGE:6299336 5', mRNA			
		sequence /clone=IMAGE:6299336		ŀ	
:7077	DOC40744	/clone_end=5' /gb=BQ649741 /gi=21773913		115 44704	
mioc7077	BQ649741	/ug=Hs.44701 /len=993		Hs.44701	NP_055301
		AGENCOURT_10227215 NIH_MGC_141		,	
		cDNA clone IMAGE:6565196 5', mRNA			
		sequence /clone=IMAGE:6565196			1
		/clone_end=5' /gb=BU536672 /gi=22847113			
fcrb4351	BU536672	/ug=Hs.380933 /len=1275	ļ	Hs.380933	NP_000974
		UI-H-FG0-bct-g-21-0-UI.s1			
		NCI_CGAP_EN1_2 cDNA clone UI-H-FG0-			
		bct-g-21-0-UI 3', mRNA sequence /clone=UI-			
		H-FG0-bct-g-21-0-UI /clone_end=3'			
		/gb=BU627064 /gi=23293278 /ug=Hs.85999			
ncrc8884	BU627064	/len=1075	ļ	Hs.85999	NP_060312
	-	UI-E-CQ1-aew-e-07-0-UI.s1 UI-E-CQ1 cDNA			
		clone UI-E-CQ1-aew-e-07-0-UI 3', mRNA			
		sequence /clone=UI-E-CQ1-aew-e-07-0-UI			1
		/clone_end=3' /gb=BU728934 /gi=23651308			1
seoc4779	BU728934	/ug=Hs.436272 /len=1132		Hs.436272	NP 060312
		BX094256 Soares fetal heart NbHH19W		1	
	1	cDNA clone IMAGp998B20783, mRNA			
	1	sequence			
		/clone=IMAGp998B20783_;_IMAGE:342835			
		/gb=BX094256 /gi=27841884 /ug=Hs.407356			
cooboses	BX094256	//len=477		Hs.407356	ND OFFOOA
36000002	DAU94250	//CII-4//	L	113.407330	NP_055301

rigure	ba Cont'd.	BX110894 Soares fetal liver spleen 1NFLS		r	T1
		· ·			
		cDNA clone IMAGp998F21129, mRNA			
		sequence			
		/clone=IMAGp998F21129_;_IMAGE:127124			
		/gb=BX110894 /gi=27836709 /ug=Hs.309257			
seob6628	BX110894	/len=612		Hs.309257	T02670
		ir24c06.y1 HR85 islet cDNA clone			
		IMAGE:6546227 5', mRNA sequence			
		/clone=IMAGE:6546227 /clone_end=5'			
		/gb=CA848700 /gi=26999906 /ug=Hs.389121			
miob0542	CA848700	/len=616		Hs.389121	NP_060312
		NISC_gj17d11.x1 NCI_CGAP_Pr28 cDNA			
		clone IMAGE:3272108 3', mRNA sequence			
		/clone=IMAGE:3272108 /clone_end=3'			
		/gb=CB050438 /gi=27788725 /ug=Hs.435309			
seob4499	CB050438	/len=534		Hs.435309	NP_060265
		mRNA for KIAA0194 gene, partial cds.			
1		/cds=(1,4310) /gb=D83778 /gi=1228038			
ncr1150	D83778	/ug=Hs.216958 /len=5245		Hs.216958	BAA12107
					5,0112101
miob6124	L24123	NRF1 protein (NRF1) mRNA	NM_003204		NP_003195
		MHC class I HLA-A10-alpha-2 chain mRNA,			
ncr5649	M24095	partial cds, clone 8/16		Hs.181244	NP 002107
11013043	10124093	partial cus, cione of to		113.101244	141 _002107
1		'			
•		·			
			NM 000757;		NP_000748;
			NM_172210;		NP_757349;
		macrophage-specific colony-stimulating	NM_172211;		NP_757350;
seob7184	M37435	factor (CSF-1) mRNA, complete cds	NM 172212		NP_757351
	11107 100	alpha-2-macroglobulin (A2M), mRNA			141 _707001
		/cds=(44,4468) /gb=NM_000014 /gi=6226959			1
ncrb5537	NIM OOOO14	/ug=Hs.74561 /len=4577	NM 000014	Uc 74561	NP 000005
ncross/	NM_000014	aspartylglucosaminidase (AGA), mRNA	NW_000014	ITS. 7430 I	NF_000005
		/cds=(171,1211) /gb=NM_000027		ĺ	
micce060	NM 000027	1	NM 000027	Hs.207776	NP 000018
mioaoaoa	1000027	/gi=4557272 /ug=Hs.207776 /len=2150 collagen, type III, alpha 1 (Ehlers-Danlos	141VI_000027	П5.201110	INF_000018
		syndrome type IV, autosomal dominant)			
		(COL3A1), mRNA /cds=(118,4518)			
	NINA 000000	/gb=NM_000090 /gi=15149480	NINA 000000	115 440574	ND 000004
mlob4512	NM_000090	/ug=Hs.119571 /len=5489	NM_000090	Hs.119571	NP_000081
		cartilage oligomeric matrix protein			1
		(pseudoachondroplasia, epiphyseal dysplasia			
		1, multiple) (COMP), mRNA /cds=(26,2299)			
		/gb=NM_000095 /gi=4557482 /ug=Hs.1584		1455:	LID COCCE
hfcr5232	NM_000095	/len=2439	NM_000095	Hs.1584	NP_000086
		ferritin, light polypeptide (FTL), mRNA			
		/cds=(189,716) /gb=NM_000146	l		
fcr0796	NM_000146	/gi=20149497 /ug=Hs.430150 /len=878	NM_000146	[Hs.430150	NP_000137

Figure	6a Contrd.				
		fucosidase, alpha-L- 1, tissue (FUCA1),			
İ		mRNA /cds=(19,1404) /gb=NM_000147			
mioa7241	NM_000147	/gi=24475878 /ug=Hs.576 /len=2035	NM_000147	Hs.576	NP_000138
		hemoglobin, gamma G (HBG2), mRNA			
1		/cds=(54,497) /gb=NM_000184 /gi=28302132			
fcrb2137	NM_000184	/ug=Hs.386655 /len=583	NM_000184	Hs.386655	NP_000175
		Kallmann syndrome 1 sequence (KAL1),			·
		mRNA /cds=(151,2193) /gb=NM_000216			
ncrc3092	NM_000216	/gi=4557682 /ug=Hs.89591 /len=6314	NM_000216	Hs.89591	NP_000207
		ligase I, DNA, ATP-dependent (LIG1), mRNA			
		/cds=(121,2880) /gb=NM_000234			
fcrc2254	NM_000234	/gi=4557718 /ug=Hs.1770 /len=3083	NM_000234	Hs.1770	NP_000225
		serine (or cysteine) proteinase inhibitor, clade			
		A (alpha-1 antiproteinase, antitrypsin),			
		member 1 (SERPINA1), mRNA			
ł		/cds=(233,1489) /gb=NM_000295			
hfcr0439	NM_000295	/gi=21361197 /ug=Hs.297681 /len=1584	NM_000295	Hs.297681	NP_000286
		protein S (alpha) (PROS1), mRNA			
		/cds=(147,2177) /gb=NM_000313			
mioa1277	NM_000313	/gi=4506116 /ug=Hs.64016 /len=3309	NM_000313	Hs.64016	NP_000304
		sarcoglycan, delta (35kDa dystrophin-			
		associated glycoprotein) (SGCD), transcript			ļ
		variant 1, mRNA /cds=(333,1205)			
		/gb=NM_000337 /gi=27477099	NM_000337;		
fcrc4935	NM_000337	/ug=Hs.151899 /len=1440	NM_172244	Hs.151899	NP_758447
		collagen, type V, alpha 2 (COL5A2), mRNA			
		/cds=(158,4648) /gb=NM_000393			
ncrc3604	NM_000393	/gi=16554580 /ug=Hs.82985 /len=6217	NM_000393	Hs.82985	NP_000384
	İ	laminin, alpha 2 (merosin, congenital			
		muscular dystrophy) (LAMA2), mRNA			
		/cds=(50,9382) /gb=NM_000426 /gi=4557708			
fcrb4616	NM_000426	/ug=Hs.75279 /len=9534	NM_000426	Hs.75279	NP_000417
		superoxide dismutase 1, soluble			
ŀ	:	(amyotrophic lateral sclerosis 1 (adult))			}
ļ	·	(SOD1), mRNA /cds=(1,465)			
		/gb=NM_000454 /gi=4507148 /ug=Hs.75428			
ncrc4376	NM_000454	/len=560	NM_000454	Hs.75428	NP_000445
	}	decay accelerating factor for complement	1		
		(CD55, Cromer blood group system) (DAF),			
		mRNA /cds=(66,1211) /gb=NM_000574	l		
mioa0577	NM_000574	/gi=10835142 /ug=Hs.1369 /len=2102	NM_000574	Hs.1369	NP_000565
		chemokine (C-C motif) receptor 5 (CCR5),			1
		mRNA /cds=(358,1416) /gb=NM_000579	NA 000775	54445	ND 000530
seoa8501	NM_000579	/gi=4502638 /ug=Hs.54443 /len=3655	NM_000579	Hs.54443	NP_000570
		CD59 antigen p18-20 (antigen identified by			
		monoclonal antibodies 16.3A5, EJ16, EJ30,			
		EL32 and G344) (CD59), mRNA			
	NIA 000044	/cds=(50,436) /gb=NM_000611 /gi=20127410	i .	11- 070570	NID OCCOO
[mlob/319	NM_000611	/ug=Hs.278573 /len=1946	NM_000611	Hs.278573	NP_000602

Application of: Liew, et. al. Our Docket #: 4231/2042 Figure 6a Cont'd.

superoxide dismutase 2, mitochondrial (SOD2), mRNA /cds=(5,673) /gb=NM 000636 /gi=10835186 ncr9165 NM 000636 /ug=Hs.372783 /len=1026 NM 000636 Hs.372783 NP 000627 aldehyde dehydrogenase 1 family, member A3 (ALDH1A3), mRNA /cds=(53,1591) /gb=NM 000693 /gi=4502040 /ug=Hs.75746 miob3618 NM 000693 /len=3442 NM_000693 Hs.75746 NP_000684 dihydrofolate reductase (DHFR), mRNA /cds=(480,1043)/gb=NM 000791 /gi=7262376 /ug=Hs.83765 /len=3900 NM 000791 Hs.83765 NP 000782 ncr2954 NM 000791 histamine receptor H1 (HRH1), mRNA /cds=(179,1642)/gb=NM 000861 /qi=13435403 /ug=Hs.1570 /len=3870 NM 000861 Hs.1570 NP 000852 seob1879 NM 000861 pyruvate dehydrogenase (lipoamide) beta (PDHB), mRNA /cds=(19,1098) /gb=NM_000925 /gi=4505686 /ug=Hs.979 NP 000916 seoa9883 NM 000925 /len=1501 NM 000925 IHs.979 phospholipase C, beta 4 (PLCB4), mRNA /cds=(231,3299) /gb=NM_000933 mioa3598 NM 000933 /gi=4505866 /ug=Hs.283006 /len=3707 NM_000933 Hs.283006 NP_877949 polymerase (RNA) II (DNA directed) polypeptide A, 220kDa (POLR2A), mRNA /cds=(387,6299) /gb=NM_000937 /gi=14589948 /ug=Hs.171880 /len=6732 NM_000937 | Hs.171880 NP_000928 seob7392 NM_000937 P450 (cytochrome) oxidoreductase (POR), nuclear gene encoding mitochondrial protein, mRNA /cds=(16,2058) /gb=NM_000941 NM_000941 Hs.167246 NM 000941 /gi=24307876 /ug=Hs.167246 /len=2446 NP 000932 fcrc4319 protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha) (PPP3CA), mRNA /cds=(407,1972) /gb=NM 000944 /gi=19923130 NP 000935 NM 000944 seob8082 NM 000944 /ug=Hs.272458 /len=4425 Hs.272458 protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha) (PPP3CA), mRNA /cds=(407,1972) /gb=NM 000944 /gi=19923130 seoa1117 NM 000944 /ug=Hs.272458 /len=4425 NM 000944 Hs.272458 NP 000935 protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha) (PPP3CA), mRNA /cds=(407,1972) /gb=NM 000944 /gi=19923130 /ug=Hs.272458 /len=4425 NM 000944 Hs.272458 NP 000935 mioc8016 NM 000944 ribosomal protein L11 (RPL11), mRNA /cds=(21,557) /gb=NM_000975 /gi=15431289 NM_000975 | Hs.388664 NP 000966 /ug=Hs.388664 /len=609 ncr3037 NM_000975 ribosomal protein L17 (RPL17), mRNA /cds=(287,841) /gb=NM 000985 NM 000985 Hs.82202 seob8311 NM 000985 /gi=14591906 /ug=Hs.82202 /len=898 NP 000976

Figure	ba Conta.				
_ _		ribosomal protein, large, P1 (RPLP1), mRNA			
		/cds=(130,474) /gb=NM_001003			
seob3513	NM_001003	/gi=16905511 /ug=Hs.424299 /len=512	NM_001003	Hs.424299	NP_000994
		ribosomal protein, large, P1 (RPLP1), mRNA			
		/cds=(130,474) /gb=NM_001003			
fcr6708	NM_001003	/gi=16905511 /ug=Hs.424299 /len=512	NM_001003	Hs.424299	NP_000994
		ribosomal protein, large, P1 (RPLP1), mRNA			
		/cds=(130,474) /gb=NM_001003			
miob9652	NM_001003	/gi=16905511 /ug=Hs.424299 /len=512	NM_001003	Hs.424299	NP_000994
			[
seob3326	NM_001004	ribosomal protein, large P2 (RPLP2), mRNA	NM_001004	Hs.297753	NP_000995
seob4140	NM_001004	ribosomal protein, large P2 (RPLP2), mRNA	NM 001004	Hs.297753	NP_000995
		ribosomal protein S4, Y-linked (RPS4Y),			<u> </u>
	:	mRNA /cds=(13,804) /gb=NM_001008			
fcr4212	NM_001008	/gi=17981706 /ug=Hs.180911 /len=931	NM 001008	Hs.180911	NP_000999
1017212	1111_001000	annexin A5 (ANXA5), mRNA			
		/cds=(193,1155) /gb=NM_001154			
senh4689	NM_001154	/gi=4809273 /ug=Hs.300711 /len=1630	NM 001154	Hs 300711	NP_001145
36004003	14141_001104	ADP-ribosylation factor-like 1 (ARL1), mRNA	14141_001104	113.000711	141 _001140_
	1	/cds=(105,650) /gb=NM_001177 /gi=4755126			
coob5804	NM 001177	//ug=Hs.242894 /len=968		Hs.242894	NP 001168
56000094	14141_001177	/ug=ris.242094 /ieii=900	14141_001177	115.242034	141 _001100
		hana marnhaganatia protein 4 (PMD4)			
		bone morphogenetic protein 4 (BMP4),	NINA 004000.		
		transcript variant 1, mRNA /cds=(478,1704)	NM_001202;		
		/gb=NM_001202 /gi=19528648	NM_130850;		ND 570040
ncrb2458	NM_001202	/ug=Hs.68879 /len=1999	NM_130851	Hs.68879	NP_570912
		BUB1 budding uninhibited by benzimidazoles			
		1 beta (yeast) (BUB1B), mRNA		į	
		/cds=(135,3287) /gb=NM_001211			
hfcr6384	NM_001211	/gi=20149508 /ug=Hs.36708 /len=3702	NM_001211	Hs.36708	NP_001202
	1	cold inducible RNA binding protein (CIRBP),			
		mRNA /cds=(81,599) /gb=NM_001280			
ncrc0696	NM_001280	/gi=4502846 /ug=Hs.119475 /len=1322	NM_001280	Hs.119475	NP_001271
		defender against cell death 1 (DAD1), mRNA			
		/cds=(67,408) /gb=NM_001344 /gi=4503252	İ		
seob5645	NM_001344	/ug=Hs.82890 /len=699	NM_001344	Hs.82890	NP_001335
		dynein, cytoplasmic, intermediate polypeptide			
	1	2 (DNCI2), mRNA /cds=(166,2082)			
		/gb=NM_001378 /gi=24307878			1
seob3464	NM_001378	/ug=Hs.66881 /len=2602	NM_001378	Hs.66881	NP_001369
		dynein, cytoplasmic, intermediate polypeptide			
		2 (DNCl2), mRNA /cds=(166,2082)			1
		/gb=NM 001378 /gi=24307878			
mioc3490	NM_001378	/ug=Hs.66881 /len=2602	NM 001378	Hs.66881	NP_001369
		dihydropyrimidinase-like 3 (DPYSL3), mRNA			
		/cds=(111,1823) /gb=NM_001387			
seoa0743	NM_001387	/gi=4503378 /ug=Hs.74566 /len=5047	NM 001387	Hs.74566	NP 001378
	1	1.3. 1		1	

riguie	ba Cont d.				
		eukaryotic translation elongation factor 1			
		alpha 1 (EEF1A1), mRNA /cds=(63,1451)			1
ŀ	:	/gb=NM_001402 /gi=25453469			
ncr3040	NM_001402	/ug=Hs.422118 /len=1837	NM_001402	Hs.422118	NP_001393
		eukaryotic translation elongation factor 1			
		alpha 1 (EEF1A1), mRNA /cds=(63,1451)			
İ		/gb=NM_001402 /gi=25453469			
fcrb0386	NM_001402	/ug=Hs.422118 /len=1837	NM_001402	Hs.422118	NP_001393
		eukaryotic translation initiation factor 4A,			
		isoform 1 (EIF4A1), mRNA /cds=(17,1237)			
		/gb=NM_001416 /gi=4503528			
fcrb1741	NM_001416	/ug=Hs.129673 /len=1383	NM_001416	Hs.129673	NP_001407
		erythrocyte membrane protein band 4.1-like 2			
		(EPB41L2), mRNA /cds=(45,3062)			
		/gb=NM_001431 /gi=4503578 /ug=Hs.7857			
mioa7361	NM_001431	/len=4336	NM_001431	Hs.7857	NP_001422
		heat shock 27kDa protein 2 (HSPB2), mRNA			
		/cds=(70,618) /gb=NM_001541 /gi=4504518			
fcrc2710	NM 001541	/ug=Hs.78846 /len=874	NM_001541	Hs.78846	NP_001532
		ATP synthase, H transporting, mitochondrial			
		F0 complex, subunit c (subunit 9) isoform 3			
		(ATP5G3), mRNA /cds=(255,683)			
		/gb=NM 001689 /gi=4502300 /ug=Hs.429			ļ
miob9529	NM_001689	/len=826	NM 001689	Hs.429	NP 001680
		ATPase, H transporting, lysosomal 70kDa,	_: -:		<u> </u>
		V1 subunit A, isoform 1 (ATP6V1A1), mRNA			
		/cds=(67,1920) /gb=NM_001690			
seob5767	NM 001690	/gi=19913423 /ug=Hs.281866 /len=4567	NM ⁻ 001690	Hs.281866	NP 001681
00000.01	00.1000	ATPase, H transporting, lysosomal 70kDa,			
		V1 subunit A, isoform 1 (ATP6V1A1), mRNA	1		
		/cds=(67,1920) /gb=NM_001690			
seoc4161	NM_001690	/gi=19913423 /ug=Hs.281866 /len=4567	NM 001690	Hs.281866	NP 001681
00001101	11111_001000	cysteine dioxygenase, type I (CDO1), mRNA			
		/cds=(255,857) /gb=NM_001801 /gi=4502754			1
sena2134	NM_001801	/ug=Hs.3229 /len=1556		Hs.3229	NP_001792
30002104	14141_001001	cytochrome c-1 (CYC1), mRNA /cds=(5,982)	1111_001001	110.0220	
		/gb=NM_001916 /gi=21359866			
fcrb1867	NM 001916	/ug=Hs.289271 /len=1273	NM 001916	Hs 289271	NP 001907
10101007	14141_001310	/ug=113.2032/17/cn=1210	14141_001010	113.200271	141 _001007
		deoxyhypusine synthase (DHPS), transcript	İ	1	
		variant 1, mRNA /cds=(98,1207)	NM 001930;		
1		/gb=NM 001930 /gi=7108341 /ug=Hs.79064	NM_013406;		
hfcr1646	NM 001930	//len=1351	NM_013407	Hs.79064	NP 037539
111011040	14141 00 1930	fibromodulin (FMOD), mRNA /cds=(21,1151)	114141_01340/	113.73004	141 _03/338
		/gb=NM 002023 /gi=5016093 /ug=Hs.230	[1
forb2210	NM 002022	//len=2863	NM 002023	He 230	NP 002014
fcrb2318	NM_002023	growth arrest-specific 1 (GAS1), mRNA	14101_002023	1115.230	1NF_002014
		1		1	
mio-0507	NIM 000040	/cds=(411,1448) /gb=NM_002048	NIM 000040	He 65020	NID 002020
mioa0597	NM_002048	/gi=4503918 /ug=Hs.65029 /len=2828	NM_002048	Hs.65029	NP_002039
		high-mobility group box 1 (HMGB1), mRNA			
f	NA 000400	/cds=(77,724) /gb=NM_002128 /gi=20149538		112 6707	ND 000440
fcrb1689	NM_002128	/ug=Hs.6727 /len=1207	NM_002128	IDS.0/2/	NP_002119

1 iguie	oa Contu.	r		r	
		avalan rasantan subfamili. A masun A			1
		nuclear receptor subfamily 4, group A,	NIM 002125		}
<u>'</u>		member 1 (NR4A1), transcript variant 1,	NM_002135;		1
fb-0404	NINA 000405	mRNA /cds=(315,2111) /gb=NM_002135	NM_173157;	Un 1110	ND 775404
fcrb6464	NM_002135	/gi=27894342 /ug=Hs.1119 /len=2699	NM_173158	Hs.1119	NP_775181
		heat shock 10kDa protein 1 (chaperonin 10)			
		(HSPE1), mRNA /cds=(42,350)			
		/gb=NM_002157 /gi=4504522 /ug=Hs.1197	000457	11- 4407	LID COOLIG
seoa87/6	NM_002157	/len=538	NM_002157	Hs.1197	NP_002148
		tenascin C (hexabrachion) (TNC), mRNA		İ	Į.
		/cds=(314,6919) /gb=NM_002160			NID COOLEA
miod3302	NM_002160	/gi=4504548 /ug=Hs.289114 /len=7560	NM_002160	Hs.289114	NP_002151
,		inhibitor of DNA binding 1, dominant negative			
		helix-loop-helix protein (ID1), mRNA			
		/cds=(36,500) /gb=NM_002165 /gi=4504568		l	l
fcrc0727	NM_002165	/ug=Hs.75424 /len=926	NM_002165	Hs.75424	NP_851998
		lysyl oxidase-like 2 (LOXL2), mRNA			
1		/cds=(248,2572) /gb=NM_002318			
ncrb5595	NM_002318	/gi=4505010 /ug=Hs.83354 /len=3432	NM_002318	Hs.83354	NP_002309
		low density lipoprotein-related protein-			
ļ		associated protein 1 (alpha-2-macroglobulin			
		receptor-associated protein 1) (LRPAP1),			
		mRNA /cds=(14,1087) /gb=NM_002337			
fcrc4408	NM_002337	/gi=4505020 /ug=Hs.75140 /len=1493	NM_002337	Hs.75140	NP_002328
		mannose-6-phosphate receptor (cation			
l		dependent) (M6PR), mRNA /cds=(171,1004)			
1		/gb=NM_002355 /gi=10947032			
mioc0760	NM_002355	/ug=Hs.134084 /len=2454	NM_002355	Hs.134084	NP_002346
		MCM3 minichromosome maintenance			
		deficient 3 (S. cerevisiae) (MCM3), mRNA			
		/cds=(45,2471) /gb=NM_002388 /gi=6631094			
hfcr4462	NM_002388	/ug=Hs.179565 /len=3061	NM_002388	Hs.179565	NP_002379
1		metaxin 1 (MTX1), mRNA /cds=(1,954)			
		/gb=NM_002455 /gi=4505280	•	ŀ	
fcrb6917	NM_002455	/ug=Hs.247551 /len=1065	NM_002455	Hs.247551	NP_002446
		NADH dehydrogenase (ubiquinone) 1 alpha			
		subcomplex, 2, 8kDa (NDUFA2), mRNA]		
		/cds=(57,356) /gb=NM_002488 /gi=4505354		1	
seob3670	NM_002488	/ug=Hs.163867 /len=590	NM_002488	Hs.163867	NP_002479
		ornithine decarboxylase antizyme 2 (OAZ2),			
		mRNA /gb=NM_002537 /gi=9845506			
ncr0851	NM_002537	/ug=Hs.74563 /len=1906	NM_002537	Hs.74563	NP_002528
		tumor necrosis factor receptor superfamily,			
]	member 11b (osteoprotegerin)		}	
		(TNFRSF11B), mRNA /cds=(252,1457)	1	1	
		/gb=NM_002546 /gi=22547122			
seoc1023	NM_002546	/ug=Hs.81791 /len=2291	NM_002546	Hs.81791	NP_002537
		prohibitin (PHB), mRNA /cds=(74,892)			
		/gb=NM_002634 /gi=6031190 /ug=Hs.75323			
miob3315	NM_002634	/len=1826	NM_002634	Hs.75323	NP_002625

Figure	ba Contu.				
		solute carrier family 25 (mitochondrial carrier;		,	
		phosphate carrier), member 3 (SLC25A3),			
		nuclear gene encoding mitochondrial protein,			
		transcript variant 1b, mRNA /cds=(49,1134)			
		/gb=NM_002635 /gi=4505774 /ug=Hs.78713	NM_002635;		
fcrb2051	NM 002635	/len=1330	NM_005888	Hs.78713	NP_005879
		protease, serine, 11 (IGF binding) (PRSS11),			
		mRNA /cds=(49,1491) /gb=NM_002775			
seoa0003	NM_002775	/gi=21327712 /ug=Hs.75111 /len=2039	NM 002775	Hs.75111	NP 002766
		proteasome (prosome, macropain) subunit,	-		
		beta type, 5 (PSMB5), mRNA /cds=(20,811)			
		/gb=NM_002797 /gi=22538468			
mioa3857	NM_002797	/ug=Hs.261927 /len=1050	NM 002797	Hs.261927	NP_002788
		proteasome (prosome, macropain) 26S			
		subunit, ATPase, 1 (PSMC1), mRNA		j	
		/cds=(49,1371) /gb=NM_002802			
miod6835	NM 002802	/gi=24430150 /ug=Hs.4745 /len=1586	NM 002802	Hs.4745	NP_002793
		3			
	1				
	•	polypyrimidine tract binding protein 1	NM 002819;		
		(PTBP1), transcript variant 1, mRNA	NM 031990;		
		/cds=(89,1762) /gb=NM_002819	NM_031991;		
seob7465	NM_002819	/gi=14165462 /ug=Hs.172550 /len=3322	NM 175847	Hs.172550	NP_787041
30001 400	1111_002010	protein tyrosine phosphatase, non-receptor		110.11.2000	
		type 12 (PTPN12), mRNA /cds=(30,2372)			
		/gb=NM_002835 /gi=18375651 /ug=Hs.62			
ncrc4633	NM_002835	/len=3161	NM 002835	Hs.62	NP 002826
110101000		pentaxin-related gene, rapidly induced by IL-1	002000		
		beta (PTX3), mRNA /cds=(68,1213)		l i	
	•	/gb=NM_002852 /gi=4506332 /ug=Hs.2050			
fcrb0354	NM_002852	//len=1837	NM 002852	Hs.2050	NP 002843
1010001	7444_002002	RAB6A, member RAS oncogene family	11111_002002	110.2000	
		(RAB6A), mRNA /cds=(427,1053)			
		/gb=NM_002869 /gi=19923230 /ug=Hs.5636			
fcrb2344	NM 002869	//en=3079	NM 002869	Hs.5636	NP_002860
10102044	1444_002000	RD RNA binding protein (RDBP), mRNA	11111_002000	110.0000	
		/cds=(109,1251) /gb=NM 002904			
fcrb2756	NM_002904	/gi=20631983 /ug=Hs.106061 /len=1464	NM 002904	Hs.106061	NP 002895
10102100	14101_002504	replication factor C (activator 1) 1, 145kDa	14141_00200+	110.100001	141 _002000
		(RFC1), mRNA /cds=(429,3875)			
		/gb=NM_002913 /gi=15011930		1	
fcrb9633	NM 002913	/ug=Hs.166563 /len=5185	NM 002913	Hs.166563	NP 002904
10103033	14141_002913	ribosomal protein L15 (RPL15), mRNA	114141_002313	113.10000	141 _002304
		/cds=(37,651) /gb=NM_002948 /gi=15431292			
mioh3800	NM 002948	//ug=Hs.74267 /len=2018	NM 002948	Hs.74267	NP 002939
1111003009	14141_002940	ribosomal protein S2 (RPS2), mRNA	14141_002340	13.14201	141 _002939
		//cds=(12,893) /gb=NM_002952 /gi=15055538			
forb2224	NM 002952	//ug=Hs.356360 /len=978	NM_002952	Hs.356360	NP_002943
fcrb2321	1141VI_00290Z	rug-113.330300 /1611-370	[141VI_UUZ90Z	1113.330300	INF_002843

rigule	ba Cont d.				
		S100 calcium binding protein A8 (calgranulin			1
		A) (S100A8), mRNA /cds=(56,337)			
		/gb=NM_002964 /gi=21614543			
seoc5858	NM_002964	/ug=Hs.416073 /len=428	NM_002964	Hs.416073	NP_002955
		splicing factor, arginine/serine-rich 2			
		(SFRS2), mRNA /cds=(156,821)			
		/gb=NM_003016 /gi=4506898 /ug=Hs.73965			
fcrb8485	NM_003016	/len=1879	NM_003016	Hs.73965	NP_003007
		splicing factor, arginine/serine-rich 2			
		(SFRS2), mRNA /cds=(156,821)			
		/gb=NM_003016 /gi=4506898 /ug=Hs.73965			1
hfcr3183	NM_003016	/len=1879	NM_003016	Hs.73965	NP_003007
		splicing factor, arginine/serine-rich 3			
		(SFRS3), mRNA /cds=(106,600)	}		1
		/gb=NM_003017 /gi=24025684			
fcr7705	NM 003017	/ug=Hs.388623 /len=1403	NM_003017	Hs.388623	NP_003008
		SHC (Src 2 domain containing) transforming			
		protein 1 (SHC1), mRNA /cds=(195,1946)] .
		/gb=NM_003029 /gi=10835030			
fcrb8668	NM_003029	/ug=Hs.81972 /len=3664	NM_003029	Hs.81972	NP_892113
		SWI/SNF related, matrix associated, actin			
Ì		dependent regulator of chromatin, subfamily			
		c, member 2 (SMARCC2), transcript variant			
		1, mRNA /cds=(33,3677) /gb=NM_003075	NM 003075;		
fcrb6436	NM 003075	/gi=21237804 /ug=Hs.236030 /len=4039	_ ·	Hs.236030	NP 620706
		sterol O-acyltransferase (acyl-Coenzyme A:			
		cholesterol acyltransferase) 1 (SOAT1),			
		transcript variant 688113, mRNA			
1	:	/cds=(64,1716) /gb=NM_003101			
seoa4289	NM_003101	/gi=24431944 /ug=Hs.14553 /len=3407	NM 003101	Hs.14553	NP_003092
		sorbitol dehydrogenase (SORD), mRNA			
		/cds=(140,1213) /gb=NM_003104		İ	
seob2958	NM_003104	/gi=21314633 /ug=Hs.878 /len=2637	NM 003104	Hs.878	NP_003095
		signal recognition particle 54kDa (SRP54),			
		mRNA /cds=(225,1739) /gb=NM_003136	1	1	
seoa7408	NM_003136	/gi=20149548 /ug=Hs.49346 /len=2164	NM 003136	Hs.49346	NP 003127
		stanniocalcin 1 (STC1), mRNA			
		/cds=(285,1028) /gb=NM_003155			
ncrb7211	NM 003155	/gi=4507264 /ug=Hs.25590 /len=3901	NM_003155	Hs.25590	NP_003146
		NIMA (never in mitosis gene a)-related	1		-
		kinase 4 (NEK4), mRNA /cds=(179,2704)	1	1	
		/gb=NM_003157 /gi=4507276 /ug=Hs.1087			
miod3600	NM 003157	/len=3698	NM_003157	Hs.1087	NP_003148
		TAF9 RNA polymerase II, TATA box binding	1		
1		protein (TBP)-associated factor, 32kDa			
		(TAF9), transcript variant 1, mRNA			
		/cds=(159,953) /gb=NM_003187	NM 003187;		
seob4127	NM_003187	/gi=21166375 /ug=Hs.60679 /len=1153	NM 016283	Hs.60679	NP 057367
		transforming growth factor, beta 3 (TGFB3),	1	1	
seoa3296	NM 003239	mRNA	NM_003239	Hs.2025	NP 003230
	<u>,</u>	<u> </u>		<u> </u>	

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		tripeptidyl peptidase II (TPP2), mRNA			
		/cds=(24,3773) /gb=NM_003291 /gi=4507656			
seob4804	NM_003291	/ug=Hs.1117 /len=4626	NM_003291	Hs.1117	NP_003282
		nuclear receptor subfamily 2, group C,			
		member 1 (NR2C1), mRNA /cds=(57,1868)			
1		/gb=NM_003297 /gi=4507672]
mioa0059	NM_003297	/ug=Hs.108301 /len=2202	NM_003297	Hs.108301	NP_003288
		tetratricopeptide repeat domain 1 (TTC1),	_		
		mRNA /cds=(51,929) /gb=NM_003314			
seob3517	NM_003314	/gi=4507710 /ug=Hs.7733 /len=1407	NM_003314	Hs.7733	NP_003305
	· <u>-</u>	tetratricopeptide repeat domain 3 (TTC3),			
		mRNA /cds=(1470,7547) /gb=NM_003316			
miob4803	NM_003316	/gi=21359840 /ug=Hs.118174 /len=9078	NM_003316	Hs.118174	NP_003307
	-	Tu translation elongation factor,			
		mitochondrial (TUFM), mRNA /cds=(72,1430)			
		/gb=NM_003321 /gi=21359836			
seob6751	NM_003321	/ug=Hs.12084 /len=1636	NM_003321	Hs.12084	NP_003312
		voltage-dependent anion channel 1 (VDAC1),			
		mRNA /cds=(100,951) /gb=NM_003374			
miob2533	NM_003374	/gi=4507878 /ug=Hs.149155 /len=1806	NM_003374	Hs.149155	NP_003365
		voltage-dependent anion channel 1 (VDAC1),			
	-	mRNA /cds=(100,951) /gb=NM_003374		•	
seob3197	NM_003374	/gi=4507878 /ug=Hs.149155 /len=1806	NM_003374	Hs.149155	NP_003365
		zinc finger protein 140 (clone pHZ-39)			
		(ZNF140), mRNA /cds=(273,1646)		İ	
	:	/gb=NM_003440 /gi=4507990		ł	j
seob1848	NM_003440	/ug=Hs.154205 /len=2407	NM_003440	Hs.154205	NP_003431
1		protein tyrosine phosphatase type IVA,			
		member 2 (PTP4A2), transcript variant 1,	NM_003479;		1
		mRNA /cds=(1011,1514) /gb=NM_003479	NM_080391;		
fcrb4360	NM_003479	/gi=18104974 /ug=Hs.82911 /len=3925	NM_080392	Hs.82911	NP_536317
		syntaxin 7 (STX7), mRNA /cds=(80,865)			
		/gb=NM_003569 /gi=4507294 /ug=Hs.8906		ŀ	
mioa0497	NM_003569	/len=1614	NM_003569	Hs.8906	NP_003560
		degenerative spermatocyte lipid desaturase			
		(Drosophila) (DEGS), transcript variant 1,	Ì		
		mRNA /cds=(112,1083) /gb=NM_003676	NM_003676;		
seoa0792	NM_003676	/gi=21614503 /ug=Hs.185973 /len=2058	NM_144780	Hs.185973	NP_659004
		eukaryotic translation initiation factor 4E			<u> </u>
		binding protein 3 (EIF4EBP3), mRNA		1]
		/cds=(73,375) /gb=NM_003732 /gi=4503536		1	
fcrb8393	NM_003732	/ug=Hs.375012 /len=698	NM_003732	Hs.375012	NP_003723
		splicing factor, arginine/serine-rich 9			1
		(SFRS9), mRNA /cds=(53,718)			
		/gb=NM_003769 /gi=4506902 /ug=Hs.77608			
hfcr2850	NM_003769	/len=1069	NM_003769	Hs.77608	NP_003760

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		chromosome 19 open reading frame 2			
		(C19orf2), transcript variant 1, mRNA			
		/cds=(31,1638) /gb=NM_003796	NM_003796;		1
ncr7967	NM_003796	/gi=19924158 /ug=Hs.7943 /len=2295	NM_134447	Hs.7943	NP_604431
		WNT1 inducible signaling pathway protein 3			
ļ		(WISP3), transcript variant 1, mRNA			
		/cds=(111,1175) /gb=NM_003880	NM_003880;		
ncr1494	NM_003880	/gi=18491002 /ug=Hs.194678 /len=1307	NM_130396	Hs.194678	NP_569080
		development and differentiation enhancing			
		factor 2 (DDEF2), mRNA /cds=(341,3361)			
		/gb=NM_003887 /gi=4502248 /ug=Hs.12802			
mioc6878	NM_003887	/len=5711	NM_003887	Hs.12802	NP_003878
		B-cell CLL/lymphoma 10 (BCL10), mRNA			
		/cds=(706,1407) /gb=NM_003921			
fcrc2613	NM_003921	/gi=20336470 /ug=Hs.193516 /len=2809	NM_003921	Hs.193516	NP_003912
		CAAX box 1 (CXX1), mRNA /cds=(335,964)			
		/gb=NM_003928 /gi=4503180			
seob2987	NM_003928	/ug=Hs.250708 /len=1209	NM_003928	Hs.250708	NP_003919
		myelin protein zero-like 1 (MPZL1), mRNA			
		/cds=(160,969) /gb=NM_003953			
seoc6666	NM_003953	/gi=20070164 /ug=Hs.287832 /len=1805	NM_003953	Hs.287832	NP_003944
		ribosomal protein L14 (RPL14), mRNA			
		/cds=(38,688) /gb=NM_003973 /gi=16753224			
mioa2213	NM_003973	/ug=Hs.235422 /len=843	NM_003973	Hs.235422	NP_003964
		;		,	ļ
		solute carrier family 7 (cationic amino acid			
		transporter, y system), member 6 (SLC7A6),			
		mRNA /cds=(262,1809) /gb=NM_003983			
mioa1353	NM_003983	/gi=4507052 /ug=Hs.10315 /len=6296	NM_003983	Hs.10315	NP_003974
		adenylate cyclase 3 (ADCY3), mRNA			
		/cds=(148,3582) /gb=NM_004036			
seoa9377	NM_004036	/gi=10947058 /ug=Hs.8402 /len=4342	NM_004036	Hs.8402	NP_004027
		cryptochrome 1 (photolyase-like) (CRY1),			
		mRNA /cds=(587,2347) /gb=NM_004075			1
ncrc3415	NM_004075	/gi=19923246 /ug=Hs.151573 /len=2999	NM_004075	Hs.151573	NP_004066
		DNA-damage-inducible transcript 3 (DDIT3),			
l		mRNA /cds=(191,700) /gb=NM_004083			ND 004074
miod7011	NM_004083	/gi=21361117 /ug=Hs.400353 /len=965	NM_004083	Hs.400353	NP_004074_
		guanylate binding protein 2, interferon-			
		inducible (GBP2), mRNA /cds=(157,1932)			
		/gb=NM_004120 /gi=6996011	NINA 004400	11- 474000	ND 004444
mioc7152	NM_004120	/ug=Hs.171862 /len=2107	NM_004120	Hs.171862	NP_004111
	[small nuclear ribonucleoprotein D3			
		polypeptide 18kDa (SNRPD3), mRNA			}
	 	/cds=(88,468) /gb=NM_004175 /gi=4759159	NINA 004475	115 4575	ND 004400
hfcr2984	NM_004175	/ug=Hs.1575 /len=626	NM_004175	Hs.1575	NP_004166
		procollagen-proline, 2-oxoglutarate 4-			
		dioxygenase (proline 4-hydroxylase), alpha			
	1	polypeptide II (P4HA2), mRNA			
	NINA 004466	/cds=(188,1795) /gb=NM_004199	NINA 004460	11- 2000	ND 004400
Incrc4189	NM_004199	/gi=4758867 /ug=Hs.3622 /len=2194	NM_004199	THS:3022	NP_004190

rigure	ba Cont d.				
		high mobility group nucleosomal binding			
		domain 3 (HMGN3), transcript variant 1,			
		mRNA /cds=(179,478) /gb=NM_004242	NM_004242;		
seoc7762	NM_004242	/gi=23238229 /ug=Hs.77558 /len=935	NM_138730	Hs.77558	NP_620058
		homer 1 (Drosophila) (HOMER1), mRNA			
		/cds=(278,1342) /gb=NM_004272			
hfcr2892	NM_004272	/gi=20127465 /ug=Hs.337737 /len=1445	NM_004272	Hs.337737	NP_004263
		ring finger protein 14 (RNF14), mRNA			
		/cds=(237,1661) /gb=NM_004290			
mioa1410	NM_004290	/gi=19923285 /ug=Hs.215857 /len=3056	NM_004290	Hs.215857	NP_004281
		neural precursor cell expressed,			
		developmentally down-regulated 5 (NEDD5),			
		mRNA /cds=(259,1344) /gb=NM_004404			
fcr2089	NM_004404	/gi=4758157 /ug=Hs.155595 /len=3433	NM_004404	Hs.155595	NP_004395
		neural precursor cell expressed,			
		developmentally down-regulated 5 (NEDD5),			
•		mRNA /cds=(259,1344) /gb=NM_004404			:
miob9393	NM_004404	/gi=4758157 /ug=Hs.155595 /len=3433	NM_004404	Hs.155595	NP_004395
•		dipeptidase 1 (renal) (DPEP1), mRNA			
		/cds=(296,1531) /gb=NM_004413			
fcrb8020	NM_004413	/gi=4758189 /ug=Hs.109 /len=1738	NM_004413	Hs.109	NP_004404
		golgi autoantigen, golgin subfamily b,			
		macrogolgin (with transmembrane signal), 1			
		(GOLGB1), mRNA /cds=(127,9906)			
•		/gb=NM_004487 /gi=4758453 /ug=Hs.7844			
seoa0023	NM_004487	/len=10300	NM_004487	Hs.7844	NP_004478
				•	
	1	nuclear factor of activated T-cells,			
		cytoplasmic, calcineurin-dependent 3	NM_004555;		
		(NFATC3), transcript variant 2, mRNA	NM_173163;	·	
		/cds=(211,3417) /gb=NM_004555	NM_173164;		
fcrb6220	NM_004555	/gi=27886542 /ug=Hs.172674 /len=4005	NM_173165	Hs.172674	NP_775188
	!	phosphoenolpyruvate carboxykinase 2			1
		(mitochondrial) (PCK2), mRNA			
		/cds=(67,1989) /gb=NM_004563 /gi=4758885		l	
ncrc4231	NM_004563	/ug=Hs.75812 /len=2165	NM_004563	Hs.75812	NP_004554
		phosphoserine phosphatase (PSPH), mRNA			
		/cds=(20,697) /gb=NM_004577 /gi=21614545			
mioc2872	NM_004577	/ug=Hs.56407 /len=1432	NM_004577	Hs.56407	NP_004568
		tubulin-specific chaperone a (TBCA), mRNA			1
		/cds=(50,376) /gb=NM_004607 /gi=4759211			
fcr1791	NM_004607	/ug=Hs.433254 /len=574	NM_004607	Hs.433254	NP_004598
		ubiquitin specific protease 9, X chromosome		1	
		(fat facets-like Drosophila) (USP9X),			
		transcript variant 1, mRNA /cds=(60,7751)		1	1
		/gb=NM_004652 /gi=11641424	NM_004652;		l
ncr5065	NM_004652	/ug=Hs.77578 /len=8171	NM_021906	[Hs.77578	NP_068706

rigure	ba Conta.	r			
1		clathrin, heavy polypeptide (Hc) (CLTC),			
1		mRNA /cds=(173,5200) /gb=NM_004859			
seob6028	NM_004859	/gi=4758011 /ug=Hs.178710 /len=6111	NM_004859	Hs.178710	NP_004850_
		prostaglandin E synthase (PTGES), mRNA			
		/cds=(36,494) /gb=NM_004878 /gi=19923282			
mioc7561	NM_004878	/ug=Hs.146688 /len=1846	NM_004878	Hs.146688	NP_004869
		mitochondrial ribosomal protein L33			
		(MRPL33), nuclear gene encoding			
		mitochondrial protein, transcript variant 1,			
		mRNA /cds=(60,257) /gb=NM_004891	NM_004891;		
seoa7897	NM_004891	/gi=21735607 /ug=Hs.14454 /len=541	NM_145330	Hs.14454	NP 663303
		protein disulfide isomerase related protein			
		(calcium-binding protein, intestinal-related)			
		(ERP70), mRNA /cds=(243,2180)			
		/gb=NM_004911 /gi=21624646			1
hfcr2544	NM 004911	/ug=Hs.93659 /len=2930	NM 004911	Hs.93659	NP 004902
		zinc finger protein 36, C3H type-like 1	<u> </u>		
		(ZFP36L1), mRNA /cds=(131,1147)			
		/gb=NM_004926 /gi=15812179			
ncrc8851	NM 004926	/ug=Hs.85155 /len=3022	NM 004926	Hs.85155	NP 004917
		deoxyribonuclease I-like 3 (DNASE1L3),			
		mRNA /cds=(71,988) /gb=NM_004944			1
ncrc2730	NM 004944	/gi=4826697 /ug=Hs.88646 /len=1079	NM 004944	Hs.88646	NP 004935
	<u> </u>	LIM and senescent cell antigen-like domains			1
seoa4174	NM_004987	1 (LIMS1), mRNA	NM_004987	Hs.112378	NP 004978
	-	myosin VI (MYO6), mRNA /cds=(140,3997)			
		/gb=NM 004999 /gi=4826845			
miod7270	NM 004999	/ug=Hs.118483 /len=5212	NM 004999	Hs.118483	NP 004990
		nucleobindin 2 (NUCB2), mRNA			
		/cds=(220,1482) /gb=NM_005013			
ncrc5608	NM 005013	/gi=4826869 /ug=Hs.3164 /len=1586	NM 005013	Hs.3164	NP 005004
		poly(rC) binding protein 2 (PCBP2), transcript	=		_
		variant 1, mRNA /cds=(89,1189)			
1		/gb=NM_005016 /gi=14141167	NM_005016;		
fcrc1654	NM_005016	/ug=Hs.63525 /len=1362	NM 031989	Hs.63525	NP_114366
		polymerase (RNA) II (DNA directed)			†
		polypeptide K, 7.0kDa (POLR2K), mRNA		}	
		/cds=(67,243) /gb=NM_005034 /gi=14589955			
seob0031	NM 005034	/ug=Hs.351475 /len=540	NM 005034	Hs.351475	NP_005025
		fragile X mental retardation, autosomal 1			
		(FXR1), mRNA /cds=(13,1878)		1	
		/gb=NM_005087 /gi=4826735 /ug=Hs.82712			
seoa2209	NM 005087	/len=2132	NM 005087	Hs.82712	NP 005078
		squamous cell carcinoma antigen recognised	<u> </u>		1 -
	ļ	by T cells (SART1), mRNA /cds=(43,2445)			
	ļ	/gb=NM_005146 /gi=21327688			
seob5147	NM_005146	/ug=Hs.288319 /len=2536	NM 005146	Hs.288319	NP 005137
		cyclin C (CCNC), mRNA /cds=(29,940)		1	1 -
		/gb=NM 005190 /gi=7382485			
seoa1056	NM 005190	/ug=Hs.118442 /len=1508	NM_005190	Hs.118442	NP_005181
	1000 100		1	1	

riguie	<u>oa co</u>	iitu.						
			defensin, beta 1 (DEFB1), mRNA					
			/cds=(72,278) /gb=NM_005218 /gi=13124884					
miod1200	NM_C	005218	/ug=Hs.32949 /len=366	NM_0	05218	Hs.32949	NP_	005209
			defensin, beta 1 (DEFB1), mRNA					
			/cds=(72,278) /gb=NM_005218 /gi=13124884					
seoa5743	NM_C	005218	/ug=Hs.32949 /len=366	NM_0	05218	Hs.32949	NP_	005209
			growth differentiation factor 8 (GDF8), mRNA					
			/cds=(134,1261) /gb=NM_005259					
fcrc2306	NM_C	005259	/gi=4885258 /ug=Hs.41565 /len=2823	NM_0	05259	Hs.41565	NP_	005250
			growth factor receptor-bound protein 10					
			(GRB10), mRNA /cds=(782,2548)					
			/gb=NM_005311 /gi=19923302				ŀ	
mioc1205	NM C	005311	/ug=Hs.81875 /len=5431	NM (005311	Hs.81875	NP	005302
				_			_	
	·		heat shock 90kDa protein 1, alpha (HSPCA),]				
			mRNA /cds=(61,2259) /gb=NM_005348				1	
fcrb6650	NM C	005348	/gi=13129149 /ug=Hs.356531 /len=2259	lnm o	005348	Hs.356531	NP	005339
			podocalyxin-like (PODXL), mRNA	_				•
	1		/cds=(251,1837) /gb=NM_005397					
hfcr6509	NM C	005397	/gi=4885556 /ug=Hs.16426 /len=5869	lnm (005397	Hs.16426	NP	005388
11101000	· · · · · · ·		insulin-like 5 (INSL5), mRNA /cds=(48,455)					
	ŀ		/gb=NM_005478 /gi=5729885					
mioc6261	l _{NM} (105478	/ug=Hs.251380 /len=726	NM (005478	Hs.251380	NP	005469
1111000201		300-170	legumain (LGMN), mRNA /cds=(142,1443)	·····-	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	110.201000	 ` -	
			/gb=NM_005606 /gi=21914880				:	
fcrc6551	NM C	005606	/ug=Hs.18069 /len=1981	NM (005606	Hs.18069	NP	005597
10100001	TAIVI_C	303000_	phenylalanyl-tRNA synthetase beta-subunit	14141_	303000	113.10003	-	_000007
			(FRSB), mRNA /cds=(14,1783)					
			/gb=NM_005687 /gi=19923332 /ug=Hs.9081					
ncrc0292	NM C	005687	/len=3118	l _{NM} (005687	Hs.9081	NP	005678
110100232	14141_0	303007	ATP-binding cassette, sub-family B	14141	300007	113.3001	-	
			(MDR/TAP), member 6 (ABCB6), nuclear					
			gene encoding mitochondrial protein, mRNA	ĺ				
			/cds=(278,2806) /gb=NM_005689					
fcrc4738	NINA C	005689	/gi=9955962 /ug=Hs.107911 /len=2993	NM (005689	Hs.107911	ND	005680
10104730	INIVI_C	000009		NIVI_	303003	113.107311	-	_000000
			interloukin 18 hinding protein (II 1980)	NINA A	005699;			
			interleukin 18 binding protein (IL18BP), transcript variant C, mRNA /cds=(929,1522)	. –	173042;			
	1		, , , , , , , , , , , , , , , , , , , ,	. –	-			
2424	NINA /	005600	/gb=NM_005699 /gi=27502394		173043;	Un 225070	ND	766622
ncr3434	INNI_(005699	/ug=Hs.325978 /len=3630	LIAIM_	173044	Hs.325978	INP_	_766632
1			accessory protein BAP31 (DXS1357E),					
	NISA 4	005745	mRNA /cds=(137,877) /gb=NM_005745	NIA .	005745	He 204004	N.D.	005700
mioc6902	INM_(JU5/45	/gi=10047078 /ug=Hs.291904 /len=1314	ININ'	005745	Hs.291904	INP_	_005736
			lipoma HMGIC fusion partner (LHFP), mRNA				1	
		00555	/cds=(357,959) /gb=NM_005780 /gi=5031864		005700	11- 00705		005774
seoa2652	INM_(005780	/ug=Hs.93765 /len=2012	MM_	005780	Hs.93765	ארן	_005771
			ATP binding protein associated with cell					
			differentiation (APACD), mRNA					
			/cds=(130,810) /gb=NM_005783				l	
seoa2734	INM_(005783	/gi=18104958 /ug=Hs.153884 /len=1494	INM_	005783	Hs.153884	<u>INP</u>	005774

90.0	oa oonta.	1			
		signal transducing adaptor molecule (SH3			
1		domain and ITAM motif) 2 (STAM2), mRNA			
		/cds=(351,1928) /gb=NM_005843			
seoa1460	NM_005843	/gi=21265030 /ug=Hs.17200 /len=3928	NM_005843	Hs.17200	NP_005834
		follistatin-like 3 (secreted glycoprotein)			
		(FSTL3), mRNA /cds=(8,799)			
		/gb=NM_005860 /gi=5031700			
fcrc0730	NM_005860	/ug=Hs.433827 /len=2500	NM_005860	Hs.433827	NP_005851
		MAD, mothers against decapentaplegic 5			,
		(Drosophila) (MADH5), mRNA			
		/cds=(193,1590) /gb=NM_005903			
mioc4145	NM_005903	/gi=20070216 /ug=Hs.37501 /len=2049	NM_005903	Hs.37501	NP_005894
		MAD, mothers against decapentaplegic 7			
		(Drosophila) (MADH7), mRNA			
		/cds=(296,1576) /gb=NM_005904			
seoc2589	NM_005904	/gi=5174516 /ug=Hs.100602 /len=3111	NM_005904	Hs.100602	NP_005895
		papillary renal cell carcinoma (translocation-			
		associated) (PRCC), mRNA /cds=(219,1694)		:	
	İ	/gb=NM_005973 /gi=20070217 /ug=Hs.9629		:	
seoa5721	NM_005973	/len=2075	NM_005973	Hs.9629	NP_005964
		ribosomal protein L10 (RPL10), mRNA			ŀ
		/cds=(42,686) /gb=NM_006013 /gi=15718685			
ncrb8056	NM_006013	/ug=Hs.412900 /len=2188	NM_006013	Hs.412900	NP_006004
		SWI/SNF related, matrix associated, actin			
		dependent regulator of chromatin, subfamily			<u> </u>
į.		f, member 1 (SMARCF1), transcript variant 1,	NM_006015;		
		mRNA /cds=(371,7228) /gb=NM_006015	NM_018450;		
seoc2030	NM_006015	/gi=21264564 /ug=Hs.123090 /len=8595	NM_139135	Hs.123090	NP_624361
		deleted in liver cancer 1 (DLC1), mRNA			
		/cds=(296,3571) /gb=NM_006094			ł
ncr3843	NM_006094	/gi=6633799 /ug=Hs.8700 /len=3821	NM_006094	Hs.8700	NP_872584
		guanine nucleotide binding protein (G			
		protein), beta polypeptide 2-like 1 (GNB2L1),			
		mRNA /cds=(96,1049) /gb=NM_006098		:	
seob0885	NM_006098	/gi=24475893 /ug=Hs.5662 /len=1093	NM_006098	Hs.5662	NP_006089
		Purkinje cell protein 4 (PCP4), mRNA			
		/cds=(59,247) /gb=NM_006198 /gi=5453857			
fcr3599	NM_006198	/ug=Hs.80296 /len=540	NM_006198	Hs.80296	NP_006189 _
	1	platelet-derived growth factor receptor-like			
		(PDGFRL), mRNA /cds=(62,1189)			
		/gb=NM_006207 /gi=5453871		1	
seob3163	NM_006207	/ug=Hs.170040 /len=1502	NM_006207	Hs.170040	NP_006198
		RAD21 (S. pombe) (RAD21), mRNA			
	İ	/cds=(185,2080) /gb=NM_006265			
fcr1068	NM_006265	/gi=5453993 /ug=Hs.81848 /len=3647	NM_006265	Hs.81848	NP_006256
		ATP synthase, H transporting, mitochondrial			
]	F0 complex, subunit d (ATP5H), mRNA			
		/cds=(46,531) /gb=NM_006356 /gi=5453558			
seob3378	NM_006356	/ug=Hs.49018 /len=628	NM_006356	Hs.49018	NP_006347

yeast) (UBE2E3), mRNA /cds=(120,743) /gb=NM_006357 /gi=5454145 /ug=Hs.4890 NP_872619 thioredoxin interacting protein (TXNIP), mRNA /cds=(222,1397) /gb=NM_006472 /gi=5454161 /ug=Hs.179526 /len=2704 thioredoxin interacting protein (TXNIP), mRNA /cds=(222,1397) /gb=NM_006472 /gi=5454161 /ug=Hs.179526 /len=2704 thioredoxin interacting protein (TXNIP), mRNA /cds=(222,1397) /gb=NM_006472 /gi=5454161 /ug=Hs.179526 /len=2704 thioredoxin interacting protein (TXNIP), mRNA /cds=(222,1397) /gb=NM_006472 /gi=5454161 /ug=Hs.179526 /len=2704 thioredoxin interacting protein (TXNIP), mRNA /cds=(221,397) /gb=NM_006472 /gi=5454161 /ug=Hs.179526 /len=2704 osteoblast specific factor 2 (fasciclin I-like) (OSF-2), mRNA /cds=(12,2522) /gb=NM_006475 /gi=5453833 seob8204 NM_006475 /ug=Hs.136348 /len=3213	Figure	6a Contid.				
gb=MM_006357 gi=5454145 /ug=Hs.4890 NM_006357 Hs.4890 NP_872619			ubiquitin-conjugating enzyme E2E 3 (UBC4/5			
NM_ 006357 Inen=1294					ŀ	
thioredoxin interacting protein (TXNIP) mRNA /cds=(222,1397) /gb=NM_006472 gi=5454161 /ug=Hs.179526 /len=2704 NM_006472 mRNA /cds=(222,1397) /gb=NM_006472 mRNA /cds=(222,1397) /gb=NM_006472 mRNA /cds=(222,1397) /gb=NM_006472 mRNA /cds=(222,1397) /gb=NM_006472 mRNA /cds=(222,1397) /gb=NM_006472 mRNA /cds=(222,1397) /gb=NM_006472 mRNA /cds=(222,1397) /gb=NM_006472 mRNA /cds=(222,1397) /gb=NM_006472 mRNA /cds=(222,1397) /gb=NM_006472 mRNA /cds=(222,1397) /gb=NM_006472 mRNA /cds=(222,1397) /gb=NM_006472 mRNA /cds=(222,1397) /gb=NM_006472 mRNA /cds=(222,1397) /gb=NM_006472 mRNA /cds=(12,2522) /gb=NM_006475 /gi=4543833 mRNA /cds=(12,2522) /gb=NM_006475 /gb=Ms333 mRNA /cds=(272,467) /gb=NM_006533 /gi=5729924 mRNA /cds=(272,467) /gb=NM_006533 /gi=5729924 mM_006533 /ug=Hs.279651 /len=538 mRNA /cds=(272,467) /gb=NM_006533 /gi=5729924 mM_006571 /gi=4826895 /ug=Hs.3913 /me=1044 mM_006571 /gi=4826895 /ug=Hs.3913 /me=1044 mM_006571 /gi=1826895 /gi=6005726 /ug=Hs.15071 mM_006571 /gi=1826895 /gi=6005726 /ug=Hs.15071 mM_006585 /gi=6005726 /ug=Hs.15071 mM_006585 /gi=5728939 /gb=NM_006603 /gi=27552576 /ug=Hs.2817 /gi=NA /cds=(405,3893) /gb=NM_006603 /gi=27552576 /ug=Hs.2817 /gi=NA /cds=(405,3893) /gb=NM_006603 /gi=27552576 /ug=Hs.2817 /gi=NA /cds=(405,3893) /gb=NM_006603 /gi=27552576 /ug=Hs.2817 /gi=NA /cds=(405,3893) /gb=NM_006603 /gi=27552576 /ug=Hs.2817 /gi=NA /cds=(42,772) /gb=NM_00659 /gi=NM_00659 /gi=S728939 /gi=Hs.13386 /gi=392337 /gi=Hs.3386 /gi=392337 /gi=Hs.3386 /gi=392337 /gi=Hs.3386 /gi=392337 /gi=Hs.35087 /gi=NA /cds=(42,872) /gb=NM_006748 /gi=3923373 /gi=Hs.75083 /gi=3755276 /gi=NM_006734 /gi=1923373 /gi=Hs.75083 /gi=S03170 /ug=Hs.75367 /gi=NM_006748 /gi=1923373 /ug=Hs.75083 /gi=S03170 /ug=Hs.75367 /gi=NM_006748 /gi=1923373 /ug=Hs.75083 /gi=S03170 /ug=Hs.75367 /gi=NM_006748 /gi=1923373 /ug=Hs.75083 /gi=S03170 /ug=Hs.75367 /gi=NM_006748 /gi=1923373 /ug=Hs.75083 /gi=S03170 /ug=Hs.75367 /gi=NM_006748 /gi=S03373 /ug=Hs.75083 /gi=S032973 /gi=NM_006748 /gi=S03373 /			/gb=NM_006357 /gi=5454145 /ug=Hs.4890			
mRNA /cds=(222, 1397) /gb=NM_006472	seoa0099	NM_006357	/len=1294	NM_006357	Hs.4890	NP_872619
Second NM 006472 dji=5454161 / lug=Hs.179526 / len=2704 hitoredoxin interacting protein (TXNIP), mRNA /cds=(222,1397) / lgh=NM_006472 dji=5454161 / lug=Hs.179526 / len=2704 hitoredoxin interacting protein (TXNIP), mRNA /cds=(222,1397) / lgh=NM_006472 dji=5454161 / lug=Hs.179526 / len=2704 hitoredoxin interacting protein (TXNIP), mRNA /cds=(222,1397) / lgh=NM_006472 mRNA /cds=(222,1397) / lgh=NM_006472 mRNA /cds=(222,1397) / lgh=NM_006472 mRNA /cds=(222,1397) / lgh=NM_006472 mRNA /cds=(222,1397) / lgh=NM_006472 mRNA /cds=(12,2522) / lgh=NM_006475 lgh=S43833 mRNA /cds=(12,2522) / lgh=NM_006475 lgh=S43833 mRNA /cds=(12,2522) / lgh=NM_006475 lgh=S43833 lgh=S2994 lgh=S			thioredoxin interacting protein (TXNIP),			
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osteoblast specific factor 2 (fasciclin I-like) (OSF-2), mRNA /cds=(12,2522) (gb=NM006475 /gi=5458833	miod/686	NM 006472	· · · · —	NM 006472	Hs 179526	NP 006463
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Crcb2306	Se008204	14141_000473		14101_000475	HS. 130340	NF_000400
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likely ortholog of mouse dynactin 6 (DCTN6), mRNA /cds=(88,660) /gb=NM_006571 /gi=18426895 /ug=Hs.39913 /len=1044 NM_006571 /gi=18426895 /ug=Hs.39913 /len=1044 NM_006571 Hs.39913 NP_006562 Chaperonin containing TCP1, subunit 8 (theta) (CCT8), mRNA /cds=(29,1675) /gb=NM_006585 /gi=6005726 /ug=Hs.15071 NM_006585 Hs.15071 NP_006576 /len=1821 NM_006585 /gi=6005726 /ug=Hs.15071 NM_006585 Hs.15071 NP_006576 /len=2817 NM_006603 /gi=27552767 /ug=Hs.8217 /len=4197 NM_006603 Hs.8217 NP_006594 tubulin, gamma complex associated protein 2 (TUBGCP2), mRNA /cds=(64,2772) /gb=NM_006659 /gi=5729839 /ug=Hs.13386 NM_006699 Hs.13386 NP_006650 /len=2846 NM_006659 /len=2846 NM_006659 /len=2846 NM_006659 /len=2846 NM_006659 /len=2846 NM_006701 /gi=20070233 /ug=Hs.433683 /len=1415 NM_006701 Hs.433683 NP_006692 immunodeficiency virus type I enhancer binding protein 2 (HIVEP2), mRNA /cds=(14,7518) /gb=NM_006734 /len=2817 NP_006734 /gi=19923373 /ug=Hs.75063 /len=9175 NM_006734 Hs.75063 NP_006725 Nr-like-adaptor (SLA), mRNA /cds=(42,872) /gb=NM_006748 /gi=5803170 /ug=Hs.75367 NM_006748 Hs.75367 NP_006739 NP_006739 NM_006793 /lg=Hs.75364 /len=1542 NM_006793 Hs.75454 NP_054817 Proline rich 2 (PROX2), nuclear gene encoding mitochondrial protein, mRNA /cds=(7,777) /gb=NM_006793 /gi=5802973 /ug=Hs.75454 /len=1542 NM_006793 /ug=Hs.75454 NP_054817 Proline rich 2 (PROX2), mRNA /cds=(114,1097) /gb=NM_006813			_	NIN 000500	LI- 070054	ND 000504
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stromal antigen 2 (STAG2), mRNA /cds=(405,3893) /gb=NM_006603 /gi=27552767 /ug=Hs.8217 /len=4197 NM_006603 Hs.8217 NP_006594			/gb=NM_006585 /gi=6005726 /ug=Hs.15071			
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fcrb3001 NM_006603 /gi=27552767 /ug=Hs.8217 /len=4197 NM_006603 Hs.8217 NP_006594 tubulin, gamma complex associated protein 2 (TUBGCP2), mRNA /cds=(64,2772) /gb=NM_006659 /gi=5729839 /ug=Hs.13386 NM_006659 Hs.13386 NP_006650 similar to S. pombe dim1 (DIM1), mRNA /cds=(141,569) /gb=NM_006701 /gi=20070233 /ug=Hs.433683 /len=1415 NM_006701 Hs.433683 NP_006692 immunodeficiency virus type I enhancer binding protein 2 (HIVEP2), mRNA /cds=(16,7518) /gb=NM_006734 /gi=19923373 /ug=Hs.75063 /len=9175 NM_006734 Hs.75063 NP_006725 Src-like-adaptor (SLA), mRNA /cds=(42,872) /gb=NM_006748 /gi=5803170 /ug=Hs.75367 NM_006748 Hs.75367 NP_006739 peroxiredoxin 3 (PRDX3), nuclear gene encoding mitochondrial protein, mRNA /cds=(7,777) /gb=NM_006793 /gi=5802973 NM_006793 Hs.75454 NP_054817 proline rich 2 (PROL2), mRNA /cds=(114,1097) /gb=NM_006813			stromal antigen 2 (STAG2), mRNA			
tubulin, gamma complex associated protein 2 (TUBGCP2), mRNA /cds=(64,2772) /gb=NM_006659 /gi=5729839 /ug=Hs.13386 NM_006659 /len=2846 NM_006659 /len=2846 NM_006659 /gi=20070233 /ug=Hs.433683 /len=1415 NM_006701 Hs.433683 NP_006692 immunodeficiency virus type I enhancer binding protein 2 (HIVEP2), mRNA /cds=(16,7518) /gb=NM_006734 /gi=19923373 /ug=Hs.75063 /len=9175 NM_006734 Hs.75063 NP_006725 Src-like-adaptor (SLA), mRNA /cds=(42,872) /gb=NM_006748 /gi=5803170 /ug=Hs.75367 NM_006748 Hs.75367 NP_006739 peroxiredoxin 3 (PRDX3), nuclear gene encoding mitochondrial protein, mRNA /cds=(7,777) /gb=NM_006793 /gi=5802973 ncrc2839 NM_006793 /ug=Hs.75454 /len=1542 NM_006793 Hs.75454 NP_054817 proline rich 2 (PROL2), mRNA /cds=(114,1097) /gb=NM_006813			/cds=(405,3893) /gb=NM_006603			
(TUBGCP2), mRNA /cds=(64,2772) /gb=NM_006659 /gi=5729839 /ug=Hs.13386 NM_006659 /len=2846 similar to S. pombe dim1 (DIM1), mRNA /cds=(141,569) /gb=NM_006701 mioa1603 NM_006701 /gi=20070233 /ug=Hs.433683 /len=1415 mmunodeficiency virus type I enhancer binding protein 2 (HIVEP2), mRNA /cds=(16,7518) /gb=NM_006734 /gi=19923373 /ug=Hs.75063 /len=9175 NM_006734 /gi=19923373 /ug=Hs.75063 /len=9175 NM_006734 /len=2665 miob3456 NM_006748 /len=2665 peroxiredoxin 3 (PRDX3), nuclear gene encoding mitochondrial protein, mRNA /cds=(7,777) /gb=NM_006793 /gi=5802973 ncrc2839 NM_006793 /ug=Hs.75454 /len=1542 proline rich 2 (PROL2), mRNA /cds=(114,1097) /gb=NM_006813	fcrb3001	NM_006603	/gi=27552767 /ug=Hs.8217 /len=4197	NM_006603	Hs.8217	NP_006594
(TUBGCP2), mRNA /cds=(64,2772) /gb=NM_006659 /gi=5729839 /ug=Hs.13386 NM_006659 /len=2846 similar to S. pombe dim1 (DIM1), mRNA /cds=(141,569) /gb=NM_006701 mioa1603 NM_006701 /gi=20070233 /ug=Hs.433683 /len=1415 mmunodeficiency virus type I enhancer binding protein 2 (HIVEP2), mRNA /cds=(16,7518) /gb=NM_006734 /gi=19923373 /ug=Hs.75063 /len=9175 NM_006734 /gi=19923373 /ug=Hs.75063 /len=9175 NM_006734 /len=2665 miob3456 NM_006748 /len=2665 peroxiredoxin 3 (PRDX3), nuclear gene encoding mitochondrial protein, mRNA /cds=(7,777) /gb=NM_006793 /gi=5802973 ncrc2839 NM_006793 /ug=Hs.75454 /len=1542 proline rich 2 (PROL2), mRNA /cds=(114,1097) /gb=NM_006813			1 • • • • • • • • • • • • • • • • • • •	_		
Application						
fcr2182 NM_006659 //len=2846 NM_006659 Hs.13386 NP_006650 similar to S. pombe dim1 (DIM1), mRNA //cds=(141,569) //gb=NM_006701 NM_006701 //gi=20070233 //ug=Hs.433683 //len=1415 NM_006701 Hs.433683 NP_006692 immunodeficiency virus type I enhancer binding protein 2 (HIVEP2), mRNA //cds=(16,7518) //gb=NM_006734 NM_006734 Hs.75063 NP_006725 Src-like-adaptor (SLA), mRNA //cds=(42,872) //gb=NM_006748 //gi=5803170 //ug=Hs.75367 NM_006748 Hs.75367 NP_006739 Peroxiredoxin 3 (PRDX3), nuclear gene encoding mitochondrial protein, mRNA //cds=(7,777) //gb=NM_006793 //gi=5802973 NM_006793 Hs.75454 NP_054817 Proline rich 2 (PROL2), mRNA //cds=(114,1097) //gb=NM_006813						
similar to S. pombe dim1 (DIM1), mRNA /cds=(141,569) /gb=NM_006701 mioa1603 NM_006701 /gi=20070233 /ug=Hs.433683 /len=1415 NM_006701 Hs.433683 NP_006692 immunodeficiency virus type I enhancer binding protein 2 (HIVEP2), mRNA /cds=(16,7518) /gb=NM_006734 /gi=19923373 /ug=Hs.75063 /len=9175 NM_006734 Hs.75063 NP_006725 Src-like-adaptor (SLA), mRNA /cds=(42,872) /gb=NM_006748 /gi=5803170 /ug=Hs.75367 miob3456 NM_006748 /len=2665 NM_006748 Hs.75367 NP_006739 peroxiredoxin 3 (PRDX3), nuclear gene encoding mitochondrial protein, mRNA /cds=(7,777) /gb=NM_006793 /gi=5802973 ncrc2839 NM_006793 /ug=Hs.75454 /len=1542 NM_006793 Hs.75454 NP_054817 proline rich 2 (PROL2), mRNA /cds=(114,1097) /gb=NM_006813	fcr2182	NM 006659	1	NM 006659	Hs.13386	INP 006650 I
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mioa1603 NM_006701 /gi=20070233 /ug=Hs.433683 /len=1415 NM_006701 Hs.433683 NP_006692 immunodeficiency virus type I enhancer binding protein 2 (HIVEP2), mRNA /cds=(16,7518) /gb=NM_006734 NM_006734 Hs.75063 NP_006725 Src-like-adaptor (SLA), mRNA /cds=(42,872) /gb=NM_006748 /gi=5803170 /ug=Hs.75367 NM_006748 Hs.75367 NP_006739 immiob3456 NM_006748 /len=2665 NM_006748 Hs.75367 NP_006739 peroxiredoxin 3 (PRDX3), nuclear gene encoding mitochondrial protein, mRNA /cds=(7,777) /gb=NM_006793 /gi=5802973 NM_006793 Hs.75454 NP_054817 proline rich 2 (PROL2), mRNA /cds=(114,1097) /gb=NM_006813						
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binding protein 2 (HIVEP2), mRNA /cds=(16,7518) /gb=NM_006734 ncr7952 NM_006734 /gi=19923373 /ug=Hs.75063 /len=9175 NM_006734 Hs.75063 NP_006725 Src-like-adaptor (SLA), mRNA /cds=(42,872) /gb=NM_006748 /gi=5803170 /ug=Hs.75367 miob3456 NM_006748 /len=2665 NM_006748 Hs.75367 NP_006739 peroxiredoxin 3 (PRDX3), nuclear gene encoding mitochondrial protein, mRNA /cds=(7,777) /gb=NM_006793 /gi=5802973 ncrc2839 NM_006793 /ug=Hs.75454 /len=1542 NM_006793 Hs.75454 NP_054817 proline rich 2 (PROL2), mRNA /cds=(114,1097) /gb=NM_006813	1111001000	14141_000701		11111_000701	110.10000	11000002
/cds=(16,7518) /gb=NM_006734 ncr7952 NM_006734 /gi=19923373 /ug=Hs.75063 /len=9175 NM_006734 Hs.75063 NP_006725 Src-like-adaptor (SLA), mRNA /cds=(42,872) /gb=NM_006748 /gi=5803170 /ug=Hs.75367 NM_006748 Hs.75367 NP_006739 peroxiredoxin 3 (PRDX3), nuclear gene encoding mitochondrial protein, mRNA /cds=(7,777) /gb=NM_006793 /gi=5802973 /ug=Hs.75454 /len=1542 NM_006793 Hs.75454 NP_054817 proline rich 2 (PROL2), mRNA /cds=(114,1097) /gb=NM_006813			1			•
ncr7952 NM_006734 /gi=19923373 /ug=Hs.75063 /len=9175 NM_006734 Hs.75063 NP_006725 miob3456 NM_006748 /len=2665 NM_006748 Hs.75367 NP_006739 miob3456 NM_006748 /len=2665 NM_006748 Hs.75367 NP_006739 ncrc2839 NM_006793 /len=1542 NM_006793 Hs.75454 NP_054817 proline rich 2 (PROL2), mRNA /cds=(114,1097) /gb=NM_006813 NM_006793 Hs.75454 NP_054817		1.	1			
Src-like-adaptor (SLA), mRNA /cds=(42,872) /gb=NM_006748 /gi=5803170 /ug=Hs.75367 NM_006748 Hs.75367 NP_006739	por7053	NIM 006724	, , , , =	NIM DOG 724	He 75063	ND 006725
/gb=NM_006748 /gi=5803170 /ug=Hs.75367 NM_006748 Hs.75367 NP_006739	11017932	14141_0007.34		14141_0007.54	1115.73003	147_000723
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peroxiredoxin 3 (PRDX3), nuclear gene encoding mitochondrial protein, mRNA /cds=(7,777) /gb=NM_006793 /gi=5802973 /ug=Hs.75454 /len=1542 NM_006793 Hs.75454 NP_054817 proline rich 2 (PROL2), mRNA /cds=(114,1097) /gb=NM_006813		NINA 000740	,	NINA 000740	75267	ND 000720
encoding mitochondrial protein, mRNA /cds=(7,777) /gb=NM_006793 /gi=5802973 /ug=Hs.75454 /len=1542 NM_006793 Hs.75454 NP_054817 proline rich 2 (PROL2), mRNA /cds=(114,1097) /gb=NM_006813	miob3456	NIVI_006748		INIVI_UU6748	IUS: \2990	INP_006/39
/cds=(7,777) /gb=NM_006793 /gi=5802973 /ug=Hs.75454 /len=1542 NM_006793 Hs.75454 NP_054817 proline rich 2 (PROL2), mRNA /cds=(114,1097) /gb=NM_006813		1				
ncrc2839 NM_006793 /ug=Hs.75454 /len=1542 NM_006793 Hs.75454 NP_054817 proline rich 2 (PROL2), mRNA /cds=(114,1097) /gb=NM_006813	•	1				
proline rich 2 (PROL2), mRNA /cds=(114,1097) /gb=NM_006813			1 · · · · ·			
/cds=(114,1097) /gb=NM_006813	ncrc2839	NM_006793		NM_006793	Hs.75454	NP_054817
		1	1'			
seob9145 NM_006813 /gi=5802981 /ug=Hs.75969 /len=2061 NM_006813 Hs.75969 NP_006804						
	seob9145	NM_006813	/gi=5802981 /ug=Hs.75969 /len=2061	NM_006813	Hs.75969	NP_006804

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· ·		coated vesicle membrane protein (RNP24),			
		mRNA /cds=(24,629) /gb=NM_006815			
mioa7239	NM_006815	/gi=21314646 /ug=Hs.75914 /len=2060	NM_006815	Hs.75914	NP_006806
	:	coated vesicle membrane protein (RNP24),			
		mRNA /cds=(24,629) /gb=NM_006815	NINA 000045	75044	LID ACCOOL
ncrc6981	NM_006815	/gi=21314646 /ug=Hs.75914 /len=2060	NM_006815	Hs.75914	NP_006806
		ALL1-fused gene from chromosome 1q			
		(AF1Q), mRNA /cds=(353,625)			1
200b6270	NM_006818	/gb=NM_006818 /gi=21626459 /ug=Hs.75823 /len=1653	NM 006818	Hs.75823	NP 006809
Se000279	141VI_0000 10	inner membrane protein, mitochondrial	14141_000010	115.73023	NF_000003
		(mitofilin) (IMMT), mRNA /cds=(93,2369)			
		/gb=NM_006839 /gi=5803114 /ug=Hs.78504			
hfcr0594	NM_006839	//len=2697	NM_006839	Hs.78504	NP 006830
111010004	14111_000000	stoned B-like factor (SBLF), mRNA	000000	110.70001	
		/cds=(11,2218) /gb=NM_006873			
mioc5772	NM 006873	/gi=26787992 /ug=Hs.54961 /len=5822	NM 006873	Hs.54961	NP 006864
		AT-binding transcription factor 1 (ATBF1),	_		
		mRNA /cds=(674,11785) /gb=NM_006885			
ncrb6357	NM_006885	/gi=19923286 /ug=Hs.101842 /len=11893	NM_006885	Hs.101842	NP_008816
	_				
		ATP synthase, H transporting, mitochondrial			
		F1 complex, epsilon subunit (ATP5E),	•		
		nuclear gene encoding mitochondrial protein,			
		mRNA /cds=(95,250) /gb=NM_006886		•	
seob0133	NM_006886	/gi=21327678 /ug=Hs.177530 /len=417	NM_006886	Hs.177530	NP_008817
		splicing factor, arginine/serine-rich 1 (splicing			
		factor 2, alternate splicing factor) (SFRS1),			
		mRNA /cds=(36,782) /gb=NM_006924		70707	ND 000055
seob1423	NM_006924	/gi=19923382 /ug=Hs.73737 /len=2708	NM_006924	Hs.73737	NP_008855
		SMT3 suppressor of mif two 3 1 (yeast)			
		(SMT3H1), mRNA /cds=(95,406) /gb=NM 006936 /gi=5902095 /ug=Hs.85119			
coob0221	NIM ODEDSE	//len=1733	NM 006936	Hs.85119	NP_008867
Seobozzi	NM_006936	HLA class II region expressed gene KE4	14141_000930	115.05119	147_000007
		(HKE4), mRNA /cds=(327,1616)			
		/gb=NM_006979 /gi=5901935			
fcrc7338	NM_006979	/ug=Hs.278721 /len=2358	NM 006979	Hs.278721	NP_008910
10/0/000	11111_000070	melanoma antigen, family D, 1 (MAGED1),		110.270721	
		mRNA /cds=(143,2479) /gb=NM_006986			
fcrb2040	NM_006986	/gi=14195633 /ug=Hs.5258 /len=2713	NM 006986	Hs.5258	NP_008917
		adhesion regulating molecule 1 (ADRM1),			
		transcript variant 1, mRNA /cds=(81,1304)	,	1	
		/gb=NM_007002 /gi=28373191	NM_007002;		
fcrb3895	NM_007002	/ug=Hs.90107 /len=1410	NM_175573	Hs.90107	NP_783163
		decidual protein induced by progesterone			
		(DEPP), mRNA /cds=(219,857)	:		
		/gb=NM_007021 /gi=5901937 /ug=Hs.93675			
ncr0238	NM_007021	/len=2114	NM_007021	Hs.93675	NP_008952

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		Tara-like protein (HRIHFB2122), transcript			
ļ		variant 1, mRNA /cds=(176,1957)			
		/gb=NM_007032 /gi=20336765	NM_007032;		
miob8630	NM_007032_	/ug=Hs.40342 /len=2687	NM_138632	Hs.40342	NP_619538
		vascular Rab-GAP/TBC-containing (VRP),			
		mRNA /cds=(1118,3811) /gb=NM_007063			
fcrb1428	NM_007063	/gi=5902153 /ug=Hs.164170 /len=4404	NM_007063	Hs.164170	NP_008994
fcr4695	NM_007104	ribosomal protein L10a (RPL10A), mRNA	NM_007104	Hs.425293	NP_009035
		transcription elongation factor B (SIII),			
		polypeptide 2 (18kDa, elongin B) (TCEB2),			
		mRNA /cds=(1,357) /gb=NM_007108			
ncr8867	NM_007108	/gi=6005889 /ug=Hs.172772 /len=357	NM_007108	Hs.172772	NP_009039
:		zinc finger protein 146 (ZNF146), mRNA			
		/cds=(857,1735) /gb=NM_007145			
seoa6038	NM_007145	/gi=6005965 /ug=Hs.301819 /len=3186	NM_007145	Hs.301819	NP_009076
		CHK2 checkpoint (S. pombe) (CHEK2),			
		transcript variant 1, mRNA /cds=(762,2393)		•	
ļ		/gb=NM_007194 /gi=22209010	NM_007194;		
mioc6898	NM_007194	/ug=Hs.146329 /len=2547	NM_145862	Hs.146329	NP_665861
				ŀ	
ŀ					
İ	1		NM_007245;		
			NM_017492;		
	:	ataxin 2 related protein (A2LP), transcript	NM_145714;		
		variant A, mRNA /cds=(169,3396)	NM_148414;		
		/gb=NM_007245 /gi=27262646	NM_148415;		
fcrb3515	NM_007245	/ug=Hs.43509 /len=4386	NM_148416	Hs.43509	NP_680782
				Ĭ	
İ		AP1 gamma subunit binding protein 1			
		(AP1GBP1), transcript variant 1, mRNA	NM_007247;	1	
		/cds=(44,2113) /gb=NM_007247	NM_080550;	ŀ	
miob7276	NM_007247	/gi=18105003 /ug=Hs.15384 /len=5115	NM_080551	Hs.15384	NP_542118
		Kruppel-like factor 8 (KLF8), mRNA			
		/cds=(439,1518) /gb=NM_007250			
fcr3163	NM_007250	/gi=28376642 /ug=Hs.320861 /len=2208	NM_007250	Hs.320861	NP_009181
		ankyrin-like with transmembrane domains 1			
		(ANKTM1), mRNA /cds=(175,3534)	-		
		/gb=NM_007332 /gi=6601589	ì		
mioa4532	NM_007332	/ug=Hs.137674 /len=5190	NM_007332	Hs.137674	NP_015628
		replication factor C (activator 1) 5, 36.5kDa	1		
	1	(RFC5), mRNA /cds=(102,1124)	-		
	1	/gb=NM_007370 /gi=19923788			
fcrb5948	NM_007370	/ug=Hs.171075 /len=2097	NM_007370	Hs.171075	NP_853556
		microtubule-actin crosslinking factor 1			
	1	(MACF1), transcript variant 1, mRNA	NM_012090;		
		/cds=(52,16344) /gb=NM_012090	NM_033024;		
seob3191		/gi=15011903 /ug=Hs.108258 /len=17532	NM 033044	Hs.108258	NP_149033

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		CASP8 associated protein 2 (CASP8AP2),			-
1		mRNA /cds=(197,6145) /gb=NM_012115			
ncrb5704	NM_012115	/gi=16306505 /ug=Hs.122843 /len=6782	NM_012115	Hs.122843	NP_036247
		eukaryotic translation initiation factor 2C, 2			
		(EIF2C2), mRNA /cds=(111,1868)			
		/gb=NM_012154 /gi=24307940			
fcrb7785	NM_012154	/ug=Hs.193053 /len=2815	NM 012154	Hs.193053	NP 036286
		golgi apparatus protein 1 (GLG1), mRNA	 		
		/cds=(27,3560) /gb=NM_012201 /gi=6912389			
ncrc0457	NM_012201	/ug=Hs.78979 /len=3909	NM_012201	Hs.78979	NP_036333
		interleukin enhancer binding factor 3, 90kDa			
		(ILF3), transcript variant 1, mRNA	NM 004516;		
1		/cds=(267,2951) /gb=NM_012218	NM 012218;		
mioc7662	NM_012218	/gi=24234749 /ug=Hs.256583 /len=6058	_	Hs.256583	NP 703194
1111001 002	1441_012210	mortality factor 4 like 2 (MORF4L2), mRNA			
		/cds=(306,1172) /gb=NM_012286		•	
fcr5211	NM_012286	/gi=6912447 /ug=Hs.173714 /len=1826	NM 012286	Hs.173714	NP 036418
1010211	14141_012200	myosin X (MYO10), mRNA /cds=(223,6399)	1111_012200	110.110711	
ŀ		/gb=NM 012334 /gi=11037056			
seob1001	NM 012334	/ug=Hs.61638 /len=7787	NM 012334	Hs 61638	NP 036466
36001001	14141_012334	olfactory receptor, family 2, subfamily F,	1410_012334	113.01000	
		member 1 (OR2F1), mRNA /cds=(1,954)			
		/gb=NM_012369 /gi=6912557			
fcrb8239	NIM 012260	/ug=Hs.159898 /len=954	NM_012369	He 150000	NP_036501
10100239	NM_012369	rearranged L-myc fusion sequence (RLF),	14141_012309	ITS. 139090	INF_030301
		mRNA /cds=(13,5757) /gb=NM_012421			
norb7944	NIM 012421	· · · · · —	NM_012421	Hs.13321	NP 036553
IICID/644	NM_012421	/gi=6912631 /ug=Hs.13321 /len=6229 ribosomal protein L13a (RPL13A), mRNA	14141_012421	П5. 1332 1	INF_030333
	N. 040402	//cds=(23,634) /gb=NM_012423 /gi=14591905		11- 200225	ND OSCEE
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		ribosomal protein L13a (RPL13A), mRNA			
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fcrc5604	NM_012423	/ug=Hs.389335 /len=1142	NM_012423	Hs.389335	NP_036555_
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		/cds=(23,634) /gb=NM_012423 /gi=14591905			ND OOSES
fcrb4470	NM_012423	/ug=Hs.389335 /len=1142	NM_012423	Hs.389335	NP_036555
	ŀ	C-type (calcium dependent, carbohydrate-			
	}	recognition domain) lectin, superfamily			
	}	member 5 (CLECSF5), mRNA			
		/cds=(198,764) /gb=NM_013252			
seoa4571	NM_013252	/gi=10281668 /ug=Hs.126355 /len=3510	NM_013252	Hs.126355	NP_037384
	[bromodomain containing 7 (BRD7), mRNA			
[/cds=(6,1964) /gb=NM_013263 /gi=7019344			\. <u>.</u>
mioa8261	NM_013263	/ug=Hs.279762 /len=2137	NM_013263	Hs.279762	NP_037395
	1	chromosome 11 open reading frame2			
fcrc4067	NM_013265	(C11orf2), mRNA	NM_013265	Hs.5258	NP_037397_
		myosin light chain 2 (HUMMLC2B), mRNA			
		/cds=(60,569) /gb=NM_013292 /gi=28372498			
fcrb1969	NM_013292	/ug=Hs.50889 /len=687	NM_013292	Hs.50889	NP_037424

Figure	6a Contd.			,	,
		transformer-2 alpha (htra-2 alpha)			
		(HSU53209), mRNA /cds=(158,1006)			
		/gb=NM_013293 /gi=9558732			
seob0976	NM_013293	/ug=Hs.130829 /len=1563	NM_013293	Hs.130829	NP_037425
		Alg5, S. cerevisiae, of (ALG5), mRNA			
		/cds=(28,1002) /gb=NM_013338 /gi=9665250			
seob5213	NM_013338	/ug=Hs.227933 /len=1125	NM_013338	Hs.227933	NP_037470
		striatin, calmodulin binding protein 4			
		(STRN4), mRNA /cds=(1,2262)			
		/gb=NM_013403 /gi=7019572			
fcrc4151	NM_013403	/ug=Hs.108665 /len=3188	NM_013403	Hs.108665	NP_037535
		isoleucine-tRNA synthetase (IARS), transcript			
		variant long, mRNA /cds=(256,4044)			
		/gb=NM_013417 /gi=7770071	NM_002161;		
fcrb8697	NM_013417	/ug=Hs.172801 /len=4508	NM_013417	Hs.172801	NP_038203
		SAC1 suppressor of actin mutations 1-like			
		(yeast) (SACM1L), mRNA /cds=(70,1833)			
		/gb=NM_014016 /gi=7662337 /ug=Hs.5867			
seob9485	NM_014016	/len=3572	NM_014016	Hs.5867	NP_054735
		mitochondrial ribosomal protein S28			
		(MRPS28), nuclear gene encoding			
		mitochondrial protein, mRNA /cds=(24,587)			
]	/gb=NM_014018 /gi=16579882			
miob8425	NM_014018	/ug=Hs.55097 /len=724	NM_014018	Hs.55097	NP_054737
		anti-silencing function 1A (DKFZP547E2110),			1
		mRNA /cds=(193,807) /gb=NM_014034			
seoc3469	NM_014034	/gi=7661591 /ug=Hs.108110 /len=2367	NM_014034	Hs.108110	NP_054753
		likely ortholog of mouse hypoxia induced			
		gene 1 (HIG1), mRNA /cds=(93,374)			
		/gb=NM_014056 /gi=7661619 /ug=Hs.7917]		
ncrc6047	NM_014056	/len=1362	NM_014056	Hs.7917	NP_054775
	_				
miob9671	NM_014129	PRO0478 protein (PRO0478), mRNA	NM_014129	Hs.279558	NP_054848
		chromosome 20 open reading frame 30			
	:	(C20orf30), mRNA /cds=(114,476)	•		
		/gb=NM_014145 /gi=15559214 /ug=Hs.3576			
miod4063	NM_014145	/len=1440	NM_014145	Hs.3576	NP_054864
		HSPC126 protein (HSPC126), mRNA		1	
		/cds=(26,838) /gb=NM_014166 /gi=7661787	1		1
ncrb3317	NM_014166	/ug=Hs.181112 /len=1424	NM_014166	Hs.181112	NP_054885
	1	signal peptidase complex (18kD) (SPC18),			
	1	mRNA /cds=(78,617) /gb=NM_014300		l	[<u>.</u>
fcr2102	NM_014300	/gi=7657608 /ug=Hs.9534 /len=1105	NM_014300	Hs.9534	NP_055115
		dTDP-D-glucose 4,6-dehydratase (TDPGD),			1
	l	mRNA /cds=(94,1146) /gb=NM_014305			 -
mioa3888	NM_014305	/gi=7657640 /ug=Hs.12393 /len=1889	NM_014305	Hs.12393	NP_055120
	İ	small membrane protein 1 (SMP1), mRNA	}		
		/cds=(151,624) /gb=NM_014313		l .	
seoa0486	NM_014313	/gi=20357549 /ug=Hs.107979 /len=2284	NM_014313	Hs.107979	NP_055128

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		mitochondrial carrier 2 (MTCH2), nuclear	1		
<u> </u>		gene encoding mitochondrial protein, mRNA			
		/cds=(49,960) /gb=NM_014342 /gi=7657346			
mioa2343	NM_014342	/ug=Hs.279609 /len=1104	NM_014342	Hs.279609	NP_055157
		3-hydroxyisobutyryl-Coenzyme A hydrolase			
		(HIBCH), mRNA /cds=(64,1209)			
		/gb=NM_014362 /gi=7657159			
fcr5895	NM_014362	/ug=Hs.236642 /len=1311	NM 014362	Hs.236642	NP_055177
		polycystic kidney disease 2-like 2 (PKD2L2),			İ
		mRNA /cds=(24,1853) /gb=NM_014386			
seoc2595	NM 014386	/gi=7657458 /ug=Hs.272418 /len=2205	NM_014386	Hs.272418	NP_055201
		Siah-interacting protein (SIP), mRNA			
		/cds=(118,804) /gb=NM_014412 /gi=7656951			
miob4760	NM_014412	/ug=Hs.27258 /len=2435	NM 014412	Hs.27258	NP_055227
		p53 regulated PA26 nuclear protein (PA26),			
		mRNA /cds=(12,1667) /gb=NM_014454			
ncr3284	NM_014454	/gi=7657436 /ug=Hs.14125 /len=2785	NM_014454	Hs.14125	NP 055269
11010201		Lsm1 protein (LSM1), mRNA /cds=(189,590)			
		/gb=NM_014462 /gi=7657312			
miod1613	NM 014462	/ug=Hs.425311 /len=935	NM 014462	Hs 425311	NP_055277
111100 10 10	14111_011102_	putative dimethyladenosine transferase	1111_011102		
		(HSA9761), mRNA /cds=(79,1020)			
		/gb=NM 014473 /gi=7657197			
fcrb3135	NM 014473	/ug=Hs.125819 /len=1505	NM 014473	Hs 125819	NP 055288
10100100	14101_014470_	ERO1-like (S. cerevisiae) (ERO1L), mRNA	11111_014470	110.120010	141_000200
		/cds=(227,1633) /gb=NM_014584			
miod/805	NM_014584	/gi=7657068 /ug=Hs.25740 /len=3334	NM 014584	Hs 25740	NP_055399
111104-1033	14141_014304	solute carrier family 11 (proton-coupled	14141_014004	113.20740	141 _000000
:		divalent metal ion transporters), member 3			
		(SLC11A3), mRNA /cds=(315,2030)	:		
		/gb=NM_014585 /gi=19923794 /ug=Hs.5944			
coop3333	NM 014585	//len=3333	NM_014585	He 50//	NP 055400
56003322	14101_014303	Rho quanine nucleotide exchange factor	14141_014303	113.0044	141_000400
		(GEF) 10 (ARHGEF10), mRNA			
		/cds=(3732,7097) /gb=NM_014629			
mioh1126	NM_014629	/gi=7662041 /ug=Hs.20695 /len=8467	NM 014629	Hs.20695	NP 055444
1111001120	141029	KIAA0391 gene product (KIAA0391), mRNA	14141_014023	113.20033	141 _000444
		/cds=(360,2063) /gb=NM_014672			
ncr1550	NM_014672	/gi=7662093 /ug=Hs.154668 /len=5677	NM_014672	He 15/1668	NP 055487
1101 1330	14072	endosome-associated FYVE-domain protein	14141_014072	113.134000	141 _000407
		(ENDOFIN), mRNA /cds=(249,4868)			
		/gb=NM 014733/gi=7662047/ug=Hs.83790			
ncr4590	NM_014733	/len=6632	NM_014733	Hs.83790	NP 055548
11014390	14101_014733	KIAA0429 gene product (KIAA0429), mRNA	14141_0 14733	113.00730	141 _000040
		/cds=(2374,3444) /gb=NM 014751			
mic22267	NM_014751	//gi=7662113 /ug=Hs.77694 /len=5645	NM 014751	Hs.77694	NP 055566
milioa3307	14/01	KIAA0107 gene product (P44S10), mRNA	14141_014731	113.77034	145_00000
		/cds=(26,1195) /gb=NM_014814 /gi=7661913			
50001000	NIM 014014	//ug=Hs.23488 /len=1308	NM 014814	He 23/99	NP_055629
1992	NM_014814	/uy=115.23400 /left=1300	[14014_U14014	1175.23400	TIAL 000058

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		KIAA0438 gene product (KIAA0438), mRNA			
		/cds=(118,2244) /gb=NM_014819			
seob2994	NM_014819	/gi=7662123 /ug=Hs.279849 /len=4765	NM_014819	Hs.279849	NP_055634
		family with sequence similarity 3, member C			
		(FAM3C), mRNA /cds=(168,851)			
		/gb=NM_014888 /gi=7661713 /ug=Hs.29882			
seoa0029	NM_014888	/len=2475	NM_014888	Hs.29882	NP_055703
		Rho-related BTB domain containing 3			
		(RHOBTB3), mRNA /cds=(336,2171)			
		/gb=NM_014899 /gi=7662355 /ug=Hs.10432			
seoc0034	NM_014899	/len=4099	NM_014899	Hs.10432	NP_055714
		KIAA1074 protein (KIAA1074), mRNA			
İ		/cds=(151,5280) /gb=NM_014915			
mioa2073	NM_014915	/gi=7662473 /ug=Hs.129218 /len=5360	NM_014915	Hs.129218	NP_055730
•		amyotrophic lateral sclerosis 2 (juvenile)			
		chromosome region, candidate 3			
		(ALS2CR3), mRNA /cds=(382,3126)			
		/gb=NM_015049 /gi=13027379		1	
seoa9160	NM_015049	/ug=Hs.154248 /len=6470	NM_015049	Hs.154248	NP_055864
		KIAA1055 protein (KIAA1055), mRNA			j
	İ	/cds=(428,1675) /gb=NM_015079			
hfcr3011	NM_015079	/gi=24307996 /ug=Hs.126084 /len=4863	NM_015079	Hs.126084	NP_055894
		RalGDS-like gene (RGL), mRNA			
		/cds=(450,2861) /gb=NM_015149			1
mioc6055	NM_015149	/gi=20127535 /ug=Hs.79219 /len=5111	NM_015149	Hs.79219	NP_055964
		KIAA0874 protein (KIAA0874), mRNA			
		/cds=(1,6189) /gb=NM_015208 /gi=14140237			
ncr7292	NM_015208	/ug=Hs.27973 /len=6189	NM_015208	Hs.27973	NP_056023
		KIAA0433 protein (KIAA0433), mRNA			
		/cds=(510,4241) /gb=NM_015216	l		
seoa4647	NM_015216	/gi=7662117 /ug=Hs.26179 /len=5814	NM_015216	Hs.26179	NP_056031
		kinesin family member 13B (KIF13B), mRNA			1
		/cds=(38,5518) /gb=NM_015254	l	l., ,,	
mioa6442	NM_015254	/gi=13194196 /ug=Hs.15711 /len=8743	NM_015254	Hs.15711	NP_056069
		kinesin family member 13B (KIF13B), mRNA			
		/cds=(38,5518) /gb=NM_015254	045054	111- 45344	ND 050000
mioc2928	NM_015254	/gi=13194196 /ug=Hs.15711 /len=8743	NM_015254	HS.15/11	NP_056069
		tripartite motif-containing 2 (TRIM2), mRNA		1	1
		/cds=(147,2381) /gb=NM_015271	NINA 045074	11- 40070	ND 050000
mioc4232	NM_015271	/gi=15011942 /ug=Hs.12372 /len=6734	NM_015271	Hs.12372	NP_056086
		KIAA0790 protein (KIAA0790), mRNA			
f	NINA 045070	/cds=(10,3204) /gb=NM_015278	NINA 045070	115 42002	ND 056003
fcrb6160	NM_015278	/gi=24308024 /ug=Hs.12002 /len=3711	NM_015278	Hs.12002	NP_056093
		tensin like C1 domain-containing			
	1	phosphatase (TENC1), transcript variant 2,	NINA 045240.		
forboos 7	NIM 045040	mRNA /cds=(196,4455) /gb=NM_015319	NM_015319;		ND 726610
fcrb8257	NM_015319	/gi=23943863 /ug=Hs.6147 /len=4944	NM_170754	Hs.6147	NP_736610
		sorbin and SH3 domain containing 1			
	1	(SORBS1), mRNA /cds=(191,2641)	NIM ODE 424:		
forb = 700	NIM 045005	/gb=NM_015385 /gi=7661699	NM_006434;	1	ND OFFICE
fcrb5720	NM_015385	/ug=Hs.108924 /len=5943	NM_015385	Hs.108924	NP_056200

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		KIAA1892 protein (KIAA1892), mRNA			•
		/cds=(308,1669) /gb=NM_015397			
seoc2518	NM_015397	/gi=22218618 /ug=Hs.102669 /len=3636	NM_015397	Hs.102669	NP_056212
		DKFZP434B168 protein (DKFZP434B168),			
		mRNA /cds=(106,2994) /gb=NM_015434		Ì	
mioc5546	NM_015434	/gi=7661565 /ug=Hs.48604 /len=3463	NM_015434	Hs.48604	NP_056249
		DKFZP586G1517 protein			
		(DKFZP586G1517), mRNA /cds=(127,2328)			
1		/gb=NM_015440 /gi=24308062			
seoc1425	NM_015440	/ug=Hs.44155 /len=2749	NM_015440	Hs.44155	NP_056255
		early hematopoietic zinc finger (EHZF),			
		mRNA /cds=(150,4085) /gb=NM_015461			
seoc1876	NM_015461	/gi=24308068 /ug=Hs.26799 /len=4869	NM_015461	Hs.26799	NP_056276
		protein tyrosine phosphatase, non-receptor			
		type 23 (PTPN23), mRNA /cds=(62,4972)			
		/gb=NM_015466 /gi=24308072			
fcrb1962	NM_015466	/ug=Hs.25524 /len=5248	NM_015466	Hs.25524	NP_056281
	<u> </u>	protein tyrosine phosphatase, non-receptor			
		type 23 (PTPN23), mRNA /cds=(62,4972)		}	
		/gb=NM_015466 /gi=24308072			
fcrb8674	NM_015466	/ug=Hs.25524 /len=5248	NM 015466	Hs.25524	NP_056281
		DKFZP564G2022 protein			
		(DKFZP564G2022), mRNA /cds=(43,1710)			
		/gb=NM 015497 /gi=13794264			
fcrb2697	NM_015497	/ug=Hs.16492 /len=2286	NM 015497	Hs.16492	NP 056312
		SET binding protein 1 (SETBP1), mRNA	-		
		/cds=(6,4634) /gb=NM_015559 /gi=7662121			
fcr5679	NM_015559	/ug=Hs.151717 /len=5744	NM 015559	Hs.151717	NP 056374
		zinc finger protein 288 (ZNF288), mRNA	 		
		/cds=(489,2495) /gb=NM_015642			
ncrc4815	NM 015642	/gi=7661651 /ug=Hs.159456 /len=2829	NM_015642	Hs.159456	NP 056457
		glioma tumor suppressor candidate region			
		gene 2 (GLTSCR2), mRNA /cds=(53,1489)			
		/gb=NM_015710 /gi=21359905			
seoa8754	NM_015710	/ug=Hs.421907 /len=1610	NM_015710	Hs.421907	NP 056525
		glioma tumor suppressor candidate region	=		
	1	gene 2 (GLTSCR2), mRNA /cds=(53,1489)			
		/gb=NM 015710 /gi=21359905			
mioc2019	NM_015710	/ug=Hs.421907 /len=1610	NM 015710	Hs.421907	NP 056525
		CGI-07 protein (CGI-07), mRNA			
		/cds=(124,1635) /gb=NM_015938			
miob5491	NM_015938	/gi=19923795 /ug=Hs.181022 /len=2762	NM 015938	Hs.181022	NP_057022
	15.5555	serologically defined breast cancer antigen		1	
	}	84 (SDBCAG84), mRNA /cds=(28,1179)			
	1	/gb=NM_015966 /gi=7706277			
hfcr0370	NM_015966	/ug=Hs.169992 /len=1337	NM 015966	Hs.169992	NP 057050
111010070	1.111_0 10000	mitochondrial ribosomal protein S17	10.0000	1	
		(MRPS17), nuclear gene encoding			
		mitochondrial protein, mRNA /cds=(31,423)			
	1	/gb=NM_015969 /gi=16554613	1		
mind3046	NM 015969	/ug=Hs.44298 /len=600	NM_015969	Hs 44298	NP_057053
1111000340	LIAINI O 19909	1/49 113.77200 /ICH-000	1.4141 0 10909	1.10.47200	1141 _007 000

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		CGI-125 protein (CGI-125), mRNA			
		/cds=(79,474) /gb=NM_016060 /gi=7705591			
ncrb8649	NM_016060	/ug=Hs.27289 /len=1196	NM_016060	Hs.27289	NP_057144
		palladin (KIAA0992), mRNA /cds=(212,3532)			
		/gb=NM_016081 /gi=21361584			
seoa3392	NM_016081	/ug=Hs.194431 /len=5773	NM_016081	Hs.194431	NP_057165
		FK506 binding protein 7 (FKBP7), mRNA			
		/cds=(96,875) /gb=NM_016105 /gi=23618828			
mioc4331	NM_016105	/ug=Hs.344379 /len=1067	NM_016105	Hs.344379	NP_851939
		PTD016 protein (LOC51136), mRNA			
		/cds=(183,809) /gb=NM_016125			
ncr9487	NM_016125	/gi=21361528 /ug=Hs.30154 /len=1917	NM_016125	Hs.30154	NP_057209
		inhibitor of growth family, member 4 (ING4),			
		mRNA /cds=(18,767) /gb=NM_016162			
hfcr6265	NM_016162	/gi=7705860 /ug=Hs.108183 /len=1377	NM_016162	Hs.108183	NP_057246
		retinoic acid repressible protein (RARG-1),			
		mRNA /cds=(33,806) /gb=NM_016167			
seob0321	NM_016167	/gi=15743546 /ug=Hs.106346 /len=896	NM_016167	Hs.106346	NP_057251
		retinal short-chain dehydrogenase/reductase			
		2 (RetSDR2), mRNA /cds=(189,1091)		1	
		/gb=NM_016245 /gi=7705904 /ug=Hs.12150	1		
ncrc0185	NM_016245	/len=1760	NM_016245	Hs.12150	NP_057329
		baculoviral IAP repeat-containing 6 (apollon)			
		(BIRC6), mRNA /cds=(1,14490)			
		/gb=NM_016252 /gi=10442821		ŀ	
ncrb5940	NM_016252	/ug=Hs.250646 /len=14490	NM_016252	Hs.250646	NP_057336
		STRIN protein (STRIN), mRNA		1	
		/cds=(100,837) /gb=NM_016271	i		
mioc6391	NM_016271	/gi=21361538 /ug=Hs.180403 /len=3226	NM_016271	Hs.180403	NP_057355
	•	RAB23, member RAS oncogene family			
	:	(RAB23), mRNA /cds=(151,864)			
		/gb=NM_016277 /gi=19923480			
mioc4842	NM_016277	/ug=Hs.94769 /len=2588	NM_016277	Hs.94769	NP_057361
		CED-6 protein (CED-6), mRNA			1
		/cds=(429,1343) /gb=NM_016315			
ncrc4132	NM_016315	/gi=7705317 /ug=Hs.107056 /len=3277	NM_016315	Hs.107056	NP_057399
		REV1-like (yeast) (REV1L), mRNA			
		/cds=(213,3968) /gb=NM_016316			
mioc8694	NM_016316	/gi=7706680 /ug=Hs.110347 /len=4276	NM_016316	Hs.110347	NP_057400
		TH1-like (Drosophila) (TH1L), mRNA			
		/cds=(8,1429) /gb=NM_016397 /gi=7705462			
fcrc6174	NM_016397	/ug=Hs.5184 /len=2130	NM_016397	Hs.5184	NP_057481
		hypothetical protein HSPC132 (HSPC132),			
		mRNA /cds=(4,234) /gb=NM_016399	1	į.	
seoa4163	NM_016399	/gi=7705466 /ug=Hs.69499 /len=1171	NM_016399	Hs.69499	NP_057483
		Huntingtin interacting protein K (HYPK),	1		
		mRNA /cds=(177,566) /gb=NM_016400			l
mioc2116	NM_016400	/gi=21361540 /ug=Hs.300954 /len=1349	NM_016400	Hs.300954	NP_057484
		chromosome 14 open reading frame 112			
	1	(C14orf112), mRNA /cds=(119,439)	1		
1	1	/gb=NM_016468 /gi=21361531			
ncrb3226	NM_016468	/ug=Hs.433630 /len=933	NM_016468	Hs.433630	NP_057552

Application of: Liew, et. al. Our Docket #: 4231/2042 Figure 6a Cont'd.

Figure (oa Conta.				
		RAB-8b protein (LOC51762), mRNA			
		/cds=(92,715) /gb=NM_016530 /gi=7706562			
seob5886	NM_016530	/ug=Hs.321245 /len=1265	NM_016530	Hs.321245	NP_057614
		calcium binding protein Cab45 precursor			
		(Cab45), mRNA /cds=(294,1340)			
		/gb=NM_016547 /gi=7706572 /ug=Hs.42806	NM_016176;		
ncrb0074	NM_016547	/len=2092	NM_016547	Hs.42806	NP_057631
	,	hypothetical protein LOC51315 (LOC51315),			1
ŀ		mRNA /cds=(395,1174) /gb=NM_016618	ļ		1
miod6292	NM_016618	/gi=7706155 /ug=Hs.5721 /len=1774	NM_016618	Hs.5721	NP_057702
		hypothetical protein BM-009 (BM-009),			
		mRNA /cds=(386,1048) /gb=NM_016623			
seoc7811	NM_016623	/gi=7705303 /ug=Hs.92918 /len=1919	NM_016623	Hs.92918	NP_057707
		mesenchymal stem cell protein DSC92			
1		(NEUGRIN), mRNA /cds=(632,1291)	İ		
		/gb=NM_016645 /gi=7706195	<u> </u>		
seob5193	NM_016645	/ug=Hs.323467 /len=1729	NM_016645	Hs.323467	NP_057729
		LIM domain kinase 2 (LIMK2), transcript			
		variant 2b, mRNA /cds=(316,2169)		}	
1		/gb=NM_016733 /gi=8051617	NM_005569;		
hfcr2693	NM_016733	/ug=Hs.278027 /len=3806	NM_016733	Hs.278027	NP_057952
		UDP-N-acetyl-alpha-D-			
		galactosamine:polypeptide N-			
		acetylgalactosaminyltransferase 7 (GalNAc-			
		T7) (GALNT7), mRNA /cds=(33,2006)	ļ		
		/gb=NM_017423 /gi=8393408			1
seob1783	NM_017423	/ug=Hs.246315 /len=4266	NM_017423	Hs.246315	NP_059119
		ankyrin repeat domain 10 (ANKRD10),	i		
		mRNA /cds=(136,1398) /gb=NM_017664			
seoc1009	NM_017664	/gi=8923103 /ug=Hs.172572 /len=2509	NM_017664	Hs.172572	NP_060134
		hypothetical protein FLJ20502 (FLJ20502),			1
		mRNA /cds=(29,580) /gb=NM_017845			
mioc6251	NM_017845	/gi=8923457 /ug=Hs.23956 /len=1373	NM_017845	Hs.23956	NP_060315
		hypothetical protein FLJ20508 (FLJ20508),			
		mRNA /cds=(191,802) /gb=NM_017850		1	
miod0080	NM_017850	/gi=8923468 /ug=Hs.272673 /len=2376	NM_017850	Hs.272673	NP_060320
		BTG3 associated nuclear protein (BANP),			
		transcript variant 1, mRNA /cds=(153,1562)		İ	
		/gb=NM_017869 /gi=17986265	NM_017869;		
ncrc0304	NM_017869	/ug=Hs.352397 /len=2136	NM_079837	Hs.352397	NP_524576
		hypothetical protein FLJ20618 (FLJ20618),			
		mRNA /cds=(319,726) /gb=NM_017903			
ncrc0324	NM_017903	/gi=8923570 /ug=Hs.52184 /len=2213	NM_017903	Hs.52184	NP_060373
	,	hypothetical protein FLJ20699 (FLJ20699),			
1		mRNA /cds=(33,1043) /gb=NM_017931			
fcrc6010	NM_017931	/gi=8923627 /ug=Hs.15125 /len=2594	NM_017931	Hs.15125	NP_060401
		hypothetical protein FLJ20729 (FLJ20729),	1		
		mRNA /cds=(135,1547) /gb=NM_017953			
lmiod4507	NM 017953	/gi=20149642 /ug=Hs.5111 /len=2821	NM_017953	Hs.5111	NP_060423

Figure	oa Conta.				
		hypothetical protein FLJ10134 (FLJ10134),			
1		mRNA /cds=(314,1141) /gb=NM_018004			
ncrc9187	NM_018004	/gi=8922242 /ug=Hs.104800 /len=1564	NM_018004	Hs.104800	NP_060474
	:	hypothetical protein FLJ10159 (FLJ10159),			
		mRNA /cds=(1,807) /gb=NM_018013			
mioc4077	NM_018013	/gi=8922262 /ug=Hs.22505 /len=2070	NM_018013	Hs.22505	NP_060483
		hypothetical protein FLJ10420 (FLJ10420),			
		mRNA /cds=(34,825) /gb=NM_018090			
fcrb3808	NM_018090	/gi=20127581 /ug=Hs.289087 /len=2046	NM_018090	Hs.289087	NP_060560
		chromosome 10 open reading frame 6			
		(C10orf6), mRNA /cds=(543,4064)			
		/gb=NM_018121 /gi=27532981	NM_018121;		
ncr1221	NM_018121	/ug=Hs.93581 /len=7284	NM_144592	Hs.93581	NP_653193
		hypothetical protein FLJ10587 (FLJ10587),	-		
		mRNA /cds=(16,2991) /gb=NM_018149			
mioc2459	NM_018149	/gi=21361713 /ug=Hs.7296 /len=3256	NM_018149	Hs.7296	NP_060619
		hypothetical protein FLJ10856 (FLJ10856),			
		mRNA /cds=(148,1233) /gb=NM_018247			
miod4066	NM_018247	/gi=8922719 /ug=Hs.108530 /len=3720	NM_018247	Hs.108530	NP_060717
		stromal cell protein (LOC55974), mRNA			
ļ		/cds=(61,726) /gb=NM_018845 /gi=10047123			
seob4676	NM_018845	/ug=Hs.292154 /len=1316	NM_018845	Hs.292154	NP_061333
		cytochrome c, somatic (CYCS), mRNA			
		/cds=(61,378) /gb=NM_018947 /gi=21361707			
mioa8919	NM_018947	/ug=Hs.169248 /len=3990	NM_018947	Hs.169248	NP_061820
		mitochondrial ribosomal protein S21			
		(MRPS21), transcript variant 2, nuclear gene			
		encoding mitochondrial protein, mRNA			
		/cds=(519,782) /gb=NM_018997	NM_018997;		
ncr9956	NM_018997	/gi=16950592 /ug=Hs.81281 /len=939	NM_031901	Hs.81281	NP_114107
		similar to DNA-directed RNA polymerase I			
		(135 kDa) (Rpo1-2), mRNA /cds=(53,1063)		}	
		/gb=NM_019014 /gi=9506618 /ug=Hs.86337	NM_019014;		
miob0171	NM_019014	/len=4684	NM_032212	Hs.86337	NP_061887
		putative membrane protein (LOC54499),			-
		mRNA /cds=(139,705) /gb=NM_019026			
mioc4112	NM_019026	/gi=24308132 /ug=Hs.93832 /len=1186	NM_019026	Hs.93832	NP_061899
		protocadherin 18 (PCDH18), mRNA			
		/cds=(388,3795) /gb=NM_019035			
fcrc5164	NM_019035	/gi=14589928 /ug=Hs.97266 /len=5157	NM_019035	Hs.97266	NP_061908
		potassium voltage-gated channel, KQT-like			
	:	subfamily, member 5 (KCNQ5), mRNA			
		/cds=(84,2882) /gb=NM_019842			
miob5012	NM_019842	/gi=28373064 /ug=Hs.283644 /len=3325	NM_019842	Hs.283644	NP_062816
		likely ortholog of mouse enhancer trap locus			
		1 (ETL1), mRNA /cds=(79,3159)			
		/gb=NM_020159 /gi=14149729			
seob4002	NM_020159	/ug=Hs.21356 /len=4935	NM_020159	Hs.21356	NP_064544
		DC11 protein (DC11), mRNA /cds=(21,398)			
	İ	/gb=NM_020186 /gi=9910179 /ug=Hs.42785			
ncr4332	NM_020186	/len=957	NM_020186	Hs.42785	NP_064571_

<u> </u>	6a Contra.				
		hypothetical protein LOC57019 (LOC57019),			
		mRNA /gb=NM_020313 /gi=10092672			
ncr1545	NM_020313	/ug=Hs.4900 /len=2105	NM_020313	Hs.4900	NP_064709_
		eukaryotic translation initiation factor 2B,			
		subunit 3 gamma, 58kDa (EIF2B3), mRNA			
		/cds=(103,1461) /gb=NM_020365			
seob4539	NM_020365	/gi=9966778 /ug=Hs.283627 /len=1602	NM_020365	Hs.283627	NP_065098
		DEAD/H (Asp-Glu-Ala-Asp/His) box			
		polypeptide 24 (DDX24), mRNA			
		/cds=(100,2679) /gb=NM_020414			
seob6853	NM_020414	/gi=14251213 /ug=Hs.155986 /len=2967	NM_020414	Hs.155986	NP_065147
		hypothetical protein DKFZp564F013			
		(DKFZP564F013), mRNA /cds=(107,2194)			
		/gb=NM_020432 /gi=24308192			
seob9406	NM_020432	/ug=Hs.128653 /len=4572	NM_020432	Hs.128653	NP_065165
		reticulon 4 (RTN4), mRNA /cds=(245,3823)	NM_007008;	İ	
		/gb=NM_020532 /gi=24638438	NM_020532;		
fcrb5389	NM_020532	/ug=Hs.65450 /len=4166	NM_153828	Hs.65450	NP_722550
		diazepam binding inhibitor (GABA receptor		ļ	
		modulator, acyl-Coenzyme A binding protein)		1	
		(DBI), mRNA /cds=(20,334) /gb=NM_020548			
ncrc6756	NM 020548	/gi=24475624 /ug=Hs.78888 /len=556	NM 020548	Hs.78888	NP 065438
		3			
ļ		diazepam binding inhibitor (GABA receptor			
		modulator, acyl-Coenzyme A binding protein)			
		(DBI), mRNA /cds=(20,334) /gb=NM_020548			
seob8031	NM_020548	/gi=24475624 /ug=Hs.78888 /len=556	NM_020548	Hs.78888	NP 065438
		cytochrome P450 monooxygenase (CYP-M),			
İ	1	mRNA /cds=(88,1395) /gb=NM_020674	NM 020674;		
ncr9572	NM 020674	/gi=10257438 /ug=Hs.352566 /len=1755	NM 177538	Hs.352566	NP 803882
		AT2 receptor-interacting protein 1 (ATIP1),			
		mRNA /cds=(1,1311) /gb=NM_020749			
miob3986	NM_020749	/gi=21361871 /ug=Hs.7946 /len=3455	NM_020749	Hs.7946	NP_065800
		Rho-GTPase activating protein 10		İ	
		(ARHGAP10), mRNA /cds=(438,6311)			
		/gb=NM 020824 /gi=20977540		,	
ncr4020	NM_020824	/ug=Hs.11611 /len=7130	NM_020824	Hs.11611	NP 065875
		WD repeat endosomal protein (KIAA1449),			
		mRNA /cds=(11,2044) /gb=NM_020839			
fcrb8855	NM 020839	/gi=21314694 /ug=Hs.109778 /len=3705	NM 020839	Hs.109778	NP 065890
		nuclear receptor subfamily 2, group F,			
		member 2 (NR2F2), mRNA /cds=(343,1587)			
		/gb=NM 021005 /gi=14149745			
ncrb8319	NM_021005	/ug=Hs.347991 /len=1740	NM 021005	Hs.347991	NP 066285
		interferon induced transmembrane protein 3	 	12.2	
		(1-8U) (IFITM3), mRNA /cds=(238,639)			
1		/gb=NM_021034 /gi=11995467			
ncrc1999	NM_021034	/ug=Hs.381234 /len=808	NM_021034	Hs.381234	NP 066362
	1.111_02 1004	1-25 110.00 120 171011 000	1.111_02 1004	1.10.00 1204	1.11 _000002

rigure	ba Conta.				
		fatty-acid-Coenzyme A ligase, long-chain 2			
		(FACL2), mRNA /cds=(14,2110)			
		/gb=NM_021122 /gi=12669906			
mioc5603	NM_021122	/ug=Hs.154890 /len=3635	NM_021122	Hs.154890	NP_066945
		cyclin D binding myb-like transcription factor			
		1 (DMTF1), mRNA /cds=(276,2558)			
		/gb=NM 021145 /gi=10863946 /ug=Hs.5671			
seob0046	NM 021145	/len=3767	NM 021145	Hs.5671	NP 066968
		cyclin D binding myb-like transcription factor			†
		1 (DMTF1), mRNA /cds=(276,2558)			
		/gb=NM 021145 /gi=10863946 /ug=Hs.5671			
fcrb1580	NM_021145	/len=3767	NM_021145	Hs.5671	NP 066968
		TcD37 (HTCD37), mRNA /cds=(137,1498)			
		/gb=NM_021222 /gi=24308262			
ncrc5760	NM_021222	/ug=Hs.78524 /len=2995	NM_021222	Hs.78524	NP_067045
		likely of rat and mouse retinoid-inducible			
		serine carboxypeptidase (RISC), mRNA			
		/cds=(33,1391) /gb=NM_021626			
ncrc3161	NM_021626	/gi=11055991 /ug=Hs.106747 /len=1921	NM 021626	Hs.106747	NP_067639
		hypothetical protein SP192 (SP192), mRNA			
		/cds=(445,1869) /gb=NM_021639		1	
mioc0690	NM_021639	/gi=21314695 /ug=Hs.169854 /len=2728	NM 021639	Hs.169854	NP_067652
***************************************		WW45 protein (WW45), mRNA			
		/cds=(339,1490) /gb=NM_021818			
mioh8146	NM_021818	/gi=18860913 /ug=Hs.288906 /len=3031	NM_021818	Hs 288906	NP 068590
11555115	02.10.10	I			
mioa5594	NM_021914	cofilin 2 (muscle) (CFL2), mRNA	NM 021914	Hs.180141	NP_619579
		chromosome 21 open reading frame 97			
		(C21orf97), mRNA /cds=(665,1351)		1	
		/gb=NM_021941 /gi=11345479 /ug=Hs.4746			
fcrb1525	NM_021941	/len=1819	NM 021941	Hs.4746	NP 068760
10121020		egl nine 3 (C. elegans) (EGLN3), mRNA			
		/cds=(327,1046) /gb=NM_022073	NM 022073;		ļ
fcrc6826	NM 022073	/gi=11545786 /ug=Hs.18878 /len=2770	NM 033344	Hs.18878	NP_071356
		golgi phosphoprotein 3 (coat-protein)			
		(GOLPH3), mRNA /cds=(241,1137)]
		/gb=NM 022130 /gi=20149665			1
fcrb5709	NM_022130	/ug=Hs.18271 /len=2655	NM 022130	Hs.18271	NP 071413
		golgi phosphoprotein 3 (coat-protein)			
		(GOLPH3), mRNA /cds=(241,1137)		ļ	ļ
		/gb=NM_022130 /gi=20149665			ŀ
ncrb8142	NM 022130	/ug=Hs.18271 /len=2655	NM 022130	Hs.18271	NP 071413
		endoplasmic reticulum chaperone SIL1, of		1	<u> </u>
	}	yeast (SIL1), mRNA /cds=(97,1482)			
		/gb=NM_022464 /gi=11968008			
fcrb5687	NM 022464	/ug=Hs.297875 /len=1702	NM 022464	Hs.297875	NP 071909
.5.2007	022304	hypothetical protein FLJ12799 (FLJ12799),	1 222,04	1	
	Ì	mRNA /cds=(485,1324) /gb=NM_022495			
miod1792	NM_022495	/gi=22095362 /ug=Hs.22549 /len=1926	NM_022495	Hs 22549	NP_071940
	1.111,_022,700	1'3'	1022-700	1.10.22070	1.41 _07 10 40

rigure	ba Conta.				
		anaphase-promoting complex 1 (meiotic			
		checkpoint regulator) (ANAPC1), mRNA			
		/cds=(263,6097) /gb=NM_022662			
ncrc2531	NM 022662	/gi=12056970 /ug=Hs.40137 /len=6282	NM 022662	Hs.40137	NP_073153
		tumor endothelial marker 6 (TEM6), mRNA			
		/cds=(93,3710) /gb=NM_022748			
ncrh8343	NM 022748	/gi=17511208 /ug=Hs.12210 /len=6702	NM_022748	Hs 12210	NP_073585
110100040	74101_0227-10	hypothetical protein FLJ22347 (FLJ22347),	100,000		
		mRNA /cds=(60,2684) /gb=NM_022830			
norh6919	NM_022830	/gi=12383073 /ug=Hs.106004 /len=2747	NM_022830	Hs.106004	NP_073741
110100010	NIVI_022630	7gi-123830737ug-113.1000047lett-2747	14101_022030	113.100004	141_0/3/41
		nucleolar protein family 6 (RNA-associated)			
			NIM 022017:		
		(NOL6), transcript variant alpha, mRNA	NM_022917;		
		/cds=(61,3501) /gb=NM_022917	NM_130793;	11- 400050	ND COACOA
seoc8306	NM_022917	/gi=22212928 /ug=Hs.183253 /len=4854	NM_139235	Hs.183253	NP_631981
				ŀ	
]	
	t				
			NM_000604;	ļ	
			NM 015850;		
			NM 023105;		
}			NM_023106;	}	
		fibroblast growth factor receptor 1 (fms-	NM_023107;		
		related tyrosine kinase 2, Pfeiffer syndrome)	NM_023108;		1
		(FGFR1), transcript variant 7, mRNA	NM_023109;		
ŀ	ĺ	/cds=(727,2715) /gb=NM_023109	NM_023110;		
fcrb7207	NM_023109	/gi=13186244 /ug=Hs.748 /len=4066	NM_023111	Hs.748	NP_075599 _
		nudix (nucleoside diphosphate linked moiety			
		X)-type motif 9 (NUDT9), mRNA			
		/cds=(326,1378) /gb=NM_024047			
fcrc0076	NM_024047	/gi=20127621 /ug=Hs.301789 /len=1718	NM 024047	Hs.301789	NP_076952
		SECIS binding protein 2 (SBP2), mRNA	<u> </u>		
		/cds=(58,2622) /gb=NM 024077			
seoh7224	NM 024077	/gi=21359954 /ug=Hs.288141 /len=3457	NM_024077	Hs.288141	NP_076982
33357224	027077	ubiquitin-like 5 (UBL5), mRNA /cds=(66,287)	02,70,7		
		/gb=NM_024292 /gi=13236509	l	1	
norhE227	NIM 024202	//ug=Hs.13836 /len=413	NM_024292	Hs.13836	NP_077268
ncrb5227	NM_024292		141VI_UZ4Z9Z	113.13030	14F_0//200
}		phospholipase A2, group IVA (cytosolic,			
	Ì	calcium-dependent) (PLA2G4A), mRNA	Ì		1
		/cds=(139,2388) /gb=NM_024420		l -	
seob4213	NM_024420	/gi=23943919 /ug=Hs.211587 /len=2875	NM_024420	Hs.211587	NP_077734
		proline-serine-threonine phosphatase			1
seoa7249	NM_024430	interacting protein 2 (PSTPIP2), mRNA	NM_024430	Hs.69149	NP_077748
		hypothetical protein FLJ11712 (FLJ11712),	1		٥
		mRNA /cds=(287,1225) /gb=NM_024570		İ	
miod1820	NM_024570	/gi=13375741 /ug=Hs.14920 /len=1515	NM_024570	Hs.14920	NP_078846
		TA		<u> </u>	

i iguic	oa contu.				
		hypothetical protein FLJ22643 (FLJ22643),			
		mRNA /cds=(15,650) /gb=NM_024635			
mioc4769	NM_024635	/gi=13375865 /ug=Hs.43579 /len=997	NM_024635	Hs.43579	NP_078911
		hypothetical protein FLJ22729 (FLJ22729),		,	
		mRNA /cds=(603,1079) /gb=NM_024683			
mioc3904	NM_024683	/gi=13375953 /ug=Hs.94891 /len=1278	NM_024683	Hs.94891	NP_078959
	-	hypothetical protein FLJ22419 (FLJ22419),		-	
		mRNA /cds=(409,1596) /gb=NM_024697			
miob9901	NM_024697	/gi=13375980 /ug=Hs.99256 /len=1674	NM_024697	Hs.99256	NP_078973
		hypothetical protein FLJ22625 (FLJ22625),			
		mRNA /cds=(694,1776) /gb=NM_024715			
seob8641	NM_024715	/gi=21362011 /ug=Hs.106534 /len=2747	NM_024715	Hs.106534	NP_078991
		hypothetical protein FLJ22415 (FLJ22415),			
		mRNA /cds=(342,1463) /gb=NM_024769			
miob9714	NM_024769_	/gi=13376114 /ug=Hs.135121 /len=2627	NM_024769	Hs.135121	NP_079045
		hypothetical protein FLJ12542 (FLJ12542),			
		mRNA /cds=(157,2136) /gb=NM_024899			
fcrb2330_	NM_024899	/gi=21314727 /ug=Hs.236940 /len=2884	NM_024899	Hs.236940	NP_079175
		F-box only protein 11 (FBXO11), mRNA	NM_012167;		
		/cds=(319,2748) /gb=NM_025133	NM_018693;		
fcr7667	NM_025133	/gi=28316723 /ug=Hs.284289 /len=3960	NM_025133	Hs.284289	NP_079409
		hypothetical protein FLJ21439 (FLJ21439),			1
		mRNA /cds=(207,1484) /gb=NM_025137			
miod3341	NM_025137	/gi=13376718 /ug=Hs.288872 /len=2010	NM_025137	Hs.288872	NP_079413
•		chromosome 1 open reading frame 22		,	
		(C1orf22), mRNA /cds=(54,2723)			
		/gb=NM_025191 /gi=19923618		1	
mioc3565	NM_025191	/ug=Hs.279951 /len=6298	NM_025191	Hs.279951	NP_079467
	1	likely ortholog of neuronally expressed			
		calcium binding protein (FLJ13612), mRNA			
	l	/cds=(101,820) /gb=NM_025202			ND 070470
mioc1596	NM_025202	/gi=20149495 /ug=Hs.24391 /len=1898	NM_025202	Hs.24391	NP_079478
		hypothetical protein DC42 (DC42), mRNA			
		/cds=(463,771) /gb=NM_030921		11. 70005	ND 440400
miod1942	NM_030921	/gi=24475707 /ug=Hs.72805 /len=1632	NM_030921	Hs.72805	NP_112183
		hypothetical protein DKFZp434B195			
		(DKFZP434B195), mRNA /cds=(514,1290)			
1440		/gb=NM_031284 /gi=21361960	NIA 004004	Un 40740	ND 440574
ncrc1140	NM_031284	/ug=Hs.10748 /len=2262	NM_031284	Hs.10748	NP_112574
	ŀ	hypothetical protein DKFZp564B1162		1	
	i	(DKFZP564B1162), mRNA /cds=(661,2628)			
	N.M. 004005	/gb=NM_031305 /gi=13775229	NIM 024205	Un 03500	ND 110505
ncr5149	NM_031305	/ug=Hs.93589 /len=4593	NM_031305	Hs.93589	NP_112595
		heterogeneous nuclear ribonucleoprotein D			
1	1	(AU-rich element RNA binding protein 1,	NIM 000430:		
		37kDa) (HNRPD), transcript variant 1, mRNA			
norcoocc	NIM 024270	/cds=(286,1353) /gb=NM_031370	NM_031369;	He 406404	ND 112729
LICICARO	NM_031370	/gi=14110419 /ug=Hs.406404 /len=2197	NM_031370	Hs.406404	NP_112738

rigure	oa Conta.				
		B aggressive lymphoma gene (BAL), mRNA			
		/cds=(229,2793) /gb=NM_031458			
mioc5636	NM_031458	/gi=13899296 /ug=Hs.47783 /len=3243	NM_031458	Hs.47783	NP_113646
		hypothetical protein MGC4415 (MGC4415),			
		mRNA /cds=(154,675) /gb=NM_031484			
fcrb1560	NM_031484	/gi=13899343 /ug=Hs.209614 /len=3243	NM_031484	Hs.209614	NP_113672
		hypothetical protein MGC4415 (MGC4415),			
		mRNA /cds=(154,675) /gb=NM_031484			
fcrb3848	NM_031484	/gi=13899343 /ug=Hs.209614 /len=3243	NM_031484	Hs.209614	NP_113672
		hypothetical protein similar to RNA-binding			
		protein lark (MGC10871), mRNA			÷
		/cds=(54,1133) /gb=NM_031492			
hfcr3160	NM_031492	/gi=13899353 /ug=Hs.49994 /len=1821	NM_031492	Hs.49994	NP_113680
		mitochondrial ribosomal protein S5 (MRPS5),			
		nuclear gene encoding mitochondrial protein,			
		mRNA /cds=(219,1511) /gb=NM_031902			
hfcr2722	NM_031902	/gi=16554614 /ug=Hs.433117 /len=1678	NM_031902	Hs.433117	NP_114108
		hypothetical protein DKFZp564D172			
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		/gb=NM_032042 /gi=21362017			1
miob0670	NM_032042	/ug=Hs.25307 /len=4204	NM_032042	Hs.25307	NP_114431
		Splicing factor, arginine/serine-rich, 46kD			
		(SRP46), mRNA /cds=(283,1131)			
		/gb=NM 032102 /gi=15055542			
ncr3971	NM 032102	/ug=Hs.155160 /len=2186	NM_032102	Hs.155160	NP 115285
		dimerization cofactor of hepatocyte nuclear			
		factor 1 (HNF1) from muscle (DCOHM),			
		mRNA /cds=(21,413) /gb=NM_032151			
mioc0214	NM_032151	/gi=14149824 /ug=Hs.150186 /len=5641	NM 032151	Hs.150186	NP_115527
······		FLJ23277 protein (FLJ23277), mRNA			
		/cds=(141,3089) /gb=NM_032236			1
seoa0488	NM_032236	/gi=18860906 /ug=Hs.334477 /len=3911	NM 032236	Hs.334477	NP 115612
		hypothetical protein DKFZp761D112			
		(DKFZp761D112), mRNA /cds=(60,464)	İ		
		/gb=NM_032297 /gi=14150051			
ncrb4101	NM 032297	/ug=Hs.103849 /len=2573	NM_032297	Hs.103849	NP_115673
		hypothetical protein MGC3047 (MGC3047),			
	İ	mRNA /cds=(41,1369) /gb=NM_032348			
ncrc1884	NM_032348	/gi=14150144 /ug=Hs.59384 /len=2299	NM 032348	Hs.59384	NP_115724
		ankyrin repeat and BTB (POZ) domain			
		containing 1 (ABTB1), transcript variant 1,	NM_032548;	I	
		mRNA /cds=(526,1536) /gb=NM 032548	NM_172027;		
fcrb5588	NM_032548	/gi=25777622 /ug=Hs.107812 /len=2020	NM 172028	Hs.107812	NP 742025
		HP43.8KD protein (HP43.8KD), mRNA		1	1
	1	/cds=(507,3635) /gb=NM_032557			
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30000410	002007	methylmalonyl CoA epimerase (MCEE),		1	1
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11010111	[141VI_002001	1/91 2 10 1-1/01 / dg 110.0-10-10 /1011-000	1	1. 10.0-10 10	1.1 1.0000

Figure	ba Cont d.				
		tubulin alpha 6 (TUBA6), mRNA			
		/cds=(1,1350) /gb=NM_032704 /gi=14389308			
fcrb1539	NM_032704	/ug=Hs.406578 /len=1350	NM_032704	Hs.406578	NP_116093
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-		junctional adhesion molecule 3 (JAM3),			
		mRNA /cds=(25,1092) /gb=NM_032801			
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		DC32 (DC32), mRNA /cds=(229,630)		-	
		/gb=NM_032936 /gi=24475725			
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ncrc6455	NM_032961	/ug=Hs.146858 /len=5384	NM_032961	Hs.146858	NP_116586
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		mRNA /cds=(268,2082) /gb=NM_052860			
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		ankylosis, progressive (mouse) (ANKH),			
•		transcript variant 2, mRNA /cds=(265,1743)		,	
		/gb=NM_054027 /gi=21536394	NM_019847;		
mioa2620	NM_054027	/ug=Hs.168640 /len=4031	NM_054027	Hs.168640	NP_473368
		vacuolar protein sorting 29 (yeast) (VPS29)			
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seoa0799	NM_057180	/ug=Hs.69192 /len=1107	NM_057180	Hs.69192	NP_476528
				İ	
		GNAS complex locus (GNAS), transcript	NM_000516;		
		variant 3, mRNA /cds=(1,2730)	NM_016592;		
		/gb=NM_080425 /gi=18426897	NM_080425;		Ì
mioa0908	NM_080425	/ug=Hs.374523 /len=3091	NM_080426	Hs.374523	NP_536351
		oxysterol binding protein-like 1A (OSBPL1A),		1	
		transcript variant OSBPL1B, mRNA	NM_018030;		ŀ
Ì		/cds=(175,3027) /gb=NM_080597	NM_080597;	}	}
miob8191	NM_080597	/gi=19718740 /ug=Hs.252716 /len=4165	NM_133268	Hs.252716	NP_579802
					Ì
		synaptotagmin-like 4 (granuphilin-a) (SYTL4),			
		mRNA /cds=(333,2348) /gb=NM_080737			l
miod4938	NM_080737	/gi=18152766 /ug=Hs.247525 /len=3914	NM_080737	Hs.247525	NP_542775

Application of: Liew, et. al. Our Docket #: 4231/2042 Figure 6a Cont'd.

CC20orf52), mRNA /cds=(164,403) /gb=NM_080748 /gi=18152784 Nm_080748 /gi=18152784 Nm_080748 /gi=18152784 Nm_080748 /gi=18152784 Nm_080748 /gi=18152784 Nm_080748 Hs.401703 NP_542786 Protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1), mRNA /cds=(28,1542) /gb=NM_080792 Nm_080792 Hs.156114 NP_542970 Nm_080792 Hs.156114 NP_542970 Nm_080792 Hs.156114 NP_542970 Nm_080792 Hs.156114 NP_542970 Nm_080792 Hs.156114 NP_542970 Nm_080792 Hs.156114 NP_542970 Nm_080792 Hs.156114 NP_542970 Nm_080792 Hs.156114 NP_542970 Nm_016628; Nm_080792 Nm_080792 Hs.156114 NP_542970 Nm_016628; Nm_100264 Nm_100264 Nm_100264 Nm_100264 Nm_100264 Nm_100264 Nm_100264 Nm_100264 Nm_100264 Nm_100264 Nm_100264 Nm_100264 Nm_100333 NP_567823 Nm_016324 Nm_016324 Nm_016324 Nm_016325 Nm_133502 Nm_133502 Nm_133502 Hs.83761 Nm_106325 Nm_133502 Nm_106325 Nm_1	riguie	ba Conto.	·		,	,
Incre5536 NM			chromosome 20 open reading frame 52			
NM_080748						[
protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1), mRNA (csc4(28,1542) (gb=NM, 080792) (gi=18426910 /ug=Hs.156114 /len=3872) NM_080792 (gi=18426910 /ug=Hs.156114 /len=3872) NM_080792 Hs.156114 NP_542970 WW domain-containing adapter with a coiled-coil region (WAC), transcript variant 2, mRNA (M_0806792) NM_100264 (gi=18379329 /ug=Hs.70333 /len=3088 NM_100264 NM_100264 /gi=18379329 /ug=Hs.70333 /len=3088 NM_100486 Hs.70333 NP_567823 Zinc finger protein 274 (ZNF274), transcript variant 2NF274c, mRNA /cds=(460,2421) (gb=NM_133502 /ug=Hs.83761 /len=2839 NM_133502 NM_133502 NM_133502 NM_133502 NM_133502 NM_133502 NM_133502 NM_133502 NM_133502 NM_133502 NM_133502 NM_133502 NM_133502 NM_134442 NM_004379; NM_134442 NM_004379; NM_134442 NM_004379; NM_134442 NM_004379; NM_134442 NM_004379; NM_134442 NM_004379; NM_134442 NM_004379; NM_134442 NM_004379; NM_134442 NM_004379; NM_134442 NM_004379; NM_134442 NM_004379; NM_134442 NM_004379; NM_134442 NM_004379; NM_134442 NM_004379; NM_134442 NM_004379; NM_134449 NM_134449 NM_004379; NM_134449 NM_134449 NM_004379; NM_134449 NM_134449 NM_004379; NM_134449 NM_134449 NM_004379; NM_134449 NM_134449 NM_004379; NM_134449 NM_134449 NM_004379; NM_134449 N			, ,			
bype substrate 1 (PTPNS1), mRNA cds=(28,1542) /gb=NM_080792 gi=18426910 /ug=Hs.156114 /len=3872 NM_080792 Hs.156114 NP_542970 WW domain-containing adapter with a coiled-coil region (WAC), transcript variant 2, mRNA NM_016628; NM_100264 NM_106325 NM_133502 /gi=19743800 NM_16325 NM_16325 NM_16325 NM_16325 NM_16326 NM_1	ncrc5536	NM_080748		NM_080748	Hs.401703	NP_542786
			1,			
Mm_080792 rig=18426910 / rig=Hs.156114 / len=3872 Mm_080792 Hs.156114 NP_542970			1 2 1			
WW domain-containing adapter with a coiled-coil region (WAC), transcript variant 2, mRNA NM_016628; NM_100264 /gj=18379329 /ug=Hs.70333 /len=3088 NM_100264; NM_100264 /gj=18379329 /ug=Hs.70333 /len=3088 NM_100264; NM_100264; NM_100264; NM_100264 /gj=18379329 /ug=Hs.70333 /len=3088 NM_100486 Hs.70333 NP_567823 NM_016324; NM_016324; NM_016325; NM_016326; NM_01632	l		/cds=(28,1542) /gb=NM_080792			
Coil region (WAC), transcript variant 2, mRNA NM_016628; NM_100264 (/cds=(332,2140) /gb=NM_100264 NM_100264 NM_100264 (/g=18379329 /ug=Hs.70333 /len=3088 NM_100486 Hs.70333 NP_567823 NM_100486 Hs.70333 NP_567823 NM_100486 Hs.70333 NP_567823 NM_104686 Hs.70333 NP_567823 NM_104686 Hs.70333 NP_567823 NM_104686 Hs.70333 NP_567823 NM_1046325; NM_1046326; NM_104629; NM_1046326; NM_104629; NM_104629; NM_104664; NM_1046326; NM_104664; NM_1046326; NM_104664; NM_1046326; NM_104664; NM_1046326; NM_104664; NM_1046326; NM_104664; NM_1046326; NM_104664; NM_1046326; NM_104664; NM_1046326; NM_104664; NM_1046326; NM_104664; NM_1046326; NM_104664; NM_1046326; NM_104664; NM_1046326; NM_104664; NM_10466; NM_104664; NM_1046326; NM_104664; NM_1046326; NM_104	mioc4910	NM_080792	/gi=18426910 /ug=Hs.156114 /len=3872	NM_080792	Hs.156114	NP_542970
Coil region (WAC), transcript variant 2, mRNA NM_016628; NM_100264 (/cds=(332,2140) /gb=NM_100264 NM_100264 NM_100264 (/g=18379329 /ug=Hs.70333 /len=3088 NM_100486 Hs.70333 NP_567823 NM_100486 Hs.70333 NP_567823 NM_100486 Hs.70333 NP_567823 NM_104686 Hs.70333 NP_567823 NM_104686 Hs.70333 NP_567823 NM_104686 Hs.70333 NP_567823 NM_1046325; NM_1046326; NM_104629; NM_1046326; NM_104629; NM_104629; NM_104664; NM_1046326; NM_104664; NM_1046326; NM_104664; NM_1046326; NM_104664; NM_1046326; NM_104664; NM_1046326; NM_104664; NM_1046326; NM_104664; NM_1046326; NM_104664; NM_1046326; NM_104664; NM_1046326; NM_104664; NM_1046326; NM_104664; NM_1046326; NM_104664; NM_1046326; NM_104664; NM_10466; NM_104664; NM_1046326; NM_104664; NM_1046326; NM_104						
Interpretation			coil region (WAC), transcript variant 2, mRNA			1
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variant ZNF274c, mRNA /cds=(460,2421)						
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Crc4734 NM_133502 Ng=Hs.83761 /len=2839 NM_133502 Hs.83761 NP_598009	•		variant ZNF274c, mRNA /cds=(460,2421)	NM_016324;		
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(CREB1), transcript variant B, mRNA /cds=(182,1207) /gb=NM_134442 Mi_2ds=(182,1207) /gb=NM_134442 Mi_2ds=(182,1207) /gb=NM_134442 Mi_2ds=(182,1207) /gb=NM_134442 Mi_2ds=(174,1055) Mi_2ds=(174,	fcrc4734	NM_133502_		NM_133502	Hs.83761	NP_598009
Independent			cAMP responsive element binding protein 1			
mioc5179 NM_134442 /gi=2219460 /ug=Hs.79194 /len=3006 NM_134442 Hs.79194 NP_604391 hypothetical protein, MGC:7199 (LOC16150), mRNA /cds=(174,1055) /gb=NM_138459 /gi=20270242 /ug=Hs.289008 /len=2645 NM_138459 /igi=20270242 /ug=Hs.289008 /len=2645 NM_138459 /igi=20270242 /ug=Hs.289008 /len=2645 NM_138459 Hs.289008 NP_612468 signal transducer and activator of transcription 3 (acute-phase response factor) (STAT3), transcript variant 1, mRNA /cds=(241,2553) /gb=NM_139276 NM_003150; hypothetical protein MGC32043 (MGC32043), mRNA /cds=(8,457) /gb=NM_144582 /gi=21389354 /ug=Hs.226138 /len=3131 NM_144582 Hs.226138 NP_653183 ATPase, H transporting, lysosomal 42kDa, V1 subunit C isoform 2 (ATP6V1C2), mRNA /cds=(21,1166) /gb=NM_144583 /gi=21389364 /ug=Hs.372429 /len=3033 NM_144583 Hs.372429 NP_653184 hypothetical protein FLJ30574 (FLJ30574), mRNA /cds=(403,1908) /gb=NM_144629 /gi=21389456 /ug=Hs.350388 /len=3113 NM_144629 Hs.350388 NP_653230 hypothetical protein MGC33371 (MGC33371), mRNA /cds=(318,1019) /gb=NM_144664 /gi=21389552 /ug=Hs.288304 /len=1399 NM_144664 Hs.288304 NP_653265 /mgNA_144664 /gi=21389506 /mgNA_144664 /gi=21389506			(CREB1), transcript variant B, mRNA			
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(LOC116150), mRNA /cds=(174,1055) /gb=NM_138459 /gi=20270242 / / /ug=Hs.289008 /len=2645	mioc5179	NM_134442	/gi=22219460 /ug=Hs.79194 /len=3006	NM_134442	Hs.79194	NP_604391
Igb=NM_138459 Igi=20270242 Igb=NM_138459 Igi=20270242 Igb=NM_138459			hypothetical protein, MGC:7199			
NM_138459			(LOC116150), mRNA /cds=(174,1055)			
Signal transducer and activator of transcription 3 (acute-phase response factor) (STAT3), transcript variant 1, mRNA /cds=(241,2553) /gb=NM_139276 NM_003150; /gi=21618339 /ug=Hs.321677 /len=3455 NM_139276 Hs.321677 NP_644805 NM_139276 NM_139276 Hs.321677 NP_644805 NM_139276 NM_14582 /gi=21389354 NM_144582 /gi=21389354 NM_144582 /gi=21389354 NM_144582 /gi=21389364 /ug=Hs.226138 /len=3131 NM_144582 Hs.226138 NP_653183 NP_653183 NM_144583 NM_144583 NM_144583 NM_144583 NM_144583 NM_144583 NM_144583 NM_144583 NM_144583 NM_144583 NM_144583 NM_144583 NM_144629 NM_144629 NM_144629 NM_144629 NM_144629 NM_144629 NM_144629 NM_144629 NM_144629 NM_144629 NM_144629 NM_144629 NM_144629 NM_144644 /gi=21389552 NM_144664 /gi=21389552 NM_144664 /gi=21389552 NM_144664 /gi=21389552 NM_144664 /gi=21389552 NM_144664 /gi=21389552 NM_144664 /gi=21389552 NM_144664 /gi=21389552 NM_144664 /gi=21389552 NM_144664 /gi=21389550 NM_144664 /gi=21389506 NM_			/gb=NM_138459 /gi=20270242			
transcription 3 (acute-phase response factor) (STAT3), transcript variant 1, mRNA //cds=(241,253) /gb=NM_139276 NM_144585 NM_144582 //gb=NM_144582 /gi=21389354 //gb=NM_144582 /gi=21389354 NM_144582 NM_144582 NM_144582 NM_144582 NM_144582 NM_144583 NM_144684 NM_14468	seoc0317	NM_138459	/ug=Hs.289008 /len=2645	NM_138459	Hs.289008	NP_612468
(STAT3), transcript variant 1, mRNA /cds=(241,2553) /gb=NM_139276 /gi=21618339 /ug=Hs.321677 /len=3455 hypothetical protein MGC32043 (MGC32043), mRNA /cds=(8,457) /gb=NM_144582 /gi=21389354 fcrb9684 NM_144582 MM_144582 MM_144582 MM_144582 MM_144583 MM_144648 MM_144649 MM_144629 MM_144629 MM_144629 MM_144629 MM_144629 MM_144629 MM_144629 MM_144629 MM_144629 MM_144629 MM_144629 MM_144629 MM_144664 MGC33371), mRNA /cds=(318,1019) /gb=NM_144664 /gi=21389552 MM_144664 MM_144664 MGC30052), mRNA /cds=(35,703) /gb=NM_144721 /gi=21389506			signal transducer and activator of			
Cds=(241,2553) /gb=NM_139276			transcription 3 (acute-phase response factor)			
fcr4699 NM_139276 /gi=21618339 /ug=Hs.321677 /len=3455 NM_139276 Hs.321677 NP_644805 hypothetical protein MGC32043 (MGC32043), mRNA /cds=(8,457) /gb=NM_144582 /gi=21389354 /ug=Hs.226138 /len=3131 NM_144582 Hs.226138 NP_653183 ATPase, H transporting, lysosomal 42kDa, V1 subunit C isoform 2 (ATP6V1C2), mRNA /cds=(21,1166) /gb=NM_144583 /gi=21389364 /ug=Hs.372429 /len=3033 NM_144583 /gi=21389364 /ug=Hs.372429 /len=3033 NM_144583 Hs.372429 NP_653184 hypothetical protein FLJ30574 (FLJ30574), mRNA /cds=(403,1908) /gb=NM_144629 /gi=21389456 /ug=Hs.350388 /len=3113 NM_144629 Hs.350388 NP_653230 hypothetical protein MGC33371 (MGC33371), mRNA /cds=(318,1019) /gb=NM_144664 /gi=21389552 NM_144664 /ug=Hs.288304 /len=1399 NM_144664 Hs.288304 NP_653265 hypothetical protein MGC30052 (MGC30052), mRNA /cds=(35,703) /gb=NM_144721 /gi=21389506			(STAT3), transcript variant 1, mRNA		İ	
hypothetical protein MGC32043 (MGC32043), mRNA /cds=(8,457) /gb=NM_144582 /gi=21389354 /ug=Hs.226138 /len=3131 NM_144582 Hs.226138 NP_653183 ATPase, H transporting, lysosomal 42kDa, V1 subunit C isoform 2 (ATP6V1C2), mRNA /cds=(21,1166) /gb=NM_144583 /gi=21389364 /ug=Hs.372429 /len=3033 NM_144583 Hs.372429 NP_653184 hypothetical protein FLJ30574 (FLJ30574), mRNA /cds=(403,1908) /gb=NM_144629 /gi=21389456 /ug=Hs.350388 /len=3113 NM_144629 Hs.350388 NP_653230 hypothetical protein MGC33371 (MGC33371), mRNA /cds=(318,1019) /gb=NM_144664 /gi=21389552 /ug=Hs.288304 /len=1399 NM_144664 Hs.288304 NP_653265 hypothetical protein MGC30052 (MGC30052), mRNA /cds=(35,703) /gb=NM_144721 /gi=21389506			/cds=(241,2553) /gb=NM_139276	NM_003150;		
(MGC32043), mRNA /cds=(8,457) /gb=NM_144582 /gi=21389354 /ug=Hs.226138 /len=3131 ATPase, H transporting, lysosomal 42kDa, V1 subunit C isoform 2 (ATP6V1C2), mRNA /cds=(21,1166) /gb=NM_144583 miod1863 NM_144583 /gi=21389364 /ug=Hs.372429 /len=3033 NM_144583 Hs.372429 NP_653184 hypothetical protein FLJ30574 (FLJ30574), mRNA /cds=(403,1908) /gb=NM_144629 seob9772 NM_144629 /gi=21389456 /ug=Hs.350388 /len=3113 NM_144629 Hs.350388 NP_653230 hypothetical protein MGC33371 (MGC33371), mRNA /cds=(318,1019) /gb=NM_144664 /gi=21389552 hypothetical protein MGC30052 (MGC30052), mRNA /cds=(35,703) /gb=NM_144721 /gi=21389506	fcr4699	NM_139276	/gi=21618339 /ug=Hs.321677 /len=3455	NM_139276	Hs.321677	NP_644805
Interpolate			hypothetical protein MGC32043			
fcrb9684 NM_144582 /ug=Hs.226138 /len=3131 NM_144582 Hs.226138 NP_653183 ATPase, H transporting, lysosomal 42kDa, V1 subunit C isoform 2 (ATP6V1C2), mRNA /cds=(21,1166) /gb=NM_144583 miod1863 NM_144583 /gi=21389364 /ug=Hs.372429 /len=3033 NM_144583 Hs.372429 NP_653184 hypothetical protein FLJ30574 (FLJ30574), mRNA /cds=(403,1908) /gb=NM_144629 /gi=21389456 /ug=Hs.350388 /len=3113 NM_144629 Hs.350388 NP_653230 hypothetical protein MGC33371 (MGC33371), mRNA /cds=(318,1019) /gb=NM_144664 /gi=21389552 /ug=Hs.288304 /len=1399 NM_144664 Hs.288304 NP_653265 hypothetical protein MGC30052 (MGC30052), mRNA /cds=(35,703) /gb=NM_144721 /gi=21389506			(MGC32043), mRNA /cds=(8,457)			
ATPase, H transporting, lysosomal 42kDa, V1 subunit C isoform 2 (ATP6V1C2), mRNA /cds=(21,1166) /gb=NM_144583			/gb=NM_144582 /gi=21389354			
V1 subunit C isoform 2 (ATP6V1C2), mRNA /cds=(21,1166) /gb=NM_144583 miod1863 NM_144583 /gi=21389364 /ug=Hs.372429 /len=3033 NM_144583 Hs.372429 NP_653184 hypothetical protein FLJ30574 (FLJ30574), mRNA /cds=(403,1908) /gb=NM_144629 seob9772 NM_144629 /gi=21389456 /ug=Hs.350388 /len=3113 NM_144629 Hs.350388 NP_653230 hypothetical protein MGC33371 (MGC33371), mRNA /cds=(318,1019) /gb=NM_144664 /gi=21389552 hypothetical protein MGC30052 (MGC30052), mRNA /cds=(35,703) /gb=NM_144721 /gi=21389506	fcrb9684	NM_144582	/ug=Hs.226138 /len=3131	NM_144582	Hs.226138_	NP_653183
Minod Mino						
miod1863 NM_144583 /gi=21389364 /ug=Hs.372429 /len=3033 NM_144583 Hs.372429 NP_653184 hypothetical protein FLJ30574 (FLJ30574), mRNA /cds=(403,1908) /gb=NM_144629 NM_144629 Hs.350388 NP_653230 hypothetical protein MGC33371 (MGC33371), mRNA /cds=(318,1019) /gb=NM_144664 /gi=21389552 NM_144664 /gi=21389552 NM_144664 /gi=21389506 NM_144664 Hs.288304 NP_653265 NP_653265			1			
hypothetical protein FLJ30574 (FLJ30574), mRNA /cds=(403,1908) /gb=NM_144629 seob9772 NM_144629 /gi=21389456 /ug=Hs.350388 /len=3113 NM_144629 Hs.350388 NP_653230 hypothetical protein MGC33371 (MGC33371), mRNA /cds=(318,1019) /gb=NM_144664 /gi=21389552 mioc7352 NM_144664 /ug=Hs.288304 /len=1399 NM_144664 Hs.288304 NP_653265 hypothetical protein MGC30052 (MGC30052), mRNA /cds=(35,703) /gb=NM_144721 /gi=21389506			/cds=(21,1166) /gb=NM_144583			
mRNA /cds=(403,1908) /gb=NM_144629 seob9772 NM_144629 /gi=21389456 /ug=Hs.350388 /len=3113 NM_144629 Hs.350388 NP_653230 hypothetical protein MGC33371 (MGC33371), mRNA /cds=(318,1019) /gb=NM_144664 /gi=21389552 /ug=Hs.288304 /len=1399 NM_144664 Hs.288304 NP_653265 hypothetical protein MGC30052 (MGC30052), mRNA /cds=(35,703) /gb=NM_144721 /gi=21389506	miod1863	NM_144583	/gi=21389364 /ug=Hs.372429 /len=3033	NM_144583	Hs.372429	NP_653184
seob9772 NM_144629 /gi=21389456 /ug=Hs.350388 /len=3113 NM_144629 Hs.350388 NP_653230 hypothetical protein MGC33371 (MGC33371), mRNA /cds=(318,1019) /gb=NM_144664 /gi=21389552 /ug=Hs.288304 /len=1399 NM_144664 Hs.288304 NP_653265 hypothetical protein MGC30052 (MGC30052), mRNA /cds=(35,703) /gb=NM_144721 /gi=21389506 NM_144629 Hs.350388 NP_653230			hypothetical protein FLJ30574 (FLJ30574),			
hypothetical protein MGC33371 (MGC33371), mRNA /cds=(318,1019) /gb=NM_144664 /gi=21389552 mioc7352 NM_144664 /ug=Hs.288304 /len=1399 NM_144664 Hs.288304 NP_653265 hypothetical protein MGC30052 (MGC30052), mRNA /cds=(35,703) /gb=NM_144721 /gi=21389506			mRNA /cds=(403,1908) /gb=NM_144629	1		
MGC33371), mRNA /cds=(318,1019) /gb=NM_144664 /gi=21389552 mioc7352 NM_144664 /ug=Hs.288304 /len=1399 NM_144664 Hs.288304 NP_653265 NP	seob9772	NM_144629	/gi=21389456 /ug=Hs.350388 /len=3113	NM_144629	Hs.350388	NP_653230
Mg			hypothetical protein MGC33371			
mioc7352 NM_144664 /ug=Hs.288304 /len=1399 NM_144664 Hs.288304 NP_653265 hypothetical protein MGC30052 (MGC30052), mRNA /cds=(35,703) /gb=NM_144721 /gi=21389506		}		}	1	
hypothetical protein MGC30052 (MGC30052), mRNA /cds=(35,703) /gb=NM_144721 /gi=21389506						
(MGC30052), mRNA /cds=(35,703) /gb=NM_144721 /gi=21389506	mioc7352	NM_144664	/ug=Hs.288304 /len=1399	NM_144664	Hs.288304	NP_653265
/gb=NM_144721 /gi=21389506			hypothetical protein MGC30052			
			(MGC30052), mRNA /cds=(35,703)			1
miod6947 NM_144721 /ug=Hs.143692 /len=2260 NM_144721 Hs.143692 NP_653322			/gb=NM_144721 /gi=21389506			
	miod6947	NM_144721	/ug=Hs.143692 /len=2260	NM_144721	Hs.143692	NP_653322

riguic						
			thymus expressed gone 3 like (MGC15476)			
			thymus expressed gene 3-like (MGC15476), mRNA /cds=(441,1655) /gb=NM_145056		:	
fcrb6676	NINA	145056	/gi=21450823 /ug=Hs.134185 /len=2544	NM_145056	He 13/185	NP 659493
ICIDO070	INIVI	143030	similar to spermatid WD-repeat protein	14101_143030	113.104100	NF_009490
			(LOC114987), mRNA /cds=(238,1338)			
			/gb=NM_145241 /gi=21687047			
seob0409	lим	145241	/ug=Hs.133331 /len=3121	NM 145241	Hs.133331	NP 660284
	_		similar to DNA-binding protein; zinc finger		-, 11 , 1	
			protein 253 (LOC199777), mRNA			
			/cds=(130,408) /gb=NM_145297			
mioa0582	NM_	145297	/gi=21699081 /ug=Hs.334568 /len=647	NM_145297	Hs.334568	NP_660340
			Williams-Beuren Syndrome critical region			
			protein 20 copy B (WBSCR20B), mRNA			
	l		/cds=(984,1448) /gb=NM_145645			ND 00000
ncr3163	NM_	145645	/gi=21717802 /ug=Hs.406306 /len=1634	NM_145645	Hs.406306	NP_663620
			lipin 1 (LPIN1), mRNA /cds=(68,2740)			
mioa0891	NINA	145603	/gb=NM_145693 /gi=22027647 /ug=Hs.81412 /len=5363	NM_145693	Hs.81412	NP 663731
moacosi	INIVI_	_143093	desmuslin (DMN), transcript variant A, mRNA	141093	115.01412	NF_003731
			/cds=(121,4818) /gb=NM_145728	NM_015286;		
seoa7943	NM	145728	/gi=22027637 /ug=Hs.10587 /len=7343	NM 145728	Hs.10587	NP 663780
			microsomal glutathione S-transferase 1	NM_020300;	1	
			(MGST1), transcript variant 1c, mRNA	NM_145764;	1	
			/cds=(144,611) /gb=NM_145791	NM_145791;		
miob6113	NM_	_145791_	/gi=22035635 /ug=Hs.389700 /len=987	NM_145792	Hs.389700	NP_665735
	İ			NM 007217;		ŀ
			programmed cell death 10 (PDCD10),	NM_145859;		
mioa3239	NM	145850	transcript variant 2, mRNA	NM 145860	Hs.28866	NP 665859
1111040200	14141-	_140000_	transcript variant 2, mixtox	140000	113.2000	
]
			A kinase (PRKA) anchor protein (yotiao) 9	NM_005751;		
			(AKAP9), transcript variant 4, mRNA	NM_147166;		
			/cds=(223,5190) /gb=NM_147166	NM_147171;		
seob2717	NM_	147166	/gi=22538388 /ug=Hs.58103 /len=6058	NM_147185	Hs.58103	NP_671714
			mitochondrial ribosomal protein L27			
	[(MRPL27), nuclear gene encoding	NIM 046504:		
			mitochondrial protein, transcript variant 2,	NM_016504;	İ	
seoa4802	NINA	1/18571	mRNA /cds=(32,316) /gb=NM_148571 /gi=22547130 /ug=Hs.7736 /len=2472	NM_148570; NM 148571	Hs.7736	NP_683412
36044002	14101	_1403/1		14101_1400/1	1113.7730	141 _000412
			choline kinase-like (CHKL), transcript variant	1		
1			2, mRNA /cds=(185,568) /gb=NM_152253	NM 005198;		
fcr6635	NM	152253	/gi=23238260 /ug=Hs.154886 /len=4914	. -	Hs.154886	NP_689466

i iguic	ba Cont d.				
		hypothetical protein FLJ23751 (FLJ23751),			
		mRNA /cds=(121,1563) /gb=NM_152282			
fcrb3776	NM_152282	/gi=22748648 /ug=Hs.37443 /len=2994	NM_152282	Hs.37443	NP_689495
		T-box 15 (TBX15), mRNA /cds=(230,1093)			
		/gb=NM_152380 /gi=23943887	450000		
seoc5833	NM_152380	/ug=Hs.164680 /len=2782	NM_152380	Hs.164680	NP_689593
		hypothetical protein MGC39497			
		(MGC39497), mRNA /cds=(9,770)			
		/gb=NM_152436 /gi=22748922			
fcr6748	NM_152436	/ug=Hs.406728 /len=1745	NM_152436	Hs.406728	NP_689649
-		hypothetical protein FLJ37318 (FLJ37318),		-	
		mRNA /cds=(226,2025) /gb=NM_152586			
ncr3944	NM_152586	/gi=22749206 /ug=Hs.130184 /len=3114	NM_152586	Hs.130184	NP_689799
		sprouty-related, EVH1 domain containing 1			
		(SPRED1), mRNA /cds=(106,1440)			
		/gb=NM_152594 /gi=22749220			
mioc7974	NM_152594	/ug=Hs.302718 /len=3816	NM_152594	Hs.302718	NP_689807_
		hypothetical protein FLJ35382 (FLJ35382),			
		mRNA /cds=(165,1235) /gb=NM_152608			İ
ncr4545	NM_152608	/gi=22749244 /ug=Hs.99210 /len=1349	NM_152608	Hs.99210	NP_689821
		hypothetical protein FLJ32001 (FLJ32001),			
		mRNA /cds=(212,2389) /gb=NM_152609			
ncrb7600	NM_152609	/gi=22749246 /ug=Hs.288742 /len=3608	NM_152609	Hs.288742	NP_689822
		hypothetical protein FLJ30162 (FLJ30162),			
		mRNA /cds=(272,841) /gb=NM_152731			
seob5859	NM_152731	/gi=22749448 /ug=Hs.311163 /len=2278	NM_152731	Hs.311163	NP_689944
		mitochondrial translational initiation factor 3			
		(MTIF3), mRNA /cds=(237,1073)			
		/gb=NM_152912 /gi=24432096		1	
mioc0734	NM_152912	/ug=Hs.406591 /len=1693	NM_152912	Hs.406591	NP_690876
		SRY (sex determining region Y)-box 5			
		(SOX5), transcript variant B, mRNA	NM_006940;		
		/cds=(373,2625) /gb=NM_152989	NM_152989;	İ	
seob0547	NM_152989_	/gi=23308714 /ug=Hs.87224 /len=4492	NM_178010	Hs.87224	NP_821078
		hypothetical protein FLJ90754 (FLJ90754),			
2005		mRNA /cds=(677,5170) /gb=NM_153366			
ncr8995	NM_153366	/gi=23503304 /ug=Hs.8963 /len=5421	NM_153366	Hs.8963	NP_699197
_		adult retina protein (LOC153222), mRNA			
		/cds=(305,2224) /gb=NM_153607			
ncr6637	NM_153607	/gi=23957697 /ug=Hs.163725 /len=5446	NM_153607	Hs.163725	NP_705835
		tropomyosin 3 (TPM3), mRNA /cds=(52,798)			
		/gb=NM_153649 /gi=24119202	NM_152263;		
fcrb2483	NM_153649	/ug=Hs.85844 /len=2089	NM_153649	Hs.85844	NP_705935
		proteasome (prosome, macropain) 26S			
		subunit, non-ATPase, 4 (PSMD4), transcript			1
		variant 2, mRNA /cds=(63,869)			
		/gb=NM_153822 /gi=25121957	NM_002810;		
fcr3575	NM_153822	/ug=Hs.148495 /len=1508	NM_153822	Hs.148495	NP_722544
		cytosolic sialic acid 9-O-acetylesterase (CSE-	_		
seoc7373	NM_170601	C), mRNA	NM_170601		NP_733746

rigure	oa Conta.				
1		ATPase, Ca transporting, cardiac muscle,			
		slow twitch 2 (ATP2A2), transcript variant 1,	•		
		mRNA /cds=(164,3292) /gb=NM_170665	NM_001681;		:
seob7402	NM_170665	/gi=27886537 /ug=Hs.1526 /len=4205	NM_170665	Hs.1526	NP_733765
1					
					1
			NINA 000044.		
			NM_003244;	:	
			NM_170695;		
1			NM_173207;		
			NM_173208;		
		TGFB-induced factor (TALE family	NM_173209;		
		homeobox) (TGIF), transcript variant 1,	NM_173210;		
		mRNA /cds=(388,1593) /gb=NM 170695	NM 173211;		
ncr0377	NM_170695	/gi=28178842 /ug=Hs.90077 /len=2076		Hs.90077	NP_777480
		mitochondrial ribosomal protein L42			
		(MRPL42), transcript variant 3, nuclear gene		l [*]	
ļ		encoding mitochondrial protein, mRNA	NM 014050;		
		/cds=(179,607) /gb=NM_172178	NM 172177;		
micc1015	NM_172178	/gi=26667173 /ug=Hs.112110 /len=2093	NM_172178	Uc 112110	NP 751918
moarors	141VI_172170	hypothetical protein FLJ35976 (FLJ35976),	14141172170	113.112110	731310
		1 * '			
	NINA 470000	mRNA /cds=(59,601) /gb=NM_173639	NIM 472620	LID 424940	ND 775010
mlob0/46	NM_173639	/gi=27735030 /ug=Hs.131810 /len=1838	NM_173639	Hs.131810	NP_775910
		hypothetical protein MGC26717	5		
		(MGC26717), mRNA /cds=(107,1090)			
		/gb=NM_173824 /gi=28376661	l		
seob3840	NM_173824	/ug=Hs.406060 /len=1387	NM_173824	Hs.406060	NP_776185
<u>'</u>		isocitrate dehydrogenase 3 (NAD) beta			
1		(IDH3B), transcript variant 3, nuclear gene			
ŀ		encoding mitochondrial protein, mRNA	NM_006899;		
ŀ		/cds=(572,1273) /gb=NM_174856	NM_174855;		
fcr1994	NM_174856	/gi=28178818 /ug=Hs.155410 /len=1645	NM_174856	Hs.155410	NP_777281
		hypothetical protein LOC221143			
1		(LOC221143), mRNA /cds=(82,726)			
		/gb=NM_174928 /gi=28372546			
seoc2232	NM 174928	/ug=Hs.32450 /len=890	NM 174928	Hs.32450	NP 777588
3000000					
			NM_018997;	1	
seoc7006	U79258	clone 23732 mRNA, partial cds	NM_031901		NP_061870
		I			
		putative protein tyrosine phosphatase (PTEN)	}		
		mRNA, complete cds /cds=(1,1212)	1		
	l	/gb=U93051 /gi=1916351 /ug=Hs.356062			Lup 00000
seoa4670		/len=1212	NM_000314	 	NP_000305
fcr7508	X56932	23 kD highly basic protein	NM_012423	Hs.389335	NP_036555
		IFNAR gene for interferon alpha/beta			
seob9187	X60459	receptor	<u></u>		CAA42992
	·				

fcr4214	X63224	ubiquinone oxidoreductase complex CI-PDSW	NM_175818	Bt.70	NP_787012
mioc2561	XM_040708	KIAA1377 protein (KIAA1377), mRNA			XP_040708
ncrc4016	XM_046097	LOC92606 (LOC92606), mRNA			XP_046097
seob2938	XM_046827	nuclear factor I/A (NFIA), mRNA	;		NP_005586
ncrc5491	XM_046853	LOC92719 (LOC92719), mRNA		-	XP_046853
	XM_058647	similar to mitochondrial ribosomal protein L52 CG1577-PA (LOC122704), mRNA			NP_851824
	XM_084654	LOC143914 (LOC143914), mRNA similar to Tropomyosin alpha 4 chain (Tropomyosin 4) (TM30p1) (LOC157784),			XP_084654
seob3462	XM_088391	mRNA			XP_088391
fcrb1763	XM_209913	similar to ring finger protein 5 (LOC286140), mRNA			NP_872402

FIGURE 6b: OA stage specific markers for moderate OA only								
Clone Name	Genbank	Description	RefSeq	UniGene	Rep_prot			
		and Constitute A						
		acyl-Coenzyme A						
		dehydrogenase, very						
		long chain (ACADVL),						
		nuclear gene encoding mitochondrial protein,						
		mRNA /cds=(86,2053)						
		/gb=NM_000018						
		/gi=4557234						
		/ug=Hs.82208						
fcrb0131	NM_000018	/len=2219	NM_000018	Hs.82208	NP_000009			
		hiotinidaea (PTD)						
		biotinidase (BTD), mRNA /cds=(36,1667)						
		/gb=NM_000060						
		/gi=4557372		İ				
		/ug=Hs.78885						
seoa0045	NM_000060	/len=2016	NM_000060	Hs.78885	NP_000051			
		complement						
		component 2 (C2),						
		mRNA /cds=(37,2295)						
		/gb=NM_000063						
		/gi=20631970						
ncrc0644	NM_000063	/ug=Hs.2253 /len=2609	NM_000063	Hs.2253	NP_000054			
		collagen, type I, alpha						
		1 (COL1A1), mRNA						
		/cds=(120,4514)	•					
		/gb=NM_000088 /gi=14719826						
		/g=147 19820 /ug=Hs.172928						
ncrb6394	NM 000088	/len=5921	NM 000088	Hs.172928	NP_000079			
		collagen, type I, alpha		110.172020				
	•	2 (COL1A2), mRNA						
		/cds=(138,4238)						
		/gb=NM_000089						
		/gi=21536289						
20000033	NIM OCCOSO	/ug=Hs.179573	NIM GOOGG	11- 470570	ND 000000			
seoa0032	NM_000089	/len=5084 collagen, type I, alpha	NM_000089	Hs.179573	NP_000080			
		2 (COL1A2), mRNA						
		/cds=(138,4238)						
		/gb=NM_000089						
		/gi=21536289						
		/ug=Hs.179573						
mioa1097	NM_000089	/len=5084	NM_000089	Hs.179573	NP_000080			

Figure 6b	Conta.				
miob4221	NM_000130	coagulation factor V (proaccelerin, labile factor) (F5), mRNA /cds=(98,6772) /gb=NM_000130 /gi=10518500 /ug=Hs.30054 /len=6914	NM_000130	Hs.30054	NP 000121
seob0370	NM_000137	fumarylacetoacetate hydrolase (fumarylacetoacetase) (FAH), mRNA /cds=(57,1316) /gb=NM_000137 /gi=4557586 /ug=Hs.73875 /len=1447	NM 000137	Hs.73875	NP 000128
seob0200	NM 000186	H factor 1 (complement) (HF1), mRNA /cds=(74,3769) /gb=NM_000186 /gi=4504374 /ug=Hs.250651 /len=3926	NM 000186	Hs.250651	NP 000177
miob4975	NM_000204	I factor (complement) (IF), mRNA /cds=(15,1766) /gb=NM_000204 /gi=4504578 /ug=Hs.36602 /len=1963	NM_000204	Hs.36602	NP_000195
mioa1445	NM_000255	methylmalonyl Coenzyme A mutase (MUT), nuclear gene encoding mitochondrial protein, mRNA /cds=(77,2329) /gb=NM_000255 /gi=4557766 /ug=Hs.155212 /len=2798	NM_000255	Hs.155212	NP_000246

Application of: Liew, et. al. Our Docket #: 4231/2042 Figure 6b Cont'd.

Figure 6b Co	onta.				
		methylmalonyl Coenzyme A mutase (MUT), nuclear gene encoding mitochondrial protein, mRNA /cds=(77,2329) /gb=NM_000255 /gi=4557766 /ug=Hs.155212			
miod0592	NM_000255	/len=2798	NM_000255	Hs.155212	NP_000246
		non-metastatic cells 1, protein (NM23A) expressed in (NME1), mRNA /cds=(85,543) /gb=NM_000269 /gi=4557796 /ug=Hs.118638			,
seoa0054	NM_000269	/len=732	NM_000269	Hs.118638	NP_000260
seoa8348	NM 000274	ornithine aminotransferase (gyrate atrophy) (OAT), nuclear gene encoding mitochondrial protein, mRNA /cds=(55,1374) /gb=NM_000274 /gi=4557808 /ug=Hs.75485 /len=2013	NM_000274	Hs.75485	NP 000265
		peroxisome receptor 1 (PXR1), mRNA /cds=(52,1947) /gb=NM_000319 /gi=21361203 /ug=Hs.158084		110.70100	W _000200
ncrb8539	NM_000319	/len=3227	NM_000319	Hs.158084	NP_000310
		transforming growth factor, beta-induced, 68kDa (TGFBI), mRNA /cds=(48,2099) /gb=NM_000358 /gi=4507466 /ug=Hs.118787			
seob3307	NM_000358	/len=2691	NM_000358	Hs.118787	NP_000349

NM 000358	transforming growth factor, beta-induced, 68kDa (TGFBI), mRNA /cds=(48,2099) /gb=NM_000358 /gi=4507466 /ug=Hs.118787 /len=2691		Hs.118787	NP 000349
	aquaporin 1 (channel- forming integral protein, 28kDa) (AQP1), mRNA /cds=(39,848) /gb=NM_000385	_		
	/ug=Hs.76152			
NM_000385	/len=1662	NM_000385	Hs.76152	NP_000376
NM_000390	choroideremia (Rab escort protein 1) (CHM), transcript variant 2950156, mRNA /cds=(31,1992) /gb=NM_000390 /gi=9966760 /ug=Hs.2010 /len=2115	NM_000390	Hs.2010	NP_000381
NM 000391	ceroid-lipofuscinosis, neuronal 2, late infantile (Jansky- Bielschowsky disease) (CLN2), mRNA /cds=(30,1721) /gb=NM_000391 /gi=5597012 /ug=Hs.20478	NIM 000301	He 20479	ND 000383
	GM2 ganglioside activator protein (GM2A), mRNA /cds=(96,677) /gb=NM_000405 /gi=16507969 /ug=Hs.289082			NP_000382 NP_000396
	NM_000358 NM_000385	factor, beta-induced, 68kDa (TGFBI), mRNA /cds=(48,2099) /gb=NM_000358 /gi=4507466 /ug=Hs.118787 /len=2691 aquaporin 1 (channelforming integral protein, 28kDa) (AQP1), mRNA /cds=(39,848) /gb=NM_000385 /gi=4755121 /ug=Hs.76152 /len=1662 /len=16507960 /len=2115 /len=16507969 /len=16507	factor, beta-induced, 68kDa (TGFBI), mRNA /cds=(48,2099) /gb=NM_000358 /gi=4507466 /ug=Hs.118787 NM_000358 /len=2691 NM_000358 aquaporin 1 (channel-forming integral protein, 28kDa) (AQP1), mRNA /cds=(39,848) /gb=NM_000385 /gi=4755121 /ug=Hs.76152 NM_000385 /len=1662 NM_000385 /gi=9966760 NM_000390 /gi=9966760 /ug=Hs.2010 /len=2115 NM_000390 /gi=9966760 /ug=Hs.2010 /len=2115 NM_000390 /gi=996760 /ug=Hs.2010 /len=2115 NM_000390 /gi=996760 /ug=Hs.2010 /len=2115 NM_000390 /gi=996760 /ug=Hs.2010 /len=2115 NM_000390 /gi=5597012 /ug=Hs.20478 /len=3502 NM_000391 /gi=5597012 /ug=Hs.20478 /len=3502 NM_000391 /gi=5597012 /ug=Hs.20478 /len=3502 NM_000391 /gi=5597012 /ug=Hs.20478 /len=3502 NM_000391 /gi=6507969 /ug=Hs.289082	factor, beta-induced, 68kDa (TGFBI), mRNA (zds=(48,2099) (gb=NM_000358 /gi=4507466 /ug=Hs.118787 /Men=2691 NM_000358 Hs.118787 /Men=2691 NM_000358 Hs.118787 /Men=2691 NM_000358 Hs.118787 /Men=268D NM_000358 Hs.118787 /Men=268D NM_000358 /gi=4755121 /ug=Hs.76152 /Mg=Hs.76152 /Mg=Hs.76152 /Mg=Hs.76152 /Mg=Hs.76156 /Mg=NM_000390 /gi=9966760 /Mg=Hs.2010 /M

Application of: Liew, et. al. Our Docket #: 4231/2042 Figure 6b Cont'd.

Figure ob	COIR G.				
seoa8399	NM_000414	hydroxysteroid (17- beta) dehydrogenase 4 (HSD17B4), mRNA /cds=(49,2259) /gb=NM_000414 /gi=4504504 /ug=Hs.75441 /len=2593		Uo 75441	ND 000405
Se0a0399	11111_000414	/len=2595	NM_000414	Hs.75441	NP_000405
for4120	NIM 000466	peroxisome biogenesis factor 1 (PEX1), mRNA /cds=(61,3912) /gb=NM_000466 /gi=4505724 /ug=Hs.99847	\		ND 000457
fcr4129	NM_000466	/len=4343	NM_000466	Hs.99847	NP_000457
fcrb4266	NM_000500	cytochrome P450, family 21, subfamily A, polypeptide 2 (CYP21A2), mRNA /cds=(119,1606) /gb=NM_000500 /gi=20522237 /ug=Hs.278430 /len=2112	NM_000500	Hs.278430	NP_000491
fcrb3298	NM_000581	glutathione peroxidase 1 (GPX1), mRNA /cds=(319,924) /gb=NM_000581 /gi=10834975 /ug=Hs.76686 /len=1134	NM 000581	Hs.76686	NP 000572
10100290	14141_000361	transporter 1, ATP-			INP_000572
		binding cassette, sub- family B (MDR/TAP) (TAP1), mRNA /cds=(165,2591) /gb=NM_000593 /gi=24797159 /ug=Hs.352018			
miob2093	NM_000593	/len=2960	NM_000593	Hs.352018	NP_000584
miob9285	NM_000596	insulin-like growth factor binding protein 1 (IGFBP1), mRNA /cds=(166,945) /gb=NM_000596 /gi=4504614 /ug=Hs.102122 /len=1514	NM 000596	Hs.102122	NP 000587
					1.11_00001

Figure 6b Co	inta.				
		insulin-like growth			
		factor binding protein 5			
j		(IGFBP5), mRNA			
}		1.			
		/cds=(752,1570)			
		/gb=NM_000599			
		/gi=10834981			
		/ug=Hs.380833			
ncr0212	NM_000599	/len=1722	NM_000599	Hs.380833	NP_000590
11010212	14141_000399	/IEII- 1722	14141_000399	115.300033	NF_000390
		serine (or cysteine)			
		proteinase inhibitor,			
		clade A (alpha-1			
		antiproteinase,			
		antitrypsin), member 5			
		(SERPINA5), mRNA		,	
		/cds=(140,1360)		•	
		/gb=NM_000624			
		/gi=21361194			
		/ug=Hs.76353			
0.400	NINA 000004	1. •		70050	
ncr0429	NM_000624	/len=2254	NM_000624	Hs.76353	NP_000615
		latent transforming			
		growth factor beta			
		binding protein 1			
		(LTBP1), mRNA			
		/cds=(91,4275)			
		1			
		/gb=NM_000627			
		/gi=4557730	,		
		/ug=Hs.241257			
miob3320	NM_000627	/len=5075	NM_000627	Hs.241257	NP 000618
			·		
		amylo-1, 6-			
		1 -			
		glucosidase, 4-alpha-			
		glucanotransferase	NM_000028;		
		(glycogen debranching	NM_000642;	•	
		enzyme, glycogen	NM_000643;		
1		storage disease type	NM_000644;		
		III) (AGL), transcript	NM_000645;	l	
fcr6054	NM_000646	variant 6, mRNA	NM_000646	Hs.904	NP_000637
		aldehyde			· · · · · · · ·
		dehydrogenase 1			
		family, member A1			
		(ALDH1A1), mRNA			
,	}	/cds=(54,1559)		}	
		/gb=NM_000689			
		/gi=25777722			
		/ug=Hs.76392			
ncrb6462	NM_000689	/len=2116	NM_000689	Hs.76392	NP 000680
	1.1.1000000	<u> </u>	1.1.11_000000	11.10.70002	141 _000000

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Figure 60 Co	1				
seoa4739	NM_000690	aldehyde dehydrogenase 2 family (mitochondrial) (ALDH2), nuclear gene encoding mitochondrial protein, mRNA /cds=(442,1995) /gb=NM_000690 /gi=25777731 /ug=Hs.195432 /len=2445		Hs.195432	NP_000681
fcrc1311	NM 000696	aldehyde dehydrogenase 9 family, member A1 (ALDH9A1), mRNA /cds=(378,1862) /gb=NM_000696 /gi=25777738 /ug=Hs.2533 /len=2713	NM 000696	Hs.2533	NP 000687
miob3968	NM_000809	gamma-aminobutyric acid (GABA) A receptor, alpha 4 (GABRA4), mRNA /cds=(39,1703) /gb=NM_000809 /gi=4557604 /ug=Hs.248112 /len=1703			
		glutathione S- transferase M3 (brain) (GSTM3), mRNA /cds=(311,988) /gb=NM_000849 /gi=23065551	NM_000809		NP_000800
seoa9777	NM_000849	/ug=Hs.2006 /len=1572 interleukin 1 receptor, type I (IL1R1), mRNA /cds=(83,1792) /gb=NM_000877 /gi=27894331 /ug=Hs.82112			NP_000840
seoa9582	NM_000877	/len=4909	NM_000877	Hs.82112	NP_000868

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Figure 6b C	onta.		·		
ncrc6012	NM 000938	polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA /cds=(44,3568) /gb=NM_000938 /gi=4505940 /ug=Hs.296014 /len=3748	NM_000938	Hs.296014	NP 000929
		ribosomal protein L3	14000000	110.200014	
		(RPL3), mRNA /cds=(27,1238) /gb=NM_000967 /gi=16507968			
fcrb4985	NM_000967	/ug=Hs.119598 /len=1311	NM_000967	Hs.119598	NP 000958
		ribosomal protein L5 (RPL5), mRNA /cds=(63,956) /gb=NM_000969 /gi=14591908 /ug=Hs.180946	_		
mioc8766	NM_000969	/len=1033	NM_000969	Hs.180946	NP 000960
mioa8076	NM_000982	ribosomal protein L21 (RPL21), mRNA /cds=(30,512) /gb=NM_000982 /gi=18104947 /ug=Hs.431927 /len=568	NM 000982	Hs.431927	NP 000973
		ribosomal protein L21 (RPL21), mRNA /cds=(30,512) /gb=NM_000982 /gi=18104947 /ug=Hs.431927		115.451921	NF_000973
seob9869	NM_000982	/len=568	NM_000982	Hs.431927	NP_000973
ncrc9749	BC032295	clone IMAGE:3921971, mRNA, partial cds ribosomal protein L23a (RPL23A), mRNA /cds=(22,492) /gb=NM_000984 /gi=17105393		Hs.326249	NP_000974
İ		/ug=Hs.419463			
seoa0429	NM_000984	/len=546	NM_000984	Hs.419463	NP_000975

Figure 6b	Cont a.		,		
		ribosomal protein L28			
		(RPL28), mRNA			
		/cds=(43,456)			
		/gb=NM_000991			
		/gi=13904865			
		/ug=Hs.356371			
fcrb5472	NM_000991	/len=500	NM_000991	Hs.356371	NP 000982
		ribosomal protein L28			
	i	(RPL28), mRNA			
		/cds=(43,456)			
		/gb=NM_000991			
		/gi=13904865			
		/ug=Hs.356371			
fcrb3181	NM_000991	/len=500	NM_000991	Hs.356371	NP 000982
		ribosomal protein L35a		113.000071	141_000302
		(RPL35A), mRNA			
		/cds=(74,406)			
		/gb=NM_000996			
		/gi=16117790]		
		/g=10117790 /ug=Hs.288544			
ncr3339	NM 000996	/len=511	NM_000996	Hs.288544	NP 000987
11010000	14141_000990	ribosomal protein L36a-		П5.200344	NP_000907
		like (RPL36AL), mRNA			
		/cds=(95,415)			
		/gb=NM_001001			
		/gi=16306559		•	
seoa4202	NM_001001	/ug=Hs.419465 /len=537	NIM 001001	11- 440405	ND 000000
36044202	14W_001001	ribosomal protein S6	NM_001001	Hs.419465	NP_000992
		•			
		(RPS6), mRNA			
		/cds=(43,792)			
		/gb=NM_001010		İ	
		/gi=17158043			
ncrb8802	NM 001010	/ug=Hs.380843	NN 004040	11- 2000 40	ND 004004
110100002	NM_001010	/len=829	NM_001010	Hs.380843	NP_001001
	1	ribosomal protein S6			
	İ	(RPS6), mRNA			
		/cds=(43,792)			
		/gb=NM_001010			
		/gi=17158043			
		/ug=Hs.380843			
mioa2156	NM_001010	/len=829	NM_001010	Hs.380843	NP_001001
		ribosomal protein S8			
		(RPS8), mRNA			
		/cds=(24,650)			
		/gb=NM_001012			
		/gi=4506742			
		/ug=Hs.399720			
fcrb3841	NM_001012	/len=705	NM_001012	Hs.399720	NP_001003

Figure 6b	Conta.				
		ribosomal protein S11			
		(RPS11), mRNA			
		/cds=(34,510)			
		/gb=NM_001015			
		/gi=14277698]
		1 =			
	NNA 004045	/ug=Hs.182740	1114 004045	1.1 400740	
ncr2926	NM_001015	/len=594	NM_001015	Hs.182740	NP_001006
ĺ		ribosomal protein S15a			
		(RPS15A), mRNA			
		/cds=(84,476)			1
		/gb=NM_001019			
		/gi=14165468		ļ	
		/ug=Hs.433406		f	
mioa3693	NM_001019	/len=541	NM_001019	Hs.433406	NP_001010
		ribosomal protein S25	1		141 _001010
		(RPS25), mRNA			
		/cds=(64,441)			
		/gb=NM_001028			
		/gi=14591916			
		/ug=Hs.409158			
seob4303	NM_001028	/len=514	NM_001028	Hs.409158	NP_001019
		topoisomerase (DNA)			
		II alpha 170kDa			
		(TOP2A), mRNA			
		/cds=(127,4722)			1
		/gb=NM_001067			
		/gi=19913405	1		
		/ug=Hs.156346			
mioa9792	NM_001067	/len=5698	NM_001067	Hs.156346	ND 004050
1111040702	14141_00 1007	procollagen-lysine, 2-	14141_00 1007	ITS. 130340	NP_001058
		oxoglutarate 5-			
		dioxygenase 3			
		(PLOD3), mRNA			
		/cds=(323,2539)			
		/gb=NM_001084			
		/gi=21361165			
		/ug=Hs.153357			
fcrb6740	NM_001084	/len=2852	NM_001084	Hs.153357	NP 001075
		actin, beta (ACTB),	1		
		mRNA /cds=(74,1201)	1		
			ļ		
		/gb=NM_001101	1		
ì	1	/gi=5016088		}	
		/ug=Hs.426930	l	1	
hfcr2832	NM_001101	/len=1793	NM_001101	Hs.426930	NP_001092
	1	actin, beta (ACTB),	İ		
		mRNA /cds=(74,1201)	ļ		
1		/gb=NM_001101			
		/gi=5016088			
		/ug=Hs.426930			
ncrc9637	NM_001101	/len=1793	NM_001101	Hs.426930	NP_001092
					

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Figure 6b	Contid.				
mioc4888	NM_001101	actin, beta (ACTB), mRNA /cds=(74,1201) /gb=NM_001101 /gi=5016088 /ug=Hs.426930 /len=1793	NM_001101	Hs.426930	NP_001092
hfcr5970	NM 001103	actinin, alpha 2 (ACTN2), mRNA /cds=(174,2858) /gb=NM_001103 /gi=4501892 /ug=Hs.83672 /len=4181	NM_001103	Hs.83672	NP 001094
11103970	14W_001103	adrenomedullin (ADM), mRNA /cds=(157,714) /gb=NM_001124 /gi=4501944		115.03072	NP_001094
ncr3442	NM_001124	(-	NM_001124	Hs.394	NP 001115
ncrc4780	NM_001124	adrenomedullin (ADM), mRNA /cds=(157,714) /gb=NM_001124 /gi=4501944 /ug=Hs.394 /len=1449	NM_001124	Hs.394	NP 001115
seoa4608	NM_001159	aldehyde oxidase 1 (AOX1), mRNA /cds=(299,4315) /gb=NM_001159 /gi=6598319 /ug=Hs.406238 /len=5125	NM_001159	Hs.406238	NP 001150
		basic transcription element binding protein 1 (BTEB1), mRNA /cds=(1265,1999) /gb=NM_001206 /gi=4557374 /ug=Hs.150557			
ncrb4351	NM_001206	/len=4859	NM_001206	Hs.150557	NP_001197
mioc3671	NM_001239	cyclin H (CCNH), mRNA /cds=(233,1204) /gb=NM_001239 /gi=17738313 /ug=Hs.514 /len=1398	NM_001239	Hs.514	NP 001230
		1.49 .10.07 .700	100 1200	11.10.017	1111 _00 1200

oyclin T1 (CCNT1), mRNA /cds=(324,2604) /gb=NM_001240 /gl=17978465 /ug=Hs.279906 NM_001240 /len=2568 NM_001240 NM_001240 NM_001240 NM_001253 /gl=16357499 /ug=Hs.155174 NM_001253 /gl=16357499 /ug=Hs.155174 NM_001253 /len=3012 Chromodomain helicase DNA binding protein 2 (CHD2), mRNA /cds=(708,5927) /gb=NM_001271 /gl=4557448 /ug=Hs.36787 NM_001271 /len=7764 NM_001271 NM_001271 /gl=4557448 /ug=Hs.36787 NM_001271 /gl=4557448 /ug=Hs.36787 NM_001310	Figure 6b Co	ntd.				
mRNA /cds=(324,2504) /gb=NM_001240 /gi=17978465 /ug=Hs.279906 /ug=Hs.279906 /ug=Hs.279906 /ug=Hs.279906 /ug=Hs.279906 /ug=Hs.279906 /ug=Hs.279906 /ug=Hs.279906 /ug=Hs.279906 /ug=Hs.279906 /ug=Hs.279906 /ug=Hs.279906 /ug=Hs.279906 /ug=Hs.279906 /ug=Hs.279906 /ug=Hs.27999 /ug=Hs.27999 /ug=Hs.27999 /ug=Hs.27999 /ug=Hs.27999 /ug=Hs.27999 /ug=Hs.27999 /ug=Hs.27999 /ug=Hs.27999 /ug=Hs.27999 /ug=Hs.27999 /ug=Hs.27999 /ug=Hs.27999 /ug=Hs.27999 /ug=Hs.27999 /ug=Hs.27999 /ug=Hs.279999 /ug=Hs.279999 /ug=Hs.2799999 /ug=Hs.2799999 /ug=Hs.2799999 /ug=Hs.27999999 /ug=Hs.27999999999999999999999999999999999999		<u> </u>	cyclin T1 (CCNT1),			
/cds=(324,2604) /gb=NM_001240 /gb=NM_001240 /gb=NM_001240 /gb=NM_001240 /gb=NM_001240 /gb=Hs.279906 NP_001231 CDC5 cell division			· · · · · · · · · · · · · · · · · · ·			
Agb=NM_001240 Agi=17978465 Aig=18.279906 Agi=17978465 Aig=18.279906 Agi=17978465 Aig=18.279906 Agi=18.279906						
/gi=17978465 /ug=Hs.279906						
NM_001240 NM_001240 NM_001240 NM_001240 NP_001231			/gb=NM_001240			
NM_001240 NM_001240 NM_001240 NM_001240 NP_001231			/gi=17978465			
ncr6745 NM_001240 /len=2568 NM_001240 Hs.279906 NP_001231			1 -			
CDC5 cell division cycle 5-like (S. pombe) (CDC5L), mRNA /cds=(260,2668) /gb=NM_001253 /gi=16357499 /ug=Hs.155174 /len=3012 NM_001253 Hs.155174 NP_001244 chromodomain helicase DNA binding protein 2 (CHD2), mRNA /cds=(708,5927) /gb=NM_001271 /gi=4557448 /ug=Hs.36787 NP_001262 cAMP responsive element binding protein like 2 (CREBL2), mRNA /cds=(277,639) /gb=NM_001310 /gi=21536277 /ug=Hs.13313 /len=3748 NM_001310 Hs.13313 NP_001301 aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxysteroid dehydrogenase, type III) (AKR1C2), mRNA /cds=(23,94) /gb=NM_001354 /gi=24497581 /ug=Hs.201967						
cycle 5-like (S. pombe) ((CDC5L), mRNA /cds=(260,2688) /gb=NM_001253 /gj=16357499 /ug=Hs.155174 /len=3012	ncr6745	NM_001240	/len=2568	NM_001240	Hs.279906	NP_001231
cycle 5-like (S. pombe) ((CDCSL), mRNA /cds=(260,2688) /gb=NM_001253 /gj=16357499 /ug=Hs.155174 /len=3012						
cycle 5-like (S. pombe) ((CDC5L), mRNA /cds=(260,2688) /gb=NM_001253 /gj=16357499 /ug=Hs.155174 /len=3012 NM_001253 Hs.155174 NP_001244 helicase DNA binding protein 2 (CHD2), mRNA /cds=(708,5927) /gb=NM_001271 /gj=4557448 /ug=Hs.36787 NM_001271 Hs.36787 NP_001262 cAMP responsive element binding protein like 2 (CREBL2), mRNA /cds=(27,7639) /gb=NM_001310 /gj=21536277 /ug=Hs.13313 NM_001310 Hs.13313 NP_001301			CDC5 cell division			
(CDC5L), mRNA /cds=(260,2668) /gb=NM_001253 /gi=16357499 //ug=Hs.155174 //miod6488 NM_001253 //me=3012 NM_001253 //me=3012 NM_001253 //me=3012 NM_001253 //me=3012 NM_001253 //me=3012 NM_001253 //me=3012 NM_001253 //me=3012 NM_001253 //me=3012 NM_001253 //me=3012 NM_001253 //me=3012 NM_001253 //me=3012 NM_001271 //me=3012 NM_001271 //me=3012 NM_001271 //me=3012 NM_001271 //me=3012 NM_001310 //me=3012 NM			1			
Icds=(260,2668) Icds=(260,						
/gb=NM_001253 /gi=16357499 /ug=Hs.155174 /len=3012 NM_001253 Hs.155174 NP_001244 /len=3012 NM_001253 Hs.155174 NP_001244 /len=3012 NM_001253 Hs.155174 NP_001244 /len=3012 /len=3012 NM_001253 Hs.155174 NP_001244 /len=3012 /len=	1		(CDC5L), mRNA			
/gb=NM_001253 /gi=16357499 /ug=Hs.155174 /len=3012 NM_001253 Hs.155174 NP_001244 /len=3012 NM_001253 Hs.155174 NP_001244 /len=3012 NM_001253 Hs.155174 NP_001244 /len=3012 /len=3012 NM_001253 Hs.155174 NP_001244 /len=3012 /len=	1		/cds=(260,2668)			
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Minde Mind						
MM_001253 /len=3012 NM_001253 Hs.155174 NP_001244						
MM_001253 /len=3012 NM_001253 Hs.155174 NP_001244			/ug=Hs.155174			
Chromodomain helicase DNA binding protein 2 (CHD2), mRNA /cds=(708,5927) /gb=NM_001271 /gi=4557448 /ug=Hs.36787 /len=7764 NM_001271 Hs.36787 NP_001262	miod6488	NM 001253		NM 001253	Hs 155174	NP 001244
helicase DNA binding protein 2 (CHD2), mRNA /cds=(708,5927) /gb=NM_001271 /gi=4557448 /ug=Hs.36787 /len=7764 CAMP responsive element binding protein like 2 (CREBL2), mRNA /cds=(277,639) /gb=NM_001310 /gi=21536277 /ug=Hs.13313 mioa4818 NM_001310 MI_00	1111040-100	1111_001200		14.41_00 1200	110.100174	141 _001244
protein 2 (CHD2), mRNA /cds=(708,5927) /gb=NM_001271 /gi=4557448 /ug=Hs.36787 /len=7764 cAMP responsive element binding protein like 2 (CREBL2), mRNA /cds=(277,639) /gb=NM_001310 /gi=21536277 /ug=Hs.13313 mioa4818 NM_001310 NM_0						
mRNA /cds=(708,5927) /gb=NM_001271 /gi=4557448 /ug=Hs.36787 /len=7764 CAMP responsive element binding protein like 2 (CREBL2), mRNA /cds=(277,639) /gb=NM_001310 /gi=21536277 /ug=Hs.13313 mioa4818 NM_001310 Iden=3748 NM_001310 Men=3748 NM_001310 Aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3- alpha hydroxysteroid dehydrogenase, type III) (AKR1C2), mRNA /cds=(23,994) /gb=NM_001354 /gi=24497581 /ug=Hs.201967			nelicase DNA binding			·
mRNA /cds=(708,5927) /gb=NM_001271 /gi=4557448 /ug=Hs.36787 /len=7764 CAMP responsive element binding protein like 2 (CREBL2), mRNA /cds=(277,639) /gb=NM_001310 /gi=21536277 /ug=Hs.13313 mioa4818 NM_001310 Iden=3748 NM_001310 Men=3748 NM_001310 Aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3- alpha hydroxysteroid dehydrogenase, type III) (AKR1C2), mRNA /cds=(23,994) /gb=NM_001354 /gi=24497581 /ug=Hs.201967			protein 2 (CHD2).			
/cds=(708,5927) /gb=NM_001271 /gi=4557448 /ug=Hs.36787 /len=7764 NM_001271 Responsive element binding protein like 2 (CREBL2), mRNA /cds=(277,639) /gb=NM_001310 /gi=21536277 /ug=Hs.13313 /len=3748 NM_001310 NM_001310 NM_001310 NM_001310 NM_001310 NM_001310 NM_001310 NM_001310 NM_001310 NM_001310 Hs.13313 NP_001301 Aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3- alpha hydroxysteroid dehydrogenase, type III) (AKR1C2), mRNA /cds=(23,994) /gb=NM_001354 /gi=24497581 /ug=Hs.201967						
/gb=NM_001271						
Vgi=4557448				·		
Vgi=4557448			/gb=NM_001271			
NM_001271 NM_001271 NM_001271 Hs.36787 NP_001262			-			
Seoc2205 NM_001271			1 ~			
cAMP responsive element binding protein like 2 (CREBL2), mRNA /cds=(277,639) /gb=NM_001310 /gi=21536277 /ug=Hs.13313 mioa4818 NM_001310 Ien=3748 NM_001310 Ien=3748 NM_001310 Ien=3748 NM_001310 Ien=3748 NM_001310 Ien=3748 Ien=			. —			
element binding protein like 2 (CREBL2), mRNA /cds=(277,639) /gb=NM_001310 /gi=21536277 /ug=Hs.13313 NM_001310 Hs.13313 NP_001301 aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2, bile acid binding protein; 3-alpha hydroxysteroid dehydrogenase, type III) (AKR1C2), mRNA /cds=(23,994) /gb=NM_001354 /gi=24497581 /ug=Hs.201967	seoc2205	NM_001271	/ien=//64	NM_001271	Hs.36787	NP_001262
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like 2 (CREBL2), mRNA /cds=(277,639) /gb=NM_001310 /gi=21536277 /ug=Hs.13313 mioa4818 NM_001310 /len=3748 NM_001310 Aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2, bile acid binding protein; 3- alpha hydroxysteroid dehydrogenase, type III) (AKR1C2), mRNA /cds=(23,994) /gb=NM_001354 /gi=24497581 /ug=Hs.201967	1					
mRNA /cds=(277,639) /gb=NM_001310 /gi=21536277 /ug=Hs.13313 mioa4818 NM_001310 /len=3748 NM_001310 Aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxysteroid dehydrogenase, type III) (AKR1C2), mRNA /cds=(23,994) /gb=NM_001354 /gi=24497581 /ug=Hs.201967						
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mioa4818 NM_001310 //en=3748 NM_001310 Hs.13313 NP_001301 aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxysteroid dehydrogenase, type III) (AKR1C2), mRNA //cds=(23,994) //gb=NM_001354 //gi=24497581 //ug=Hs.201967						
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aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3- alpha hydroxysteroid dehydrogenase, type III) (AKR1C2), mRNA /cds=(23,994) /gb=NM_001354 /gi=24497581 /ug=Hs.201967	mioa4818	NM 001310	/len=3748	NM 001310	Hs.13313	NP 001301
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(dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxysteroid dehydrogenase, type III) (AKR1C2), mRNA /cds=(23,994) /gb=NM_001354 /gi=24497581 /ug=Hs.201967						
dehydrogenase 2; bile acid binding protein; 3- alpha hydroxysteroid dehydrogenase, type III) (AKR1C2), mRNA /cds=(23,994) /gb=NM_001354 /gi=24497581 /ug=Hs.201967						
dehydrogenase 2; bile acid binding protein; 3- alpha hydroxysteroid dehydrogenase, type III) (AKR1C2), mRNA /cds=(23,994) /gb=NM_001354 /gi=24497581 /ug=Hs.201967			[(dihydrodiol			
acid binding protein; 3- alpha hydroxysteroid dehydrogenase, type III) (AKR1C2), mRNA /cds=(23,994) /gb=NM_001354 /gi=24497581 /ug=Hs.201967						
alpha hydroxysteroid dehydrogenase, type III) (AKR1C2), mRNA /cds=(23,994) /gb=NM_001354 /gi=24497581 /ug=Hs.201967						
dehydrogenase, type III) (AKR1C2), mRNA /cds=(23,994) /gb=NM_001354 /gi=24497581 /ug=Hs.201967						
III) (AKR1C2), mRNA /cds=(23,994) /gb=NM_001354 /gi=24497581 /ug=Hs.201967						
III) (AKR1C2), mRNA /cds=(23,994) /gb=NM_001354 /gi=24497581 /ug=Hs.201967			dehydrogenase, type			
/cds=(23,994) /gb=NM_001354 /gi=24497581 /ug=Hs.201967						
/gb=NM_001354 /gi=24497581 /ug=Hs.201967			1 7 7			
/gi=24497581 /ug=Hs.201967						
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Application of: Liew, et. al. Our Docket #: 4231/2042 Figure 6b Cont'd.

Figure 6b Co	onta.				
		aldo-keto reductase			
		family 1, member C2			
		(dihydrodiol			
		dehydrogenase 2; bile			1
		acid binding protein; 3-			
		alpha hydroxysteroid			
		dehydrogenase, type			
		III) (AKR1C2), mRNA			
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		1			
		/gb=NM_001354			
		/gi=24497581			
		/ug=Hs.201967			
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		dihydropyrimidinase-			
		like 2 (DPYSL2),	}		
		mRNA			
		/cds=(275,1993)			
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		/gi=19923654			
		/ug=Hs.173381			
seob4972	NM_001386	/len=4459	NM 001386	Hs.173381	NP 001377
		enoyl Coenzyme A			
		hydratase 1,			
		peroxisomal (ECH1),			
		mRNA /cds=(28,1014)			
		/gb=NM_001398			
		/gi=4503446			
fo=0704	NINA 004200	/ug=Hs.196176	NIA 004000	11 100170	
fcr0781	NM_001398	/len=1196	NM_001398	Hs.196176	NP_001389
ļ					
		eukaryotic translation			
	1	elongation factor 1			
		alpha 1 (EEF1A1),			
		mRNA /cds=(63,1451)			
		. /gb=NM_001402			
		/gi=25453469			
		/ug=Hs.422118			·
fcrb2346	NM_001402	/len=1837	NM_001402	Hs.422118	NP 001393
					
		eukaryotic translation			
		elongation factor 1		1	
		alpha 1 (EEF1A1),			
		mRNA /cds=(63,1451)		1	
		/gb=NM_001402			
		/gi=25453469			
foro1115	NM 004400	/ug=Hs.422118	NIM 004400	115 400440	ND 004000
fcrc1115	NM_001402	/len=1837	NM_001402	Hs.422118	NP_001393

Application of: Liew, et. al. Our Docket #: 4231/2042 Figure 6b Cont'd.

Cont'd.		,		
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	/gb=NM_001439			
	/gi=14149608			
	/ug=Hs.61152			
NM 001439	/len=2833	NM 001439	Hs.61152	NP 001430
	four and a half LIM			
	domains 1 (FHL1).			
	mRNA `			
	/cds=(218,1060)			
	1 · _			
	1 -			
NM 001449		NM 001449	Hs 239069	NP 001440
1111_001410		14111_001440	113.20000	141 _001440
	· ·			
	1			
	1.			
BC028089	•		He 105464	NP 001447
DC020003			113.133404	INF_001447
	_			
	1 · · · · · · · · · · · · · · · · · · ·			
	1 -			
NIM 004 404	, •			
NWI_001461		NM_001461	Hs.14286	NP_001452
	1.			
	1 -			
	1 9			
NM_001463		NM_001463	Hs.153684	NP_001454
	• • • • • • • • • • • • • • • • • • • •			
	/gb=NM_001514	ļ		
	/gi=13435384	,		
	/ug=Hs.258561			
NM_001514	/len=1268	NM_001514	Hs.258561	NP_001505
	general transcription			
	factor IIB (GTF2B),			
	mRNA /cds=(39,989)			
	/gb=NM_001514			
	/gi=13435384			
	/ug=Hs.258561			
NM_001514	/len=1268	NM 001514	Hs.258561	NP 001505
	NM_001449 BC028089 NM_001461 NM_001463 NM_001514	exostoses (multiple)- like 2 (EXTL2), mRNA /cds=(288,1280) /gb=NM_001439 /gi=14149608 /ug=Hs.61152 /len=2833 four and a half LIM domains 1 (FHL1), mRNA /cds=(218,1060) /gb=NM_001449 /gi=21361121 /ug=Hs.239069 NM_001449 /len=2407 Similar to filamin A, alpha (actin binding protein 280), clone IMAGE:4156935, mRNA flavin containing monoxygenase 5 (FMO5), mRNA /cds=(82,1683) /gb=NM_001461 /gi=4503760 /ug=Hs.14286 NM_001461 /len=2326 frizzled-related protein (FRZB), mRNA /cds=(209,1186) /gb=NM_001463 /gi=4503788 /ug=Hs.153684 NM_001463 /len=1476 general transcription factor IIB (GTF2B), mRNA /cds=(39,989) /gb=NM_001514 /gi=13435384 /ug=Hs.258561 NM_001514 /len=1268 general transcription factor IIB (GTF2B), mRNA /cds=(39,989) /gb=NM_001514 /gi=13435384 /ug=Hs.258561	exostoses (multiple)- like 2 (EXTL2), mRNA /cds=(288,1280) /gb=NM_001439 /gi=14149608 /ug=Hs.61152 /len=2833 NM_001439 four and a half LIM domains 1 (FHL1), mRNA /cds=(218,1060) /gb=NM_001449 /gi=21361121 /ug=Hs.239069 NM_001449 /gi=2407 NM_001449 /gi=21361121 /ug=Hs.239069 NM_001449 /len=2407 NM_001449 /len=2407 NM_001449 /len=2407 NM_001449 /len=2407 NM_001449 /len=2407 NM_001449 /len=2407 NM_001449 /len=2407 NM_001449 /len=2407 NM_001449 /len=2407 NM_001449 /len=2407 NM_001449 /len=2407 NM_001449 /len=2407 NM_001449 /len=2407 NM_001449 /len=2407 /len=2407 /len=2407 /len=2407 /len=2407 /len=2407 /len=2408 /len=2408 /len=2408 /len=2326 /len=2326 /len=2326 /len=2326 /len=2326 /len=2326 /len=2326 /len=3268 /len=3268 /len=4176 /len=476 /len=476 /len=476 /len=476 /len=476 /len=476 /len=476 /len=476 /len=1476 /len=1476 /len=1476 /len=1468 /len=1476 /len=1268 /len=1476 /len=1268 /len=1268 /len=1268 /len=1268 /len=1268 /len=1268 /len=1268 /len=1268 /len=1268 /len=1268 /len=1268 /len=1268 /len=2	exostoses (multiple)- like 2 (EXTL2), mRNA /cds=(288,1280) /gb=NM_001439 /gi=14149608 /ug=Hs.61152 /len=2833 NM_001439 /len=2833 NM_001439 /len=2833 NM_001439 /len=2833 NM_001439 /len=2833 NM_001439 /len=2833 NM_001439 /len=2831 NM_001449 /len=21361121 /ug=Hs.239069 /len=2407 NM_001449 /len=2407 NM_001449 /len=2407 NM_001449 /len=2407 NM_001449 /len=2407 NM_001449 /len=2407 NM_001449 /len=2407 NM_001449 /len=2407 NM_001449 /len=2407 NM_001449 /len=2407 NM_001449 /len=2407 NM_001449 /len=2407 NM_001449 /len=2407 NM_001449 /len=2407 NM_001449 /len=2407 NM_001449 /len=2407 NM_001449 /len=2407 NM_001449 /len=4503760 /len=4503760 /len=4503760 /len=4503768 /len=4503768 /len=4503768 /len=4176 NM_001463 /len=4176 NM_001463 /len=4176 NM_001463 /len=4176 NM_001463 /len=1476 NM_001463 /len=1476 NM_001514 /len=1268 NM_001

Figure ob Co	onta.				
		general transcription			
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		(GTF3C2), mRNA			
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		/ug=Hs.75782			
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110100010	11111_001021	7.0.1. 000 1	11111_001021	113.70702	- 141 _001012
		hant about 27kDs			
		heat shock 27kDa			
		protein 1 (HSPB1),			
		mRNA /cds=(108,725)			
		/gb=NM_001540			
		/gi=4996892			1
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200h6260	A D007025		NIM 004540	11- 04004	ND 004500
seob6268	AB007935	protein, partial cds	NM_001542	Hs.81234	NP_001533
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		(ICT1), mRNA			
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		/gb=NM_001545			
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seoa6175	NM 001545	1 -	NIM 001545	Un 0070	ND 004520
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		alpha 1 (IL13RA1),			
		mRNA /cds=(44,1327)			
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	1	/ug=Hs.285115			
seob4945	NM_001560	/len=4006	NIM OO1560	Un 205115	ND 004554
36004340	14141 00 1000		NM_001560	Hs.285115	NP_001551
	1	eukaryotic translation			
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		subunit 6 48kDa			
	1	(EIF3S6), mRNA			
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	1	/gb=NM 001568			
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		muscle, aorta	1		
		(ACTA2), mRNA			
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		1 -	,		
	NN4 004040	/ug=Hs.195851		<u>.</u>	
ncrb3585	NM_001613	/len=1330	NM_001613	Hs.195851	NP_001604

Figure 6b Co	onica.	T*			<u>, — </u>
seob7906	NM_001642	amyloid beta (A4) precursor-like protein 2 (APLP2), mRNA /cds=(73,2364) /gb=NM_001642 /gi=4502146 /ug=Hs.279518 /len=3727	NM_001642	Hs.279518	NP_001633
		ATP synthase, H transporting, mitochondrial F0 complex, subunit F6 (ATP5J), nuclear gene encoding mitochondrial protein, mRNA /cds=(693,1019) /gb=NM_001685 /gi=19913429 /ug=Hs.73851			
miob6615	NM_001685	/len=1178	NM_001685	Hs.73851	NP_001676
fcr4166	BC016512	Similar to ATP synthase, H transporting, mitochondrial F1 complex, beta polypeptide, clone MGC:5231 IMAGE:2900336, mRNA, complete cds	NM_001686	Hs.406510	NP_001677
fcrc0591	NM_001686	ATP synthase, H transporting, mitochondrial F1 complex, beta polypeptide (ATP5B), nuclear gene encoding mitochondrial protein, mRNA /cds=(46,1665) /gb=NM_001686 /gi=4502294 /ug=Hs.406510 /len=1807	NM_001686	Hs.406510	ND 001677
10,00001	114141 00 1000	1/10/1-1007	[14141 OO 1000	113.400010	NP_001677

Figure 60 Co	JILU.				
mioc4534	NM_001686	ATP synthase, H transporting, mitochondrial F1 complex, beta polypeptide (ATP5B), nuclear gene encoding mitochondrial protein, mRNA /cds=(46,1665) /gb=NM_001686 /gi=4502294 /ug=Hs.406510 /len=1807	NM_001686	Hs.406510	NP_001677
seob6758	NM_001688	ATP synthase, H transporting, mitochondrial F0 complex, subunit b, isoform 1 (ATP5F1), mRNA /cds=(98,868) /gb=NM_001688 /gi=21361564 /ug=Hs.81634 /len=1230	NM_001688	Hs.81634	NP_001679
		ATP synthase, H transporting, mitochondrial F0 complex, subunit b, isoform 1 (ATP5F1), mRNA /cds=(98,868) /gb=NM_001688 /gi=21361564 /ug=Hs.81634			
ncrc7127 fcrc6228	NM_001688	/len=1230 B-cell translocation gene 1, anti- proliferative (BTG1), mRNA /cds=(309,824) /gb=NM_001731 /gi=4502472 /ug=Hs.77054 /len=1783	NM_001688 NM_001731	Hs.81634 / Hs.77054	NP_001679 NP_001722
ncr3165	NM_001743	calmodulin 2 (phosphorylase kinase, delta) (CALM2), mRNA /cds=(69,518) /gb=NM_001743 /gi=20428653 /ug=Hs.425808 /len=1128	NM_001743	Hs.425808	NP_001734

Figure ob C	Offica.			- , 	
		calpain 2, (m/II) large subunit (CAPN2), mRNA /cds=(143,2245) /gb=NM_001748 /gi=12408645 /ug=Hs.76288			
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		chaperonin containing TCP1, subunit 6A (zeta 1) (CCT6A), mRNA /cds=(56,1651) /gb=NM_001762 /gi=22095341 /ug=Hs.82916			
seoa9627	NM_001762	/len=2562	NM_001762	Hs.82916	NP_001753
		cyclin-dependent kinase 7 (MO15 Xenopus laevis, cdk- activating kinase) (CDK7), mRNA /cds=(89,1129) /gb=NM_001799 /gi=16950659 /ug=Hs.184298			
mioa4667	NM_001799	/len=1427	NM_001799	Hs.184298	NP_001790
seoa2004	NM_001826	CDC28 protein kinase regulatory subunit 1B (CKS1B), mRNA /cds=(10,249) /gb=NM_001826 /gi=4502856 /ug=Hs.348669 /len=717	NM 001826	Hs.348669	NP 001917
SEU42004		//6/1-///	111111_00 1826	IDS.348009	NP_001817
forb7525	NIM 004846	collagen, type IV, alpha 2 (COL4A2), mRNA /cds=(289,5427) /gb=NM_001846 /gi=17986276 /ug=Hs.75617		U- 75047	ND 004007
fcrb7535	NM_001846	/len=6276	NM_001846	Hs.75617	NP_001837

Figure ob C	John G.				
seoc2218	NM_001863	cytochrome c oxidase subunit VIb (COX6B), nuclear gene encoding mitochondrial protein, mRNA /cds=(163,423) /gb=NM_001863 /gi=17999530 /ug=Hs.431668 /len=578	NM_001863	Hs.431668	, NP_001854
seoa4708	NM_001865	cytochrome c oxidase subunit VIIa polypeptide 2 (liver) (COX7A2), nuclear gene encoding mitochondrial protein, mRNA /cds=(76,327) /gb=NM_001865 /gi=18105035 /ug=Hs.70312 /len=470	NM_001865	Hs.70312	NP_001856
seob0876	NM_001865	cytochrome c oxidase subunit VIIa polypeptide 2 (liver) (COX7A2), nuclear gene encoding mitochondrial protein, mRNA /cds=(76,327) /gb=NM_001865 /gi=18105035 /ug=Hs.70312 /len=470	NM_001865	Hs.70312	NP_001856
miod1714	NM_001892	casein kinase 1, alpha 1 (CSNK1A1), mRNA /cds=(140,1153) /gb=NM_001892 /gi=19923745 /ug=Hs.283738 /len=2080	NM_001892	Hs.283738	NP_001883
ncr0679	NM_001932	membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3) (MPP3), mRNA /cds=(337,2094) /gb=NM_001932 /gi=21536463 /ug=Hs.423809 /len=3012	NM_001932	Hs.423809	NP_001923

rigure ob	Conta.				
		dermatopontin, clone MGC:45278 IMAGE:5176855,			
ncrc4219	BC033736	mRNA, complete cds		Hs.80552	NP 001928
		dermatopontin (DPT), mRNA /cds=(7,612) /gb=NM_001937 /gi=4755134			
mioa2290	NM_001937	/ug=Hs.80552 /len=71	7 NM_001937	Hs.80552	NP_001928
miod1108	NM 001040	E2F transcription facto 3 (E2F3) mRNA, complete cds /cds=(67,1464) /gb=NM_001949 /gi=12669913		Uo 1190	NID 004040
miod i 108	NM_001949	/ug=Hs.1189 /len=4744	4[NIVI_001949	Hs.1189	NP_001940
		E2F transcription facto 3 (E2F3) mRNA, complete cds /cds=(67,1464) /gb=NM_001949 /gi=12669913	r		
seob6041	NM_001949	/ug=Hs.1189 /len=4744	NM 001949	Hs.1189	NP 001940
		eukaryotic translation elongation factor 2 (EEF2), mRNA /cds=(69,2645) /gb=NM_001961 /gi=25453476 /ug=Hs.75309			M _001040
fcrb2979	NM_001961	/len=3148	NM_001961	Hs.75309	NP_001952
		early growth response 1 (EGR1), mRNA /cds=(271,1902) /gb=NM_001964 /gi=4503492 /ug=Hs.326035			
fcrb8215	NM_001964	/len=3132	NM_001964	Hs.326035	NP_001955
		farnesyltransferase, CAAX box, alpha (FNTA), mRNA /cds=(7,1146) /gb=NM_002027 /gi=4503770 /ug=Hs.356463			
seoa6155	NM_002027	/len=1644	NM_002027	Hs.356463	NP_002018

	onta.			·	
		ferritin, heavy polypeptide 1 (FTH1), mRNA /cds=(92,664)			
		/gb=NM_002032 /gi=4503794			
		/ug=Hs.418650			
fcrb1329	NM_002032	/len=801	NM_002032	Hs.418650	NP_002023
		ferritin, heavy polypeptide 1 (FTH1),			
		mRNA /cds=(92,664)			
		/gb=NM_002032			
		/gi=4503794			
		/ug=Hs.418650			
seob8333	NM_002032	/len=801	NM_002032	Hs.418650	NP_002023
		glyceraldehyde-3-			
		phosphate dehydrogenase			İ
		(GAPD), mRNA			ľ
		/cds=(76,1083)			
		/gb=NM_002046		:	
		/gi=7669491			
		/ug=Hs.169476			
fcr1772	NM_002046	/len=1283	NM_002046	Hs.169476	NP_002037
		glutamine-fructose-6-			
		phosphate			
		transaminase 1			
		(GFPT1), mRNA			
		/cds=(123,2168)			
		/gb=NM_002056			
seob3131	NIM OCCOS	/gi=4503980	NIM COCCEC	110 4074	ND 000047
Seobs 131	NM_002056	/ug=Hs.1674 /len=3082	14141_002056	Hs.1674	NP_002047
		clone IMAGE:4391536,			
mioc1135	BC017742	mRNA	NM_002076	Hs.334534	NP 002067
fcr1404	NM_002087	granulin (GRN), mRNA		Hs.180577	NP_002078
		H factor (complement)-		1	
		like 1 (HFL1), mRNA /cds=(78,1070)			
		/gb=NM_002113			
		/gi=11321586			
,		/ug=Hs.278568			
seob9946	NM_002113	/len=1266	NM_002113	Hs.278568	NP_002104

Figure ob	Oonea.				
seob3370	NM_002124	major histocompatibility complex, class II, DR beta 1 (HLA-DRB1), mRNA /cds=(63,863) /gb=NM_002124 /gi=4504410 /ug=Hs.375570 /len=1182	NM_002124	Hs.375570	NP_002115
:		high-mobility group box 2 (HMGB2), mRNA /cds=(191,820)			
fcrb8915	NM_002129	/gb=NM_002129 /gi=14141173 /ug=Hs.80684 /len=1277	NIM 002420	LI- 90694	ND 000400
10100915		heat shock 10kDa	NM_002129	Hs.80684	NP_002120
		protein 1 (chaperonin 10) (HSPE1), mRNA /cds=(42,350) /gb=NM_002157 /gi=4504522			
ncrc5738	NM_002157	/g=4504522 /ug=Hs.1197 /len=538	NM_002157	Hs.1197	NP_002148
		heat shock 10kDa protein 1 (chaperonin 10) (HSPE1), mRNA /cds=(42,350) /gb=NM_002157 /gi=4504522			
miob2087	NM_002157	/ug=Hs.1197 /len=538 tenascin C	NM_002157	Hs.1197	NP_002148
seoa5366	NM_002160	(hexabrachion) (TNC), mRNA	NM_002160	Hs.289114	NP_002151
		integrin, beta 5 (ITGB5), mRNA /cds=(307,2706) /gb=NM_002213 /gi=20127445 /ug=Hs.149846			
mioa0485	NM_002213	/len=3401	NM_002213	Hs.149846	NP_002204
coch4660		karyopherin (importin) beta 1 (KPNB1), mRNA /cds=(337,2967) /gb=NM_002265 /gi=24797084 /ug=Hs.180446			
seob4669	NM_002265	/len=4205	NM_002265	Hs.180446	NP_002256

Application of: Liew, et. al. Our Docket #: 4231/2042 Figure 6b Cont'd.

Figure 6b Co	nt'd.				
		laminin, alpha 4			
		(LAMA4), mRNA			
		/cds=(284,5734)			
		/gb=NM_002290			
		/gi=9845494			
		/ug=Hs.78672			
hfcr1716	NM_002290	/len=6297	NM_002290	Hs.78672	NP 002281
1110111110	1111_002230	matrilin 3 (MATN3)	14141_002230	113.70072	141_002201
		precursor, mRNA			
		1.			
		/cds=(64,1524)			
		/gb=NM_002381			
		/gi=13518040			
		/ug=Hs.278461	l		
ncrc5091	NM_002381	/len=2599	NM_002381	Hs.278461	NP_002372
		CD99 antigen (CD99),			
		mRNA /cds=(184,741)			
	~	/gb=NM_002414			
		/gi=20149541			
		/ug=Hs.433387			
miob8992	NM_002414	/len=1264	NM 002414	Hs.433387	NP 002405
	_				
		macrophage migration			
		inhibitory factor			
		(glycosylation-inhibiting			
		factor) (MIF), mRNA		ļ	
		/cds=(98,445)			
		/gb=NM_002415			
		/gi=4505184			
60004	NINA 000445	/ug=Hs.407995	NINA 000445	11- 407005	ND 000400
fcr2861	NM_002415	/len=561	NM_002415	Hs.407995	NP_002406
		chemokine (C-X-C			
		motif) ligand 9			
		(CXCL9), mRNA			
		/cds=(40,417)			
		/gb=NM_002416			
		/gi=4505186			
		/ug=Hs.77367			
miob6562	NM_002416	/len=2545	NM_002416	Hs.77367	NP_002407
		menage a trois 1 (CAK			
		assembly factor)			
!		(MNAT1), mRNA			
		/cds=(35,964)			
		/gb=NM_002431		Ì	
		/gi=4505224			
		/ug=Hs.433410			
seob6696	NM_002431	/len=1281	NM_002431	Hs.433410	NP_002422
0000000	[1414]_002401	/1011= 120 1	11111 002 70 1	1113.700710	141_002422

Figure 60 C	onta.				
		mutS 3 (E. coli)			
		(MSH3), mRNA		1	
		/cds=(17,3403)			
		/gb=NM_002439			
		/gi=4505248			
		/ug=Hs.42674			
ncr6878	NM_002439	/len=4374	NM_002439	Hs.42674	NP_002430
		myosin, heavy			
		polypeptide 9, non-			
		muscle (MYH9),			
		mRNA /cds=(1,5883)			
		/gb=NM_002473			
		/gi=22507396			
		/ug=Hs.146550			
seoc2447	NM_002473	/len=7274	NM_002473	Hs.146550	NP_002464
		NADH dehydrogenase			
		(ubiquinone) 1 alpha			
		subcomplex, 2, 8kDa			
		(NDUFA2), mRNA			
		/cds=(57,356)			
		/gb=NM_002488			
		/gi=4505354			
		/ug=Hs.163867			
fcrb8605	NM_002488	/len=590	NM_002488	Hs.163867	NP_002479
		NA DIL dahada asasa			
		NADH dehydrogenase			
		(ubiquinone) Fe-S			
		protein 4, 18kDa			
		(NADH-coenzyme Q			
		reductase) (NDUFS4),			
		mRNA /cds=(9,536)			
		/gb=NM_002495			
seoa8543	NIM 002405	/gi=4505368 /ug=Hs.10758 /len=668	NIM 002405	Uo 10759	ND 000400
56040040	NM_002495	/uy-ns. 10/30 /len=008	114101_002495	Hs.10758	NP_002486
		NADH dehydrogenase			
		(ubiquinone) Fe-S			
		protein 4, 18kDa			
		(NADH-coenzyme Q	1		
		reductase) (NDUFS4),			
		mRNA /cds=(9,536)			
	1	/gb=NM_002495			
		/gi=4505368			
mioc1991	NM_002495	/ug=Hs.10758 /len=668	NM_002495	Hs.10758	NP 002486

Figure 6b Co	int u.				y
fcrb4294	NM_002496	NADH dehydrogenase (ubiquinone) Fe-S protein 8, 23kDa (NADH-coenzyme Q reductase) (NDUFS8), mRNA /cds=(93,725) /gb=NM_002496 /gi=4505370 /ug=Hs.90443 /len=779	NM_002496	Hs.90443	NP_002487
seoa5578	NM_002520	nucleophosmin (nucleolar phosphoprotein B23, numatrin) (NPM1), mRNA /cds=(100,984) /gb=NM_002520 /gi=20070168 /ug=Hs.355719 /len=1347	NM_002520	Hs.355719	NP_002511
ncrc9039	NM_002520	nucleophosmin (nucleolar phosphoprotein B23, numatrin) (NPM1), mRNA /cds=(100,984) /gb=NM_002520 /gi=20070168 /ug=Hs.355719 /len=1347	NM_002520	Hs.355719	NP_002511
fcrb6301	NM_002520	nucleophosmin (nucleolar phosphoprotein B23, numatrin) (NPM1), mRNA /cds=(100,984) /gb=NM_002520 /gi=20070168 /ug=Hs.355719 /len=1347	_ NM_002520	Hs.355719	NP_002511
miod4332	BC039158	Similar to pyruvate dehydrogenase kinase, isoenzyme 1, clone MGC:24867 IMAGE:4778360, mRNA, complete cds		Hs.61712	NP 002601

Figure 6b (Jonea.				
		pinin, desmosome associated protein (PNN), mRNA /cds=(31,2262) /gb=NM_002687 /gi=4505922 /ug=Hs.44499			
ncrc1633	NM_002687	/len=2617	NM_002687	Hs.44499	NP_002678
		polymerase (RNA) II (DNA directed) polypeptide G (POLR2G), mRNA /cds=(107,625) /gb=NM_002696 /gi=4505946			
seoa8432	NM_002696	/ug=Hs.14839 /len=828	NM_002696	Hs.14839	NP_002687
		phosphoribosyl pyrophosphate synthetase 1 (PRPS1), mRNA /cds=(101,1057) /gb=NM_002764 /gi=19923737			
ncr3705	NM 002764	/ug=Hs.56 /len=2078	NM 002764	Hs.56	NP 002755
		prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy) (PSAP), mRNA /cds=(39,1613) /gb=NM_002778 /gi=11386146 /ug=Hs.406455			
mioa1513	NM_002778	/len=2767	NM_002778	Hs.406455	NP_002769
		proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1), mRNA /cds=(48,773) /gb=NM_002793 /gi=22538462 /ug=Hs.407981			
ncrc6875	NM_002793	/len=872	NM_002793	Hs.407981	NP_002784

Conta.				
NM_002794	proteasome (prosome, macropain) subunit, beta type, 2 (PSMB2), mRNA /cds=(111,716) /gb=NM_002794 /gi=22538463 /ug=Hs.432607 /len=850	NM_002794	Hs.432607	NP_002785
NM 002705	macropain) subunit, beta type, 3 (PSMB3), mRNA /cds=(79,696) /gb=NM_002795 /gi=22538464		110 92702	ND 000700
NIVI_002795		NM_002795	Hs.82793	NP_002786
				·
	subunit, ATPase, 5			
	-			
	1 ~			
NM 002805	/len=1332	NM 002805	Hs.79387	NP 002796
	proteasome (prosome,			
	macropain) 26S			
	1			
	/ug=Hs.79357			
NM_002806	/len=1590	NM_002806	Hs.79357	NP_002797
			1	
			1	
	<u> </u>		1	
NM_002823	/len=1233	NM_002823	Hs.250655	NP_002814
	NM_002794 NM_002795 NM_002805	proteasome (prosome, macropain) subunit, beta type, 2 (PSMB2), mRNA /cds=(111,716) /gb=NM_002794 /gi=22538463 /ug=Hs.432607 /len=850 /gi=22538463 /ug=Hs.432607 /len=850 /gi=22538464 /ug=Hs.82793 /len=784 /gi=22538464 /ug=Hs.82793 /len=784 /gi=22538464 /ug=Hs.82793 /len=784 /gi=22538464 /ug=Hs.82793 /len=784 /gi=22538464 /ug=Hs.82793 /len=784 /gi=24349434 /gi=NM_002805 /gi=24497434 /ug=Hs.79387 /len=1332 /gi=24497434 /ug=Hs.79387 /len=1332 /gi=24497434 /ug=Hs.79387 /len=1332 /gi=24430159 /ug=Hs.79357 /len=1590 /gi=24430159 /ug=Hs.79357 /len=1590 /gi=24430159 /ug=Hs.79357 /len=1590 /gi=24430159 /ug=Hs.250655 /gi=21359859 /ug=Hs.250655	proteasome (prosome, macropain) subunit, beta type, 2 (PSMB2), mRNA /cds=(111,716) /gb=NM_002794 /gi=22538463 /ug=Hs.432607 /len=850 NM_002794 /gi=22538463 /ug=Hs.432607 NM_002794 /gi=22538464 /gi=22538464 /ug=Hs.82793 /len=784 NM_002795 /gi=22538464 /ug=Hs.82793 /len=784 NM_002795 /gi=22538464 /ug=Hs.82793 /len=784 NM_002795 /gi=24497434 /ug=Hs.79387 /len=1332 NM_002805 /gi=24497434 /ug=Hs.79387 /len=1332 NM_002805 /gi=24497434 /ug=Hs.79387 /len=1332 NM_002805 /gi=24430159 /ug=Hs.79357 /len=1590 NM_002806 /gi=24430159 /ug=Hs.79357 /len=1590 NM_002806 /gi=24430159 /ug=Hs.79357 /len=1590 NM_002806 /gi=24430159 /ug=Hs.79357 /len=1590 NM_002806 /gi=24430159 /ug=Hs.79357 /len=1590 NM_002806 /gi=24359859 /ug=Hs.250655	proteasome (prosome, macropain) subunit, beta type, 2 (PSMB2), mRNA /cds=(111,716) /gb=NM_002794 /gi=22538463 /ug=Hs.432607 /len=850 NM_002794 Hs.432607 NM_002794 /len=850 NM_002794 Hs.432607 NM_002794 /len=850 NM_002794 Hs.432607 NM_002794 /len=850 NM_002794 Hs.432607 NM_002795 /gi=22538464 NM_002795 /gi=22538464 NM_002795 /gi=22538464 NM_002795 Hs.82793 /len=784 NM_002795 Hs.82793 Proteasome (prosome, macropain) 26S subunit, ATPase, 5 (PSMC5), mRNA /cds=(42,1262) /gb=NM_002805 /gi=24497434 /ug=Hs.79387 NM_002805 Hs.79387 Proteasome (prosome, macropain) 26S subunit, ATPase, 6 (PSMC6), mRNA /cds=(21,1190) /gb=NM_002806 /gi=24430159 /ug=Hs.79357 NM_002806 Hs.79357 NM_002806 /gi=2430159 /ug=Hs.79357 NM_002806 Hs.79357 Prothymosin, alpha (gene sequence 28) (PTMA), mRNA /cds=(182,514) /gb=NM_002823 /gi=21359859 /ug=Hs.250655

	į.	İ		
NM 002851	type, Z polypeptide 1 (PTPRZ1), mRNA /cds=(148,7092) /gb=NM_002851 /gi=4506328 /ug=Hs.78867		∐c 79967	ND 002842
111111_002651		NIVI_002851	HS./886/	NP_002842
NM 002865	oncogene family (RAB2), mRNA /cds=(209,847) /gb=NM_002865 /gi=4506364 /ug=Hs.78305	NM 002865	Hs 78305	NP 002856
11111_002000	nen-1140	14141_002000	113.70000	NF_002030
NM_002901	reticulocalbin 1, EF- hand calcium binding domain (RCN1), mRNA /cds=(53,1048) /gb=NM_002901 /gi=4506454 /ug=Hs.167791 /len=2104	NM_002901	Hs.167791	NP 002892
	7.0		11.0.107701	111 _002002
NM_002947	replication protein A3, 14kDa (RPA3), mRNA /cds=(1182,1547) /gb=NM_002947 /gi=19923751 /ug=Hs.1608 /len=1622	NM_002947	Hs.1608	NP_002938
	ribosomal protein S2 (RPS2), mRNA /cds=(12,893) /gb=NM_002952 /gi=15055538 /ug=Hs.356360			
NM 002952	/len=978	NM 002952	Hs.356360	NP 002943
NM_002958	RYK receptor-like tyrosine kinase (RYK), mRNA /cds=(104,1918) /gb=NM_002958 /gi=11863158 /ug=Hs.79350 /len=3031	NM_002958	Hs.79350	NP 002949
	NM_002947	phosphatase, receptor- type, Z polypeptide 1 (PTPRZ1), mRNA /cds=(148,7092) /gb=NM_002851 /gi=4506328 /ug=Hs.78867 NM_002851 RAB2, member RAS oncogene family (RAB2), mRNA /cds=(209,847) /gb=NM_002865 /gi=4506364 /ug=Hs.78305 NM_002865 NM_002865 NM_002865 reticulocalbin 1, EF- hand calcium binding domain (RCN1), mRNA /cds=(53,1048) /gb=NM_002901 /gi=4506454 /ug=Hs.167791 NM_002901 /replication protein A3, 14kDa (RPA3), mRNA /cds=(1182,1547) /gb=NM_002947 /gi=19923751 NM_002947 replication protein S2 (RPS2), mRNA /cds=(12,893) /gb=NM_002952 /gi=15055538 /ug=Hs.356360 NM_002952 /len=978 RYK receptor-like tyrosine kinase (RYK), mRNA /cds=(104,1918) /gb=NM_002958 /gi=11863158 /ug=Hs.79350	phosphatase, receptor- type, Z polypeptide 1 (PTPRZ1), mRNA /cds=(148,7092) /gb=NM_002851 /gi=4506328 /ug=Hs.78867 NM_002851 RAB2, member RAS oncogene family (RAB2), mRNA /cds=(209,847) /gb=NM_002865 /gi=4506364 /ug=Hs.78305 NM_002865 reticulocalbin 1, EF- hand calcium binding domain (RCN1), mRNA /cds=(53,1048) /gb=NM_002901 /gi=4506454 /ug=Hs.167791 NM_002901 replication protein A3, 14kDa (RPA3), mRNA /cds=(1182,1547) /gb=NM_002947 /gi=19923751 NM_002947 ribosomal protein S2 (RPS2), mRNA /cds=(12,893) /gb=NM_002952 /gi=15055538 /ug=Hs.36360 NM_002952 RYK receptor-like tyrosine kinase (RYK), mRNA /cds=(104,1918) /gb=NM_002958 /gj=11863158 /ug=Hs.79350	phosphatase, receptor- type, Z polypeptide 1 (PTPRZ1), mRNA /cds=(148,7092) /gb=NM_002851 /gi=4506328 /ug=Hs.78867 NM_002851 RAB2, member RAS oncogene family (RAB2), mRNA /cds=(209,847) /gb=NM_002865 /gi=4506364 /ug=Hs.78305 NM_002865 reticulocalbin 1, EF- hand calcium binding domain (RCN1), mRNA /cds=(53,1048) /gb=NM_002901 /gi=4506454 /ug=Hs.167791 NM_002901 /len=2104 NM_002901 /len=2104 NM_002901 /replication protein A3, 14kDa (RPA3), mRNA /cds=(1182,1547) /gb=NM_002947 /gi=19923751 NM_002947 /gi=19923751 NM_002947 /gi=19923751 NM_002947 /gi=19505538 /ug=Hs.356360 NM_002952 /len=978 RYK receptor-like tyrosine kinase (RYK), mRNA /cds=(104,1918) /gb=NM_002958 /gi=11863158 /ug=Hs.79350

Figure 6b Co	711t G.				
		spermidine/spermine			
		N1-acetyltransferase			1
		(SAT), mRNA			
		/cds=(166,681)			
		/gb=NM_002970			
		/gi=4506788			
		/ug=Hs.28491			
ncrc9944	NM_002970	/len=1060	NM_002970	Hs.28491	NP 002961
		1.0		1.0.20.0	
		secreted frizzled-			
		related protein 1			
		(SFRP1), mRNA			
		• • • • • • • • • • • • • • • • • • • •			
		/cds=(303,1244)			
		/gb=NM_003012			
U.S. 4045	NIA 000040	/gi=8400731		7000	
hfcr4645	NM_003012	/ug=Hs.7306 /len=4469	NM_003012	Hs.7306	NP_003003
		splicing factor,			
		arginine/serine-rich 3			
		(SFRS3), mRNA			
		/cds=(106,600)			
		/gb=NM_003017			
		/gi=24025684			
		/ug=Hs.388623			
seoa1065	NM_003017	/len=1403	NM_003017	Hs.388623	NP_003008
		intersectin short			
		isoform (ITSN) mRNA,			
mioa4771	AF114488	complete cds	NM_003024	Hs.66392	NP_003015
		solute carrier family 4,			
		anion exchanger,			
		member 2 (erythrocyte			
		membrane protein			
		band 3-like 1)			
		(SLC4A2), mRNA			
		/cds=(175,3900)			}
		/gb=NM_003040			
		/gi=21361550			
		1 •			
f===0000	NINA 002040	/ug=Hs.79410	NM 002040	11- 70440	ND 000004
fcrc2089	NM_003040	/len=4078	NM_003040	Hs.79410	NP_003031
		snail 2 (Drosophila)			
		(SNAI2), mRNA			
		/cds=(165,971)		1	
		/gb=NM_003068			ŧ
		/gi=24497625			
		/ug=Hs.93005			
seob4160	NM_003068	/len=2101	NM_003068	Hs.93005	NP_003059

Figure 6b	Conta.		y		
seoa8486	NM_003096	small nuclear ribonucleoprotein polypeptide G (SNRPG), mRNA /cds=(89,319) /gb=NM_003096 /gi=21359839 /ug=Hs.77496 /len=606	NM_003096	Hs.77496	NP_003087
		signal recognition			
		particle 9kDa (SRP9), mRNA /cds=(107,367) /gb=NM_003133 /gi=4507216 /ug=Hs.75975			
seob5081	NM_003133	/len=1466	NM_003133	Hs.75975	NP_003124
seoa3852	NM_003144	signal sequence receptor, alpha (translocon-associated protein alpha) (SSR1), mRNA /cds=(112,972) /gb=NM_003144 /gi=6552340 /ug=Hs.250773 /len=3285	NM_003144	Hs.250773	NP_003135
seoa5258	NM 003203	chromosome 2 open reading frame 3 (C2orf3), mRNA /cds=(69,2414) /gb=NM_003203 /gi=7108364 /ug=Hs.184175 /len=2661	NM 003203	Hs.184175	NP 003194
56040200	NM_003203	testis enhanced gene transcript (TEGT), mRNA /cds=(41,754) /gb=NM_003217 /gi=4507432 /ug=Hs.74637	NM_003203	пѕ.1041/5	NP_003194
ncrc1631	NM_003217	/len=2600 thrombospondin 4 (THBS4), mRNA /cds=(28,2913) /gb=NM_003248 /gi=4507488 /ug=Hs.75774	NM_003217	Hs.74637	NP_003208
miob3329	NM_003248	/len=3074	NM_003248	Hs.75774	NP_003239

Figure 6b	Conta.				
		thymidine kinase 1,			
		soluble (TK1), mRNA			
		/cds=(58,762)			
		/gb=NM_003258			
		/gi=4507518			
		/ug=Hs.105097			
fcr4503	NM_003258	/len=1421	NM_003258	Hs.105097	NP 003249
		transmembrane 4			11, 2002 10
		superfamily member 6			
		(TM4SF6), mRNA			
ĺ		/cds=(104,841)	•		
		/gb=NM_003270			
		/gi=21265115			
		/g=Hs.121068			
ncrc5162	NM_003270	/len=2069	NM 002270	Hs.121068	ND 002264
110100102	14141_003270	troponin C2, fast	NM_003270	ПS. 12 1000	NP_003261
		(TNNC2), mRNA			
		/cds=(65,547)			
		/gb=NM_003279			
		/gi=4507616			
f 0000		/ug=Hs.182421			
fcrc6389	NM_003279	/len=677	NM_003279	Hs.182421	NP_003270
		topoisomerase (DNA) I			
		(TOP1), mRNA			
		/cds=(247,2544)			
		/gb=NM_003286			
		/gi=19913404			
hfcr5905	NM_003286		NM_003286	Hs.317	NP_003277
		tumor protein,			
		translationally-			
		controlled 1 (TPT1),			
		mRNA /cds=(95,613)			
		/gb=NM_003295			
		/gi=4507668			
		/ug=Hs.401448			
seoa0044	NM_003295	/len=830	NM_003295	Hs.401448	NP_003286
		tumor protein,			
		translationally-			
		controlled 1 (TPT1),			
		mRNA /cds=(95,613)			
		/gb=NM_003295			
		/gi=4507668			
		/ug=Hs.401448			
seob7500	NM_003295	/len=830	NM_003295	Hs.401448	NP_003286
		thyroid hormone			
		receptor interactor 6			
		(TRIP6), mRNA			
		/cds=(76,1506)			
		/gb=NM_003302			
		/gi=23308730			
		/ug=Hs.380230			
fcrb3795	NM_003302	/len=1695	NM_003302	Hs.380230	NP 003293
10100100	[141VI_000302	Men 1090	[141VI_00330Z	1113.300230	

Application of: Liew, et. al. Our Docket #: 4231/2042 Figure 6b Cont'd.

Figure 6b	Conta.				
		ubiquitin-conjugating			
		enzyme E2 variant 2			
		(UBE2V2), mRNA			
		/cds=(22,459)			
		/gb=NM_003350			
		/gi=12025664			
		/ug=Hs.79300			
seob7022	NM_003350	/len=1535	NM 003350	Hs.79300	NP 003341
		ubiquitin-conjugating	1 -		
		enzyme E2 variant 2	1		
		(UBE2V2), mRNA			
		/cds=(22,459)			
		/gb=NM_003350			
		/gi=12025664			
		/ug=Hs.79300			
mioc0206	NM 003350	/len=1535	NM_003350	Hs.79300	NP 003341
1111000200	14141_000000	vascular endothelial	14141_000000	113.7 3300	INF_003341
		growth factor B			
		17			
		(VEGFB), mRNA			
		/cds=(50,673)			
		/gb=NM_003377			
		/gi=20070172			
		/ug=Hs.78781	•		
miod3079	NM_003377	/len=1181	NM_003377	Hs.78781	NP_003368
		very low density			
		lipoprotein receptor			
		(VLDLR), mRNA			
		/cds=(86,2707)			
		/gb=NM_003383			
		/gi=4507900			
		/ug=Hs.73729			
seoa0396	NM_003383	/len=3355	NM_003383	Hs.73729	NP_003374
		zinc finger protein 36,			
		C3H type, (mouse)			
	·	(ZFP36), mRNA			
		/cds=(60,1040)		1	
		/gb=NM_003407			
		/gi=4507960			
		/ug=Hs.343586			
ncr9337	NM_003407	/len=1746	NM_003407	Hs.343586	NP_003398
		zinc finger protein 36,	<u> </u>		
		C3H type, (mouse)		1	
		(ZFP36), mRNA		1	
	Ì	/cds=(60,1040)		1	
		/gb=NM_003407			
		/gi=4507960		1	
		/ug=Hs.343586			
fcrb9843	NM 003407	/len=1746	NM_003407	Hs.343586	NP_003398
10100070	114141_000407	pion 11-10	1.4141_000407	1110.0-10000	111 _000000

Figure ob C	Ont G.				
17.10		zinc finger protein 9 (a cellular retroviral nucleic acid binding protein) (ZNF9), mRNA /cds=(103,636) /gb=NM_003418 /gi=4827070			
seoa1749	NM_003418	/ug=Hs.2110 /len=1500 zinc finger protein 143 (clone pHZ-1)	NM_003418	Hs.2110	NP_003409
		(CONE P112-1) (ZNF143), mRNA /cds=(155,2035) /gb=NM_003442 /gi=24475652 /ug=Hs.374355			
fcrb1311	NM_003442	/len=2641	NM_003442	Hs.374355	NP_003433
ncrc6871	NM_003455	zinc finger protein 202 (ZNF202), mRNA /cds=(11,1957) /gb=NM_003455 /gi=10835040 /ug=Hs.9443 /len=4053	NM 003455	Hs.9443	NP 003446
increder i	NW_000400	ubiquitin specific protease 7 (herpes virus-associated) (USP7), mRNA /cds=(200,3508) /gb=NM_003470 /gi=4507856 /ug=Hs.78683	NN_000433	113.3443	NF_003440
ncr8337	NM_003470	/len=4022	NM_003470	Hs.78683	NP_003461
fcrc5138	NM_003504	CDC45 cell division cycle 45-like (S. cerevisiae) (CDC45L), mRNA /cds=(71,1771) /gb=NM_003504 /gi=16357475 /ug=Hs.114311 /len=1932	NIM 003504	He 114244	ND 002405
1000100	14101_003504	MCH-1832	NM_003504	Hs.114311	NP_003495
ncrc5327	NM_003563	speckle-type POZ protein (SPOP), mRNA /cds=(158,1282) /gb=NM_003563 /gi=4507182 /ug=Hs.129951 /len=1642	NM_003563	Hs.129951	NP_003554
					

Figure 6b	Cont a.				
ncrc4302	NM_003576	serine/threonine kinase 24 (STE20 yeast) (STK24), mRNA /cds=(146,1477) /gb=NM_003576 /gi=20070157 /ug=Hs.168913 //len=2505	NM_003576	Hs.168913	NP 003567
110104302	14141_003370	neutral	1410 003370	115.100913	NP_003367
		sphingomyelinase (N-SMase) activation associated factor (NSMAF), mRNA /cds=(13,2766) /gb=NM_003580 /gi=4505464 /ug=Hs.78687			
mioa7544	NM_003580	/len=3380	NM_003580	Hs.78687	NP_003571
mioa5540	NM_003596	tyrosylprotein sulfotransferase 1 (TPST1), mRNA /cds=(328,1440) /gb=NM_003596 /gi=21361092 /ug=Hs.421194 /len=2033	NM_003596	Hs.421194	NP_003587
20022620	NM 002645	solute carrier family 4, sodium bicarbonate cotransporter, member 7 (SLC4A7), mRNA /cds=(72,3716) /gb=NM_003615 /gi=19923175 /ug=Hs.132904		U- 122004	ND 000000
seoa2620	NM_003615	/len=7785 histone	NM_003615	Hs.132904	NP_003606
mioa1149	NM 003642	acetyltransferase 1 (HAT1), mRNA /cds=(37,1296) /gb=NM_003642 /gi=4504340 /ug=Hs.13340	NM 002642	He 12240	ND 002622
mioa i 149	NM_003642	/len=1568	NM_003642	Hs.13340	NP_003633

Figure 6b Cont'd.	Figure	6b C	ont'd.
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Figure 60	Conta.				
		CGG triplet repeat			
		binding protein 1	}		
		(CGGBP1), mRNA			
		/cds=(357,863)			
		/gb=NM_003663			
		/gi=21361098			
ł		1 =			
id4007	NIM OCCCO	/ug=Hs.86041	NINA 000000	11- 00044	ND 000054
miod4867	NM_003663	/len=4279	NM_003663	Hs.86041	NP_003654
		basic helix-loop-helix			
	1	domain containing,			
		class B, 2 (BHLHB2),			
		mRNA			
		/cds=(197,1435)			
		/gb=NM_003670			
		/gi=4503298			
		/ug=Hs.171825			
seoa8638	NM 003670	/len=2922	NM 003670	Hs.171825	NP_003661
		protein kinase,			
		interferon-inducible			
		double stranded RNA			
		dependent activator			
		(PRKRA), mRNA			
		/cds=(108,1049)			
		/gb=NM_003690			
		/gi=20149526			
		/ug=Hs.18571			
mioa3514	NM_003690	/len=1843	NM_003690	Hs.18571	NP_003681
		aldo-keto reductase	į		
		family 1, member C3			
		(3-alpha hydroxysteroid			
		dehydrogenase, type			
		II) (AKR1C3), mRNA			
		/cds=(70,1041)			
		/gb=NM_003739			
		/gi=24497582			
		/ug=Hs.78183			
mioc2681	NM 003739	/len=1224	NM 003739	Hs.78183	NP_003730
		clone MGC:39731		1	
ŀ		IMAGE:5275603,			
miob8663	BC031264	mRNA, complete cds	1	Hs.6651	NP 003753
	50001204	catenin (cadherin-		1110.0001	
l		associated protein),			
ĺ		alpha-like 1	1	}	
		1 *			
		(CTNNAL1), mRNA			
		/cds=(44,2248)	1		
		/gb=NM_003798			
		/gi=4503128			
		/ug=Hs.58488			
seoa3989	NM_003798	/len=2446	NM_003798	Hs.58488	NP_003789

nt'd.	·			
NM_003800	RNA guanylyltransferase and 5'-phosphatase (RNGTT), mRNA /cds=(289,2082) /gb=NM_003800 /gi=4506562 /ug=Hs.27345 /len=4546	NM_003800	Hs.27345	NP_003791
	succinate-CoA ligase, ADP-forming, beta subunit (SUCLA2), mRNA /cds=(58,1449) /gb=NM_003850 /gi=11321582 /ug=Hs.182217			
NM_003850	/len=2178	NM_003850	Hs.182217	NP_003841
NM_003859	dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit (DPM1), mRNA /cds=(1,783) /gb=NM_003859 /gi=4503362 /ug=Hs.5085 /len=1047	NM_003859	Hs.5085	NP_003850
NM_003870	IQ motif containing GTPase activating protein 1 (IQGAP1), mRNA /cds=(468,5441) /gb=NM_003870 /gi=4506786 /ug=Hs.1742 /len=7573	NM_003870	Hs.1742	NP_003861
NM_003878	gamma-glutamyl hydrolase (conjugase, folylpolygammaglutam yl hydrolase) (GGH), mRNA /cds=(60,1016) /gb=NM_003878 /gi=4503986 /ug=Hs.78619 /len=1280	NM_003878	Hs.78619	NP 003869
	NM_003859 NM_003870	and 5-phosphatase (RNGTT), mRNA /cds=(289,2082) /gb=NM_003800 /gi=4506562 /ug=Hs.27345 /len=4546 succinate-CoA ligase, ADP-forming, beta subunit (SUCLA2), mRNA /cds=(58,1449) /gb=NM_003850 /gi=11321582 /ug=Hs.182217 /len=2178 dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit (DPM1), mRNA /cds=(1,783) /gb=NM_003859 /gi=4503362 /ug=Hs.5085 /len=1047 IQ motif containing GTPase activating protein 1 (IQGAP1), mRNA /cds=(468,5441) /gb=NM_003870 /gi=4506786 /ug=Hs.1742 /len=7573 gamma-glutamyl hydrolase (conjugase, folylpolygammaglutam yl hydrolase) (GGH), mRNA /cds=(60,1016) /gb=NM_003878 /gi=4503986 /ug=Hs.78619	guanylyltransferase and 5'-phosphatase (RNGTT), mRNA /cds=(289,2082) /gb=NM_003800 /gi=4506562 /ug=Hs.27345 NM_003800 /len=4546 NM_003800 Succinate-CoA ligase, ADP-forming, beta subunit (SUCLA2), mRNA /cds=(58,1449) /gb=NM_003850 /gi=11321582 /ug=Hs.182217 NM_003850 /len=2178 NM_003850 /gi=11321582 /ug=Hs.182217 NM_003850 /gi=4503362 NM_003859 /gi=4503362 NM_003859 /gi=450362 NM_003870 /gi=NM_003870 /gi=4506786 NM_003870 /gi=4506786 NM_003870 /gi=4506786 /ug=Hs.78619 NM_003870 /gi=NM_003878 /gi=4503986 /ug=Hs.78619	guanylyltransferase and 5-phosphatase (RNGTT), mRNA /cds=(289,2082) /gb=NM_003800 /gj=4505662 /ug=Hs.27345 NM_003800 /len=4546 NM_003800 Hs.27345 NM_003800 Hs.27345 NM_003800 Hs.27345 NM_003800 Hs.27345 NM_003800 Hs.27345 NM_003800 Hs.27345 NM_003800 Hs.27345 NM_003800 Hs.27345 NM_003800 Hs.27345 NM_003800 Hs.27345 NM_003850 /gj=11321582 /ug=Hs.182217 NM_003850 Hs.182217 NM_003850 Hs.182217 NM_003850 Hs.182217 NM_003850 Hs.182217 NM_003850 Hs.182217 NM_003850 Hs.182217 NM_003850 NM

Figure 6b C	onta.				
ncrc8903	NM_003879	CASP8 and FADD-like apoptosis regulator (CFLAR), mRNA /cds=(482,1924) /gb=NM_003879 /gi=21361768 /ug=Hs.195175 /len=2243	NM_003879	Hs.195175	NP_003870
hfa=0045	NIM 002022	suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein) (ST13), mRNA /cds=(144,1253) /gb=NM_003932 /gi=21237722 /ug=Hs.119222		U. 440000	
hfcr0045	NM_003932	/len=3214	NM_003932	Hs.119222	NP_003923
ncr0721	NM 003945	ATPase, H transporting, lysosomal 9kDa, V0 subunit e (ATP6V0E), mRNA /cds=(76,321) /gb=NM_003945 /gi=19913435 /ug=Hs.415629 /len=849	NM 003945	Hs.415629	NP 003936
		ATPase, H transporting, lysosomal 9kDa, V0 subunit e (ATP6V0E), mRNA /cds=(76,321) /gb=NM_003945 /gi=19913435 /ug=Hs.415629	_		i
seoa8960	NM_003945	/len=849	NM_003945	Hs.415629	NP_003936
		BTAF1 RNA polymerase II, B-TFIID transcription factor- associated, 170kDa (Mot1 S. cerevisiae) (BTAF1), mRNA /cds=(118,5667) /gb=NM_003972 /gi=27477069 /ug=Hs.180930			
mioa9891	NM_003972	/len=6345	NM_003972	Hs.180930	NP_003963

Figure 6b	Conta.				
ncr0733	NM 004048	beta-2-microglobulin (B2M), mRNA /cds=(14,373) /gb=NM_004048 /gi=4757825		Hc 19516	ND 004030
ncr0733	INIVI_004048	/ug=Hs.48516 /len=925	NN_004048	Hs.48516	NP_004039
ncrc1687	NM_004064	cyclin-dependent kinase inhibitor 1B (p27, Kip1) (CDKN1B), mRNA /cds=(466,1062) /gb=NM_004064 /gi=17978497 /ug=Hs.238990 /len=2422	NM 004064	Hs.238990	NP 004055
110101007	14141_004004	cyclin-dependent	14141_004004	HS.230990	INF_004055
miob8639	NM 004064	kinase inhibitor 1B (p27, Kip1) (CDKN1B), mRNA /cds=(466,1062) /gb=NM_004064 /gi=17978497 /ug=Hs.238990 /len=2422	NM 004064	Hs.238990	NP 004055
111000000	14141_004004	cerebellar	14141_00-100-1	113.230330	141 _004035
		degeneration-related protein 1, 34kDa (CDR1), mRNA /cds=(61,732) /gb=NM_004065 /gi=4757963 /ug=Hs.278427			
ncrc0672	NM_004065	/len=1165	NM 004065	Hs.278427	NP 004056
	_	cerebellar degeneration-related protein 1, 34kDa (CDR1), mRNA /cds=(61,732) /gb=NM_004065 /gi=4757963 /ug=Hs.278427			
ncrc2693	NM_004065	/len=1165	NM_004065	Hs.278427	NP_004056
norh8227	BC018149	delta sleep inducing peptide, immunoreactor, clone MGC:9719 IMAGE:3851403,	NM 004090	He 75450	ND 004090
ncrb8237	BC018148	mRNA, complete cds	NM_004089	Hs.75450	NP_004080

Figure 6b C	zoni a.				
hfcr6515	NM_004102	fatty acid binding protein 3, muscle and heart (mammary- derived growth inhibitor) (FABP3), mRNA /cds=(46,447) /gb=NM_004102 /gi=10938020 /ug=Hs.49881 /len=679	NM_004102	Hs.49881	NP_004093
miod3591	NM 004117	FK506 binding protein 5 (FKBP5), mRNA /cds=(154,1527) /gb=NM_004117 /gi=17149847 /ug=Hs.7557 /len=3781	NIM 004117	He 7557	ND 004109
	_	FK506 binding protein 5 (FKBP5), mRNA /cds=(154,1527) /gb=NM_004117 /gi=17149847		Hs.7557	NP_004108
mioc0090 seoa6364	NM_004117	/ug=Hs.7557 /len=3781 glia maturation factor, beta (GMFB), mRNA /cds=(98,526) /gb=NM_004124 /gi=4758441 /ug=Hs.151413 /len=4131	NM_004117	Hs.7557	NP_004108
seob6415	NM_004134	heat shock 70kDa protein 9B (mortalin-2) (HSPA9B), nuclear gene encoding mitochondrial protein, mRNA /cds=(94,2133) /gb=NM_004134 /gi=24234687 /ug=Hs.3069 /len=2852		Hs.3069	NP_004125
fcrb5259	NM_004147	developmentally regulated GTP binding protein 1 (DRG1), mRNA /cds=(66,1169) /gb=NM_004147 /gi=4758795 /ug=Hs.115242 /len=1383	NM_004147	Hs.115242	NP_004138

Figure 6b Co	onta.		·		
seob6601	AK055927	cDNA FLJ31365 fis, clone NB9N41000135, highly similar to RAS- RELATED PROTEIN RAB-1A	NM_004161	Hs.227327	NP_004152
		estrogen receptor			
		binding site associated,	,		
		antigen, 9 (EBAG9),			
		mRNA			
		/cds=(362,1003)			
		/gb=NM_004215 /gi=14577926			
miod4518	NM 004215	/ug=Hs.9222 /len=1182	NM 004215	Hs.9222	NP 004206
111104-1010	14101_004210	RAB9A, member RAS	14141_004213	113.3222	NF_004200
		oncogene family			
		(RAB9A), mRNA			
		/cds=(192,797)			
		/gb=NM_004251			
		/gi=20070189			
	1	/ug=Hs.330994			
ncrc5553	NM_004251	/len=1106	NM_004251	Hs.330994	NP_004242
		cofactor required for			
		Sp1 transcriptional			
		activation, subunit 6,			
		77kDa (CRSP6), mRNA			
		/cds=(196,2151)			
		/gb=NM_004268			
		/gi=10835074			
		/ug=Hs.22630			
mioc1416	NM_004268	/len=2546	NM_004268	Hs.22630	NP 004259
		Rho GDP dissociation			
		inhibitor (GDI) alpha			
		(ARHGDIA), mRNA			
		/cds=(102,716)			
		/gb=NM_004309			
		/gi=20149550 /ug=Hs.159161			
mioa3361	NM 004309	/len=1921	NM 004309	Hs.159161	NP 004300
111000001	114141 004303	ADP-ribosylation factor-		115.138101	INF_UU43UU
		like 3 (ARL3), mRNA			
		/cds=(16,564)	Ì		
		/gb=NM_004311			
		/gi=4757773			
		/ug=Hs.182215			
seob5454	NM_004311	/len=900	NM_004311	Hs.182215	NP_004302

Figure ob	Oonea.				
seob5021	NM_004313	arrestin, beta 2 (ARRB2), mRNA /cds=(234,1463) /gb=NM_004313 /gi=21626464 /ug=Hs.18142 /len=1941	NM_004313	Hs.18142	NP 004304
Seob3021	14141_004313	/leii-1941	14141_004313	П5. 10 142	INP_004304
		BCL2-associated athanogene (BAG1), mRNA /cds=(66,1103) /gb=NM_004323 /gi=7549801 /ug=Hs.41714	·		
mioa0466	NM_004323	/len=1311	NM_004323	Hs.41714	NP_004314
		chromosome 18 open reading frame 1 (C18orf1), mRNA /cds=(243,989) /gb=NM_004338 /gi=4757883 /ug=Hs.153498			
fcrc1957	NM_004338	/len=8093	NM_004338	Hs.153498	NP_004329
		CD81 antigen (target of antiproliferative antibody 1) (CD81), mRNA /cds=(41,751) /gb=NM_004356 /gi=21237760 /ug=Hs.54457			
hfcr2930	NM_004356	/len=1332	NM_004356	Hs.54457	NP_004347
20000074		cytochrome c oxidase subunit VIa polypeptide 1 (COX6A1), nuclear gene encoding mitochondrial protein, mRNA /cds=(27,356) /gb=NM_004373 /gi=17999527 /ug=Hs.180714		Ua 190744	ND 004224
seoa9874	NM_004373	/len=548	NM_004373	Hs.180714	NP_004364

Figure 60	Ochta.	100744			
1		COX11 cytochrome c			
		oxidase assembly	İ		
		protein (yeast)			
		(COX11), nuclear gene			
		encoding mitochondrial			
		protein, mRNA			
		/cds=(48,878)			
		/gb=NM_004375			
		/gi=17921983			
		/ug=Hs.241515			
mioc2039	NM 004275	/len=2717	NIM 004275	Un 241515	ND 004366
1111002039	NM_004375	chondroitin sulfate	NM_004375	Hs.241515	NP_004366
1		1			
		proteoglycan 2			
		(versican) (CSPG2),			
		mRNA			
		/cds=(267,10457)			
		/gb=NM_004385			
		/gi=21361115		·	
		/ug=Hs.81800			
mioc3220	NM_004385	/len=11185	NM_004385	Hs.81800	NP_004376
		Down syndrome critical			
		region gene 1			
		(DSCR1), mRNA			
		/cds=(66,659)			
		/gb=NM_004414			
		/gi=20149552			
		/ug=Hs.184222			
ncr0265	NM 004414	/len=2289	NM 004414	Hs.184222	NP 004405
11010200	11111_001111	isopentenyl-		110.101222	141 _004400
1		diphosphate delta			
1		isomerase (IDI1),			
		mRNA /cds=(51,737)			
1					
		/gb=NM_004508			
		/gi=4758583			
70400	NIM 004500	/ug=Hs.76038	NIM 004500	LI- 70000	ND 004400
ncrc0439	NM_004508	/len=1807	NM_004508	Hs.76038	NP_004499
		6-phosphofructo-2-			
1		kinase/fructose-2,6-			
		biphosphatase 3			
		(PFKFB3), mRNA			
		/cds=(115,1677)			
		/gb=NM_004566			
]		/gi=4758899			
		/ug=Hs.195471			
mioa9821	NM_004566	/len=4322	NM_004566	Hs.195471	NP_004557

Figure 6b	Conta.				
		serine (or cysteine)			
		proteinase inhibitor,			
		clade B (ovalbumin),			
		member 6			
		(SERPINB6), mRNA			
		/cds=(75,1205)			
		/gb=NM_004568			
		/gi=28077084			
		/gr 2007/007 /ug=Hs.41072		}	
miob2656	NM_004568	/len=1361	NM 004568	Hs.41072	NP_004559
111002000	14141_004300	serine (or cysteine)	14141_004300	113.41072	147_004339
		proteinase inhibitor,			
		clade B (ovalbumin),			
		member 6			
		•			
		(SERPINB6), mRNA			
		/cds=(75,1205)			
		/gb=NM_004568			
		/gi=28077084			
		/ug=Hs.41072			
ncr0018	NM_004568	/len=1361	NM_004568	Hs.41072	NP_004559
		Rab			
		geranylgeranyltransfer	}		
		ase, beta subunit			
		(RABGGTB), mRNA			
		/cds=(72,1067)			
	-	/gb=NM_004582			
		/gi=21359853			
		/ug=Hs.78948			
seoa9712	NM_004582	/len=1526	NM_004582	Hs.78948	NP_004573
	}	Fanconi anemia,			
		complementation			
		group G (FANCG),			
		mRNA `			
		/cds=(493,2361)			•
		/gb=NM_004629			
		/gi=4759335			
hfcr2250	NM 004629	/ug=Hs.8047 /len=2649	NM 004629	Hs.8047	NP 004620
	7411_00 1020	mRNA; cDNA	11111_00 1020	110.0017	741 _004020
		DKFZp434M2216			
		(from clone			
mioa8028	AL137295	DKFZp434M2216)	NM 004641	Hs.199429	NP 004632
111000020	AL 131 233	DIXI ZP434IVIZZ 10)	14141_004041	113.133423	INF_004032
		ash2 (absent, small, or			
			ĺ		
		homeotic)-like			
		(Drosophila) (ASH2L),	i		
		mRNA /cds=(5,1891)			
		/gb=NM_004674			
	100 00 107 1	/gi=4757789			
miob3695	NM_004674	/ug=Hs.6856 /len=2381	INM_UU46/4	Hs.6856	NP_004665

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Figure 6b	Conta.				
1		serologically defined			
		colon cancer antigen 1			
		(SDCCAG1), mRNA			
		/cds=(183,1271)			
		/gb=NM_004713			
		/gi=4759077			
		/g=Hs.388584			
	NIM 004742	1 -	NIM 004742	110 200504	ND 004704
mioa6102	NM_004713	/len=2078	NM_004713	Hs.388584	NP_004704
		cytochrome c oxidase			
		subunit VIIa			
		polypeptide 2 like			
		(COX7A2L), nuclear			
		gene encoding			
		mitochondrial protein,			
		mRNA /cds=(56,400)			
		/gb=NM_004718	1		
		/gi=18105036			
		/ug=Hs.30888			
seoa0729	NM_004718	/len=1145	NM_004718	Hs.30888	NP 004709
		DEAD/H (Asp-Glu-Ala-			
		Asp/His) box			
		polypeptide 21			
		(DDX21), mRNA			
		1			
		/cds=(266,2413)			
		/gb=NM_004728			
		/gi=13787208			
		/ug=Hs.169531			
mioc3593	NM_004728	/len=3319	NM_004728	Hs.169531	NP_004719
		eukaryotic translation			
		termination factor 1			
		(ETF1), mRNA			
		/cds=(136,1449)	İ		
		/gb=NM_004730			
		/gi=4759033	1		
		/ug=Hs.77324			
fcrb2849	NM_004730	/len=3653	NM_004730	Hs.77324	NP_004721
70.000		CCR4-NOT			
	1	transcription complex,			
		subunit 8 (CNOT8),			
		mRNA			
		· · · · · · · · · · · · · · · · · · ·			
		/cds=(245,1123)			
		/gb=NM_004779			
	}	/gi=24496777	ļ		
		/ug=Hs.26703			
seob9092	NM_004779	/len=2489	NM_004779	Hs.26703	NP_004770

Figure 6b Co	nica.		,		
seob3139	NM_004832	glutathione-S- transferase like; glutathione transferase omega (GSTTLp28), mRNA /cds=(10,735) /gb=NM_004832 /gi=4758483 /ug=Hs.11465 /len=793 eukaryotic translation		Hs.11465	NP_004823
seoa1083	NM_004836	initiation factor 2-alpha kinase 3 (EIF2AK3), mRNA /cds=(303,3650) /gb=NM_004836 /gi=21361154 /ug=Hs.102506 /len=4662	NM_004836	Hs.102506	NP_004827
seob6856	NM 004850	Rho-associated, coiled-coil containing protein kinase 2 (ROCK2), mRNA /cds=(455,4621) /gb=NM_004850 /gi=6633807 /ug=Hs.58617 /len=6409	NM 004850	Hs.58617	NP 004841
fcrb1787	NM_004859	clathrin, heavy polypeptide (Hc) (CLTC), mRNA /cds=(173,5200) /gb=NM_004859 /gi=4758011 /ug=Hs.178710 /len=6111	NM_004859	Hs.178710	NP_004850
seob3904	NM_004862	LPS-induced TNF- alpha factor (PIG7), mRNA /cds=(234,920) /gb=NM_004862 /gi=4758913 /ug=Hs.76507 /len=1773	NM_004862	Hs.76507	NP_004853
seoa4717	NM_004872	chromosome 1 open reading frame 8 (C1orf8), mRNA /cds=(251,1222) /gb=NM_004872 /gi=27545320 /ug=Hs.416495 /len=1709	NM_004872	Hs.416495	NP_004863

Figure 6b	Cont a.				
seob3189	NIM 004904	chromosome 14 open reading frame 2 (C14orf2), mRNA /cds=(61,237) /gb=NM_004894 /gi=4758939 /ug=Hs.109052	NM 004204	11- 400050	ND 004005
seob3189	NM_004894	/len=627	NM_004894	Hs.109052	NP_004885
seob3226	NM_004896	vacuolar protein sorting 26 (yeast) (VPS26), mRNA /cds=(80,1063) /gb=NM_004896 /gi=17978518 /ug=Hs.67052 /len=2652	NM_004896	Hs.67052	NP 004887
		RNA-binding region (RNP1, RRM) containing 2 (RNPC2), mRNA /cds=(150,1724) /gb=NM_004902 /gi=4757925 /ug=Hs.145696			
seob6015	NM_004902	/len=2595	NM_004902	Hs.145696	NP_004893
mine2967	NM 004003	RNA-binding region (RNP1, RRM) containing 2 (RNPC2), mRNA /cds=(150,1724) /gb=NM_004902 /gi=4757925 /ug=Hs.145696	NIM COACCO	Uo 4 45000	ND 004000
mioc3867	NM_004902	/len=2595 cerebral cavernous malformations 1 (CCM1), mRNA /cds=(26,1615) /gb=NM_004912 /gi=4758657 /ug=Hs.93810	NM_004902	Hs.145696	NP_004893
mioc4190	NM_004912	/len=2004	NM_004912	Hs.93810	NP_004903
fcrb6939	NM 004926	zinc finger protein 36, C3H type-like 1 (ZFP36L1), mRNA /cds=(131,1147) /gb=NM_004926 /gi=15812179 /ug=Hs.85155 /len=3022	NM_004926	Hs.85155	NP 004917
			1	1	1. 100 70 17

Figure 6b Co	JIILU.				
		FK506 binding protein			
		12-rapamycin			
	ļ	associated protein 1			
		(FRAP1), mRNA			
		/cds=(80,7729)			
		/gb=NM_004958			
'		_			
		/gi=19924298			
		/ug=Hs.338207			
ncr1122	NM_004958	/len=8680	NM_004958	Hs.338207	NP_004949
		integrin-binding			
		sialoprotein (bone			
		sialoprotein, bone	•		
		sialoprotein II) (IBSP),			
		mRNA			
		/cds=(143,1096)			
		/gb=NM_004967			
		/gi=13259536			
		/ug=Hs.49215			. <u></u>
ncr0491	NM_004967	/len=1108	NM_004967	Hs.49215	NP_004958
		methyl CpG binding			
		protein 2 (Rett		1	
		syndrome) (MECP2),			
		mRNA			
		/cds=(168,1628)	į		
		/gb=NM_004992			
		/gi=7710148			
		/ug=Hs.3239			
mioa5511	NM_004992	/len=10182	NINA OO 4000	Un 2020	ND 004000
1111045511	14141_004992	<u> </u>	NM_004992	Hs.3239	NP_004983
		mRNA for 3'5' cyclic			
		nucleotide			
		phosphodiesterase			
seob4363	AJ401610	(PDE1A5 gene)		Hs.41717	NP_005010
		serine (or cysteine)			
]		proteinase inhibitor,			
		clade I (neuroserpin),			
		member 1 (SERPINI1),			
		mRNA /cds=(82,1314)			
		/gb=NM_005025			
		/gi=4826903			
		1 ~			
	N	/ug=Hs.78589			
miob6688	NM_005025	/len=1559	NM_005025	Hs.78589	NP_005016
}					
		proteasome (prosome,			
		macropain) 26S			
		subunit, non-ATPase,			
		5 (PSMD5), mRNA			
		/cds=(20,1534)			
		/gb=NM_005047			
		/gi=25777613			
		/ug=Hs.193725			
fcrc5233	NM_005047	/len=3411	NM_005047	Hs.193725	NID OUEUSO
10100200	114101_000047	/ C -0 +		[113.133123	NP_005038

Application of: Liew, et. al. Our Docket #: 4231/2042 Figure 6b Cont'd.

Figure 6b	Conta.				
		transducin-like			
		enhancer of split 1			
		(E(sp1) Drosophila)			
		(TLE1), mRNA			
		/cds=(451,2763)			
		/gb=NM_005077			
		/gi=21541823			
		/ug=Hs.28935			
ncr9125	NM_005077	/len=3292	NM_005077	Hs.28935	NP_005068
		sarcospan (Kras	1	110.2000	141_000000
		oncogene-associated			
		gene) (SSPN), mRNA			
		/cds=(85,816)			
		/gb=NM_005086			
		/gi=16933560			
		/ug=Hs.183428			
ncr2391	NM 005086	/len=2707	NIM OOFOOG	Un 402420	ND 005077
11012391			NM_005086	Hs.183428	NP_005077
ļ		nuclear receptor subfamily 1, group D,			
		member 2, clone			
		MGC:33914			
2004	20045040	IMAGE:5274113,			
ncr9881	BC045613	mRNA, complete cds		Hs.37288	NP_005117
		ATP synthase, H			
		transporting,			
		mitochondrial F0			
		complex, subunit c			
		(subunit 9), isoform 1			
		(ATP5G1), mRNA			
		/cds=(120,530)			
		/gb=NM_005175			
ŀ		/gi=4885080	1		
mioa0707	NM_005175	/ug=Hs.80986 /len=631	NM_005175	Hs.80986	NP_005166
		ATP synthase, H			
		transporting,			
		mitochondrial F0			
		complex, subunit c			
		(subunit 9), isoform 1			
1		(ATP5G1), mRNA			
		/cds=(120,530)]		
		/gb=NM_005175	1		
1		/gi=4885080	1	1	
ncrc4994	NM 005175	/ug=Hs.80986 /len=631	NM 005175	Hs.80986	NP 005166
		CCAAT/enhancer	000170	110.00000	141 _000 100
		binding protein			
		(C/EBP), beta			
seoa4436	NM_005194	(CEBPB), mRNA	NM_005194	Hs.99029	NP_005185
220047700	11111_000104	LOCAL D), IIIXIAA	TAIN 000 194	1113.33023	111F_000100

Figure 6b	Conta.	 ,			
mioa8857	NM_005245	FAT tumor suppressor 1 (Drosophila) (FAT), mRNA /cds=(187,13959) /gb=NM_005245 /gi=4885228 /ug=Hs.166994 /len=14756	NM_005245	Hs.166994	NP 005236
IIIIOaooo7		glucose regulated	114141_005245	HS. 100994	NP_005236
		protein, 58kDa (GRP58), mRNA /cds=(90,1607) /gb=NM_005313 /gi=21361656 /ug=Hs.13751			
ncr4009	NM_005313	/len=2074	NM_005313	Hs.13751	NP_005304
fcr3181	NM_005318	H1 histone family, member 0 (H1F0), mRNA	NM_005318	Hs.226117	NP_005309
miob2375	NM_005324	H3 histone, family 3B (H3.3B) (H3F3B), mRNA /cds=(118,528) /gb=NM_005324 /gi=21264598 /ug=Hs.180877 /len=1662	NM_005324	Hs.180877	NP_005315
fcrb2926	NM_005324	H3 histone, family 3B (H3.3B) (H3F3B), mRNA /cds=(118,528) /gb=NM_005324 /gi=21264598 /ug=Hs.180877 /len=1662	NM_005324	Hs.180877	NP_005315
ncr6137	NM 005340	histidine triad nucleotide binding protein 1 (HINT1), mRNA /cds=(108,488) /gb=NM_005340 /gi=4885412 /ug=Hs.256697 /len=641	NM 005340	Hs.256697	NP 005331

Figure 6b Co	onta.				
		heat shock 70kDa			
		protein 5 (glucose-			
		regulated protein,			
		78kDa) (HSPA5),			
		mRNA '			
		/cds=(205,2169)			
-		/gb=NM_005347			
		1 -		1	
		/gi=21361242			
		/ug=Hs.75410		l	
seoa5429	NM_005347	/len=3925	NM_005347	Hs.75410	NP_005338
		heat shock 70kDa			
		protein 5 (glucose-			
		regulated protein,			
		78kDa) (HSPA5),			
		mRNA			
		/cds=(205,2169)			
		/gb=NM 005347			
		/gi=21361242			
		/ug=Hs.75410			
seob1191	NM 005347	/len=3925	NM_005347	Hs.75410	ND 005220
26001191	NIVI_005347	heat shock 70kDa	NIVI_005347	INS. 754 10	NP_005338
		protein 5 (glucose-			
		regulated protein,			
		78kDa) (HSPA5),			
		mRNA			
		/cds=(205,2169)			
		/gb=NM_005347			
		/gi=21361242			
		/ug=Hs.75410			
fcrb4788	NM_005347	/len=3925	NM_005347	Hs.75410	NP 005338
	,	v-maf			
	}	musculoaponeurotic			
		fibrosarcoma			
		oncogene (avian)			
		(MAF), mRNA	1		
1		/cds=(808,2019)	1		
		/gb=NM_005360			
		/gi=5453735			
		/ug=Hs.30250			
ncrc9729	NM_005360	/len=2145	NM_005360	Hs.30250	NP_005351
		protein phosphatase 1,			
		regulatory (inhibitor)	ľ		
	1	subunit 3C			
1		(PPP1R3C), mRNA	1		}
•		/cds=(58,1011)			
		/gb=NM_005398			
		/gi=21314622			
		1 ~			
mioo0211	NIM 005300	/ug=Hs.303090	NINA DOESOO	11- 202000	ND 005000
mioa0311	NM_005398	/len=2524	NM_005398	Hs.303090	NP_005389

Figure ob Co	nica.				
		protein phosphatase 1,			
		regulatory (inhibitor)			
		subunit 3C			
		(PPP1R3C), mRNA			
					•
		/cds=(58,1011)			
		/gb=NM_005398			
		/gi=21314622			
		/ug=Hs.303090			
miod2007	NM_005398	/len=2524	NM_005398	Hs.303090	NP 005389
		protein phosphatase 1,		·	
1		regulatory (inhibitor)			
1		subunit 3C			
		(PPP1R3C), mRNA			
		/cds=(58,1011)			
		/gb=NM_005398			
		/gi=21314622	,		
		/ug=Hs.303090			
ncrc3541	NM_005398	/len=2524	NM_005398	Hs.303090	NP 005389
		chondroitin sulfate			
		proteoglycan 6			
		(bamacan) (CSPG6),			
		mRNA /cds=(92,3745)			
		1 ' '			
		/gb=NM_005445			
		/gi=24475891			
	l	/ug=Hs.24485			
ncr6881	NM_005445	/len=4096	NM_005445	Hs.24485	NP_005436
		zinc finger protein 265			
		(ZNF265), mRNA			
		/gb=NM_005455			
		/gi=19923317			
		/ug=Hs.194718			
mioc2219	NM_005455	/len=2837	NM_005455	Hs.194718	NP 005446
		ADP-ribosyltransferase			
		(NAD ; poly(ADP-			
		ribose) polymerase)-			
		like 2 (ADPRTL2),			
		mRNA			
		/cds=(150,1754)			
1		/gb=NM_005484			
		/gi=11496991			
	ļ	/ug=Hs.24284			
mioa7069	NM_005484	/len=1887	NM_005484	Hs.24284	NP 005475
		inhibitor of growth			——————————————————————————————————————
,	i .				
3		Itamily, member 1			1
		family, member 1			
		(ING1), mRNA			
		(ING1), mRNA /cds=(433,1701)			
		(ING1), mRNA /cds=(433,1701) /gb=NM_005537			
		(ING1), mRNA /cds=(433,1701) /gb=NM_005537 /gi=19923770			
fcrc2775	NM_005537	(ING1), mRNA /cds=(433,1701) /gb=NM_005537	NM_005537	Hs.46700	NP 005528

Figure 60	Contu.		, 		
fcrb2218 ncrc0408	NM_005594 AK024964	nascent-polypeptide- associated complex alpha polypeptide (NACA), mRNA /cds=(26,673) /gb=NM_005594 /gi=5031930 /ug=Hs.32916 /len=797 cDNA: FLJ21311 fis, clone COL02167. /gb=AK024964 /gi=10437390 /ug=Hs.173933 /len=3216 ATPase, Class I, type	7 NM_005594	Hs.32916 Hs.173933	NP_005585 NP_005586
ncr5975	NM_005603	8B, member 1 (ATP8B1), mRNA /cds=(1,3756) /gb=NM_005603 /gi=5031696 /ug=Hs.406187 /len=3756	NM_005603	Hs.406187	NP_005594
seob8483	NM_005605	protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform (calcineurin A gamma) (PPP3CC), mRNA /cds=(337,1875) /gb=NM_005605 /gi=21361289 /ug=Hs.75206 /len=2230	NM 005605	Hs.75206	NP 005596
seob1538	NM_005611	retinoblastoma-like 2 (p130) (RBL2), mRNA /cds=(70,3489) /gb=NM_005611 /gi=21361291 /ug=Hs.79362 /len=4853	NM_005611	Hs.79362	NP_005602
ncrc0907	NM_005623	chemokine (C-C motif) ligand 8 (CCL8), mRNA /cds=(456,755) /gb=NM_005623 /gi=22538815 /ug=Hs.271387 /len=1351	NM_005623	Hs.271387	NP_005614

Cont'd.				
NM_005627	serum/glucocorticoid regulated kinase (SGK), mRNA /cds=(58,1353) /gb=NM_005627 /gi=25168262 /ug=Hs.296323 /len=2386	NM_005627	Hs.296323	NP_005618
NM_005642	TAF7 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 55kDa (TAF7), mRNA /cds=(741,1790) /gb=NM_005642 /gi=14717406 /ug=Hs.155188 /len=2310	NM_005642	Hs.155188	NP_005633
NIM 005642	II, TATA box binding protein (TBP)-associated factor, 55kDa (TAF7), mRNA/cds=(741,1790)/gb=NM_005642/gi=14717406/ug=Hs.155188		Ua 455400	NID 005022
	TGFB inducible early growth response (TIEG), mRNA /cds=(124,1566) /gb=NM_005655 /gi=5032176 /ug=Hs.82173	_		NP_005633
NM_005655	TGFB inducible early growth response (TIEG), mRNA /cds=(124,1566) /gb=NM_005655 /gi=5032176 /ug=Hs.82173 /len=2899	NM_005655	Hs.82173	NP_005646
	NM_005642 NM_005645	regulated kinase (SGK), mRNA /cds=(58,1353) /gb=NM_005627 /gi=25168262 /ug=Hs.296323 /len=2386 TAF7 RNA polymerase II, TATA box binding protein (TBP)- associated factor, 55kDa (TAF7), mRNA /cds=(741,1790) /gb=NM_005642 /gi=14717406 /ug=Hs.155188 /len=2310 TAF7 RNA polymerase II, TATA box binding protein (TBP)- associated factor, 55kDa (TAF7), mRNA /cds=(741,1790) /gb=NM_005642 /gi=14717406 /ug=Hs.155188 NM_005642 /gi=14717406 /ug=Hs.155188 NM_005642 /gi=14717406 /ug=Hs.155188 NM_005655 /gi=14717406 /ug=Hs.155188 NM_005655 /gi=5032176 /ug=Hs.82173 /len=2899 TGFB inducible early growth response (TIEG), mRNA /cds=(124,1566) /gb=NM_005655 /gi=5032176 /ug=Hs.82173 /ug=Hs.82173 /ug=Hs.82173	regulated kinase (SGK), mRNA /cds=(58,1353) /gb=NM_005627 /gi=25168262 /ug=Hs.296323 NM_005627 TAF7 RNA polymerase II, TATA box binding protein (TBP)- associated factor, 55kDa (TAF7), mRNA /cds=(741,1790) /gb=NM_005642 /gi=14717406 /ug=Hs.155188 NM_005642 TAF7 RNA polymerase II, TATA box binding protein (TBP)- associated factor, 55kDa (TAF7), mRNA /cds=(741,1790) /gb=NM_005642 /gi=14717406 /ug=Hs.155188 NM_005642 /gi=14717406 /ug=Hs.155188 NM_005642 /gi=14717406 /ug=Hs.155188 NM_005642 /gi=14717406 /ug=Hs.155188 NM_005642 /gi=14717406 /ug=Hs.155188 NM_005655 /gi=5032176 /ug=Hs.82173 NM_005655 /gi=5032176 /ug=Hs.82173 /ug=Hs.82173 /ug=Hs.82173 /ug=Hs.82173 /ug=Hs.82173 /ug=Hs.82173 /ug=Hs.82173	regulated kinase (SGK), mRNA /cds=(58,1353) /gb=NM_005627 /gi=25168262 //gi=45168262 //gi=45168263 NM_005627 TAF7 RNA polymerase II, TATA box binding protein (TBP)- associated factor, 55KDa (TAF7), mRNA /cds=(741,1790) //gb=NM_005642 //gi=14717406 //ug=Hs.155188 NM_005642 TAF7 RNA polymerase II, TATA box binding protein (TBP)- associated factor, 55KDa (TAF7), mRNA /cds=(741,1790) //gb=NM_005642 //gi=14717406 //ug=Hs.155188 NM_005642 TAF7 RNA polymerase II, TATA box binding protein (TBP)- associated factor, 55KDa (TAF7), mRNA /cds=(741,1790) //gb=NM_005642 //gi=14717406 //ug=Hs.155188 NM_005642 TGFB inducible early growth response (TIEG), mRNA //cds=(124,1566) //gb=NM_005655 //gi=5032176 //ug=Hs.82173 NM_005655 //gi=5032176 //ug=Hs.82173 //ug=Hs.82173 //ug=Hs.82173 //ug=Hs.82173 //ug=Hs.82173 //ug=Hs.82173 //ug=Hs.82173 //ug=Hs.82173 //ug=Hs.82173 //ug=Hs.82173 //ug=Hs.82173 //ug=Hs.82173 //ug=Hs.82173 //ug=Hs.82173 //ug=Hs.82173 //ug=Hs.82173 //ug=Hs.82173 //ug=Hs.82173 //ug=Hs.82173

Figure 6b Co	onta.	· · · · · · · · · · · · · · · · · · ·			
		tetraspan 3 (TSPAN- 3), mRNA /cds=(218,979) /gb=NM_005724 /gi=21264581 /ug=Hs.100090			
miod1044	NM_005724	/len=1842	NM_005724	Hs.100090	NP_005715
20004034	T00422	yc77a06.s1 Soares infant brain 1NIB cDNA clone IMAGE:21844 3', mRNA sequence /clone=IMAGE:21844 /clone_end=3' /gb=T66132 /gi=675177 /ug=Hs.332583		U- 220502	ND 005706
seoc1034	T66132	/len=246		Hs.332583	NP_005728
seob9818	NM_005738	ADP-ribosylation factor- like 4 (ARL4), mRNA /cds=(154,756) /gb=NM_005738 /gi=5031602 /ug=Hs.245540 /len=1077	NM 005738	Hs.245540	NP 005729
300000	0007.00	transducer of ERBB2,		110.2 100 10	741 _000720
seob5726	NM_005749	1 (TOB1), mRNA /cds=(36,1073) /gb=NM_005749 /gi=22035666 /ug=Hs.178137 /len=1830	NM_005749	Hs.178137	NP 005740
		C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 1 (cartilage-derived) (CLECSF1), mRNA /cds=(80,673) /gb=NM_005752 /gi=5031636 /ug=Hs.287364	1.1.1_000140		TH _000/40
seoc6745	NM_005752	/len=673	NM_005752	Hs.287364	NP_005743
ncr0791	NM_005759	abl-interactor 2 (ABI-2), mRNA /cds=(35,1462) /gb=NM_005759 /gi=20127476 /ug=Hs.343575 /len=1735	NM_005759	Hs.343575	NP_005750

61
61
61
61
61
74
82

Figure ob	COIR G.				
		neuroepithelial cell			
		transforming gene 1	1		
		(NET1), mRNA			
		/cds=(147,1775)			
					1
		/gb=NM_005863			
		/gi=19923326			
		/ug=Hs.25155			
ncrb8396	NM_005863	/len=3236	NM_005863	Hs.25155	NP_005854
		neuroepithelial cell			
		transforming gene 1			
		(NET1), mRNA			
		/cds=(147,1775)			
		/gb=NM_005863			
		/gi=19923326			
		/ug=Hs.25155			
ncrc9004	NM_005863	/len=3236	NM_005863	Hs.25155	NP_005854
		formin-like (FMNL),			
		mRNA			
		/cds=(635,2026)			
		/gb=NM_005892			
1		/gi=21735573			
1010		/ug=Hs.100217			
seoc1218	NM_005892	/len=2384	NM_005892	Hs.100217	NP_005883
		sarcoma amplified		· ·	
		sequence (SAS),			
	į	mRNA /cds=(155,787)			
	İ	/gb=NM_005981			
		/gi=21264346			
		1 -			
0004		/ug=Hs.50984			l
seoa9931	NM_005981	/len=1809	NM_005981	Hs.50984	NP_005972
ļ		ubiquitin carboxyl-			
		terminal esterase L3			
		(ubiquitin thiolesterase)			
}		(UCHL3), mRNA			
		/cds=(43,735)			
		/gb=NM_006002			•
		/gi=20149578			
seob3090	NM_006002	/ug=Hs.77917 /len=911	NM_006002	Hs.77917	NP_005993
		ubiquinol-cytochrome c			
		reductase hinge	İ	1	
		protein (UQCRH),			
		mRNA /cds=(37,312)			
		/gb=NM_006004			
ĺ		1 · -			
4005	NINA 000004	/gi=5174744		70040	
seoa4395	NM_006004	/ug=Hs.73818 /len=515	NM_006004	Hs.73818	NP_005995

fcrb4252 NN	M_006009	tubulin, alpha 3 (TUBA3), mRNA /cds=(100,1455) /gb=NM_006009 /gi=17986282 /ug=Hs.433394 /len=1677 ribosomal protein L10 (RPL10), mRNA	NM_006009	Hs.433394	
fcrb4252 NM	M_006009	/len=1677 ribosomal protein L10	NM_006009	Hs 433394	
		•	 	1.13.700007	NP_006000
ncrc9709 NN		/cds=(42,686) /gb=NM_006013 /gi=15718685 /ug=Hs.412900 /len=2188	NM_006013	Hs.412900	NP_006004
ncr0634 NA		paraneoplastic antigen MA1 (PNMA1), mRNA /cds=(665,1726) /gb=NM_006029 /gi=14719429 /ug=Hs.194709 /len=2530	NM_006029	Hs.194709	NP 006020
		LanC lantibiotic synthetase component C-like 1 (bacterial) (LANCL1), mRNA /cds=(105,1304) /gb=NM_006055 /gi=5174444 /ug=Hs.13351			
seob1617 NA		/len=4544 tubulin, alpha, ubiquitous (K-ALPHA- 1), mRNA /cds=(68,1423) /gb=NM_006082 /gi=5174476 /ug=Hs.334842	NM_006055	Hs.13351	NP_006046
fcrb1618 NN	M_006082	/len=1596	NM_006082	Hs.334842	NP_006073
seob4726 NN		N-myc downstream regulated gene 1 (NDRG1), mRNA /cds=(111,1295) /gb=NM_006096 /gi=5174656 /ug=Hs.75789 /len=3020	NM_006096	Hs.75789	NP_006087

Figure 6b Co	iii u.				<u>. </u>
		iduronate 2-sulfatase			
		(Hunter syndrome)			
		(IDS), transcript variant			
		1, mRNA			
		/cds=(332,1984)			
		/gb=NM_000202			
		/gi=5360215	NIA 000000		
		/ug=Hs.172458	NM_000202;		
miob9902	NM_000202	/len=2504	NM_006123	Hs.172458	NP_006114
		chromosome 21 open			
		reading frame 4			
		(C21orf4), mRNA			
		/cds=(159,635)			
		/gb=NM_006134			
		/gi=8659558			
		/ug=Hs.284142			
mioa4674	NM_006134	/len=750	NM_006134	Hs.284142	NP 006125
1111047017	11111_000104	LIM and SH3 protein 1	14141_000104	113.207172	141 _000120
		(LASP1), mRNA			
		`			
		/cds=(76,861)			
		/gb=NM_006148			
		/gi=5453709			
		/ug=Hs.334851			
seoa5784	NM_006148	/len=3846	NM_006148	Hs.334851	NP_006139
		NCK adaptor protein 1			
		(NCK1), mRNA			
		/cds=(117,1250)			
		/gb=NM_006153			
		/gi=20070226			
		/ug=Hs.54589			
seoa4587	NM 006153	/len=1947	NIM 000452	LI- 54500	ND 000444
5004307	14141_000133	/len=1947	NM_006153	Hs.54589	NP_006144
		nuclear transcription			
		factor Y, beta (NFYB),			
		mRNA /cds=(101,724)			
		/gb=NM_006166			
		/gi=11496976			
mioc7559	NM 006166	/ug=Hs.84928 /len=734	NM 006166	Hs.84928	NP 006157
		<u> </u>			
		poly(rC) binding protein			
		1 (PCBP1), mRNA			
1		, , , , ,			
1		/cds=(178,1248)			
		/gb=NM_006196			
		/gi=14141164			
fcrb0265	NM_006196	/ug=Hs.2853 /len=1634	NM_006196	Hs.2853	NP_006187

Figure 6b Co	ont'd.				
seob7082	NM_006196	poly(rC) binding protein 1 (PCBP1), mRNA /cds=(178,1248) /gb=NM_006196 /gi=14141164 /ug=Hs.2853 /len=1634 platelet-derived growth factor receptor, alpha polypeptide (PDGFRA), mRNA /cds=(395,3664)		Hs.2853	NP_006187
ncrc9910	NM_006206	/gb=NM_006206 /gi=15451787 /ug=Hs.74615 /len=6633	NM_006206	Hs.74615	NP_006197
ncr4793	D30036	mRNA for phosphatidylinositol transfer protein (Pl-TPalpha), complete cds	NM_006224	Hs.433429	NP 006215
seoc1906	NM_006241	protein phosphatase 1, regulatory (inhibitor) subunit 2 (PPP1R2), mRNA /cds=(235,852) /gb=NM_006241 /gi=19923357 /ug=Hs.267819 /len=3355	NM_006241	Hs.267819	NP_006232
ncr0766	NM_006286	transcription factor Dp- 2 (E2F dimerization partner 2) (TFDP2), mRNA /cds=(141,1301) /gb=NM_006286 /gi=5454111 /ug=Hs.379018 /len=2320	NM_006286	Hs.379018	NP_006277
seoa1132	NM_006294	ubiquinol-cytochrome c reductase binding protein (UQCRB), mRNA /cds=(54,389) /gb=NM_006294 /gi=20070231 /ug=Hs.131255 /len=965	NM_006294	Hs.131255	NP_006285

brain abundant, membrane attached signal protein 1 (BASP1), mRNA /cds=(53,736)/gb=NM_006317 /gi=5453749 /ug=Hs.79516 seob6535 NM 006317 /len=1486 NM_006317 Hs.79516 NP_006308 brain abundant. membrane attached signal protein 1 (BASP1), mRNA /cds=(53,736) /gb=NM 006317 /gi=5453749 /ug=Hs.79516 fcrc4669 NM_006317 /len=1486 NM 006317 Hs.79516 NP_006308 translocase of inner mitochondrial membrane 17 A (yeast) (TIMM17A), mRNA /cds=(8,523) /gb=NM 006335 /gi=5454119 /ug=Hs.20716 miob4238 NM_006335 /len=1645 NM_006335 Hs.20716 NP 006326 translocase of inner mitochondrial membrane 17 A (yeast) (TIMM17A), mRNA /cds=(8,523) /gb=NM_006335 /gi=5454119 /ug=Hs.20716 seoc2504 NM 006335 /len=1645 NM_006335 Hs.20716 NP 006326 ATP synthase, H transporting, mitochondrial F0 complex, subunit d (ATP5H), mRNA /cds=(46,531) /gb=NM 006356 /gi=5453558 ncrc0327 NM 006356 /ug=Hs.49018 /len=628 NM 006356 Hs.49018 NP 006347

ont'd.			·	
NM_006367	adenylyl cyclase- associated protein (CAP), mRNA /cds=(63,1490) /gb=NM_006367 /gi=10938021 /ug=Hs.104125 /len=2614	NM_006367	Hs.104125	NP_006358
NM_006369	MUF1 protein (MUF1), mRNA /cds=(1,1854) /gb=NM_006369 /gi=5453747 /ug=Hs.172210 /len=2165	NM_006369	Hs.172210	NP_006360
NM_006371	cartilage associated protein (CRTAP), mRNA /cds=(12,1217) /gb=NM_006371 /gi=21536278 /ug=Hs.155481 /len=2307	NM_006371	Hs.155481	NP_006362
	amyloid beta precursor protein (cytoplasmic tail) binding protein 2 (APPBP2), mRNA /cds=(289,2046) /gb=NM_006380 /gi=18104961 /ug=Hs.84084			
	regulated in glioma (RIG), mRNA /cds=(26,358) /gb=NM_006394 /gi=5454007 /ug=Hs.278503	_		NP_006371
NM_006402	hepatitis B virus x interacting protein (HBXIP), mRNA /cds=(56,331) /gb=NM_006402 /gi=5454169 /ug=Hs.433355 /len=605	NM_006402	Hs.433355	NP_006385
	NM_006369 NM_006371 NM_006380	associated protein (CAP), mRNA /cds=(63,1490) /gb=NM_006367 /gi=10938021 /ug=Hs.104125 /len=2614 MUF1 protein (MUF1), mRNA /cds=(1,1854) /gb=NM_006369 /gi=5453747 /ug=Hs.172210 /len=2165 cartilage associated protein (CRTAP), mRNA /cds=(12,1217) /gb=NM_006371 /gi=21536278 /ug=Hs.155481 /len=2307 amyloid beta precursor protein (cytoplasmic tail) binding protein 2 (APPBP2), mRNA /cds=(289,2046) /gb=NM_006380 /gi=18104961 /ug=Hs.84084 NM_006380 /len=6468 regulated in glioma (RIG), mRNA /cds=(26,358) /gb=NM_006394 /gi=5454007 /ug=Hs.278503 NM_006394 /len=2569 hepatitis B virus x interacting protein (HBXIP), mRNA /cds=(56,331) /gb=NM_006402 /gi=5454169 /ug=Hs.433355	associated protein (CAP), mRNA /cds=(63,1490) /gb=NM_006367 /gi=10938021 /ug=Hs.104125 NM_006367 MUF1 protein (MUF1), mRNA /cds=(1,1854) /gb=NM_006369 /gi=5453747 /ug=Hs.172210 NM_006369 cartilage associated protein (CRTAP), mRNA /cds=(12,1217) /gb=NM_006371 /gi=21536278 /ug=Hs.155481 NM_006371 amyloid beta precursor protein (cytoplasmic tail) binding protein 2 (APPBP2), mRNA /cds=(289,2046) /gb=NM_006380 /gi=18104961 /ug=Hs.84084 NM_006380 regulated in glioma (RIG), mRNA /cds=(26,358) /gb=NM_006394 /gi=5454007 /ug=Hs.278503 NM_006394 NM_006394 len=2569 NM_006394 /ds=569 NM_006394 /gb=NM_006402 /gi=5454169 /ug=Hs.433355	associated protein (CAP), mRNA (Ids=(63,1490) (gb=NM_006367 (gi=10938021 (gi=10938021 (gi=10938021 (gi=10938021 (gi=5453747 (gi=10938021 (gi=5453747 (gi=10) (gi=5453747 (gi=10) (gi=5453747 (gi=10) (gi=5453747 (gi=10) (gi=5453747 (gi=10) (

Figure ob	Conta.				
		protein C receptor, endothelial (EPCR) (PROCR), mRNA /cds=(83,799) /gb=NM_006404 /gi=21361313 /ug=Hs.82353	,		
mioc4174	NM_006404	/len=1381	NM 006404	Hs.82353	NP 006395
ncrc6712	NM_006407	vitamin A responsive; cytoskeleton related (JWA), mRNA /cds=(90,656) /gb=NM_006407 /gi=7669496 /ug=Hs.92384 /len=2088			
miob4322	NM_006449	CDC42 effector protein (Rho GTPase binding) 3 (CDC42EP3), mRNA /cds=(969,1733) /gb=NM_006449 /gi=19923355 /ug=Hs.260024 /len=2768		Hs.92384 Hs.260024	NP_006398 NP_006440
fcrc2099	NM_006449	CDC42 effector protein (Rho GTPase binding) 3 (CDC42EP3), mRNA /cds=(969,1733) /gb=NM_006449 /gi=19923355 /ug=Hs.260024 /len=2768	NM_006449	Hs.260024	NP_006440
ncr8420	NM_006449	CDC42 effector protein (Rho GTPase binding) 3 (CDC42EP3), mRNA /cds=(969,1733) /gb=NM_006449 /gi=19923355 /ug=Hs.260024 /len=2768	NM_006449	Hs.260024	NP_006440
fcr6039	NM_006482	dual-specificity tyrosine- (Y)-phosphorylation regulated kinase 2 (DYRK2), transcript variant 2, mRNA	NM_003583; NM_006482	Hs.173135	NP_006473

Figure 6b	Conta.				
		SET domain and			
		mariner transposase			
		fusion gene			ľ
seoc4132	NM_006515	(SETMAR), mRNA	NM_006515	Hs.265855	NP 006506
	- 	t-complex-associated-			
		testis-expressed 1-like			
		1 (TCTEL1), mRNA			
		/cds=(1,342)			
		/gb=NM_006519			
		/gi=5730084			
		/ug=Hs.266940	Ì		
miob0178	NM_006519	/len=713	NM_006519	Hs.266940	NP_006510
1111000170	14141_000010	melanoma inhibitory	14141_000313	113.200340	147_000010
		activity (MIA), mRNA			
		/cds=(72,467)			
		•			
		/gb=NM_006533			
		/gi=5729924			
fcr3322	NIM OOGESS	/ug=Hs.279651	NIM OCCESS	110 070054	ND 000504
1013322	NM_006533	/len=538	NM_006533	Hs.279651	NP_006524
		KH domain containing,]	
		RNA binding, signal			
		transduction			
		associated 1			
	:				
		(KHDRBS1), mRNA			
		/cds=(107,1438)			
		/gb=NM_006559			
		/gi=5730026			
f	NINA 000550	/ug=Hs.119537			<u>.</u>
fcrb1633	NM_006559	/len=2685	NM_006559	Hs.119537	NP_006550
		SnRNP assembly			
		defective 1 (SAD1),			
		mRNA		1	
		/cds=(493,1467)	·		
		/gb=NM_006590			
		/gi=5730024]		
0704		/ug=Hs.12820			
mioa6734	NM_006590	/len=2166	NM_006590	Hs.12820	NP_006581
		otromal artists 2			
		stromal antigen 2			
		(STAG2), mRNA			
		/cds=(405,3893)			
		/gb=NM_006603			
	NIM OCCOO	/gi=27552767			
seob3303	NM_006603	/ug=Hs.8217 /len=4197	NM_006603	Hs.8217	NP_006594
		otromol options 2			
		stromal antigen 2			
		(STAG2), mRNA			
		/cds=(405,3893)	ł		
		/gb=NM_006603	· .		
minoSOSE	NM 00000	/gi=27552767	NINA COCCO	11- 0047	ND coord
mioc6925	NM_006603	/ug=Hs.8217 /len=4197	[NN] 006603	Hs.8217	NP_006594

Figure 6b Co	nt u.				
		HBS1-like (S.			
		cerevisiae) (HBS1L),			
		mRNA			
		/cds=(194,2248)			
		/gb=NM_006620			
		/gi=24431963			
		1 -			
		/ug=Hs.221040			
mioa5085	NM_006620	/len=7163	NM_006620	Hs.221040	NP_006611
		hydrolase-like 1			
		(AHCYL1), mRNA			
		/cds=(369,1961)			
		/gb=NM_006621			
		/gi=21361646			
miob9228	NM 006621	/ug=Hs.4113 /len=2677	NM 006621	Hs.4113	NP 006612
1111003220	14101_000021	/ug=119.41137len=2077	14141_000021	115.4113	NP_000012
		ovelie AMD			
		cyclic AMP			
		phosphoprotein, 19 kD			
		(ARPP-19), mRNA			
		/cds=(125,463)			
		/gb=NM_006628			
1		/gi=19923363			
seoa3514	NM_006628	/ug=Hs.7351 /len=5171	NM 006628	Hs.7351	NP 006619
		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	11111_000020	110.7001	
		methylene			
		tetrahydrofolate			
		dehydrogenase (NAD			
		dependent),			
		methenyltetrahydrofola			
		te cyclohydrolase			
		(MTHFD2), nuclear			
		gene encoding			
		mitochondrial protein,			
		mRNA /cds=(77,1111)			
		/gb=NM_006636			
		/gi=13699869			
0700	NINA 000000	/ug=Hs.154672			
seoa9709	NM_006636	/len=2154	NM_006636	Hs.154672	NP_006627
		WAS protein family,			
		member 3 (WASF3),			
		mRNA			
		/cds=(179,1687)			
		/gb=NM_006646			
		/gi=21237780			}
		/ug=Hs.82318			
mioc3011	NM 006646	/len=4768	NIM OOGG46	 La 00040	ND 000007
IIIIOCOUTT	14141_000040	/ICH-4/00	NM_006646	Hs.82318	NP_006637

Serologically defined Colon cancer antigen 16 (SDCCAG16) mRNA /cds=(29.2344) /gb=NM_006849 /gb=21361347 /ug=Hs.271926 /len=2509 NM_006649 Hs.271926 NP_006640 /len=2509 NM_006649 Hs.271926 NP_006640 /len=2509 NM_006649 Hs.271926 NP_006640 /len=2509 NM_006700 /lg=5729827 /lg=Hs.5148 /len=2618 NM_006700 /lg=5729827 /lg=Hs.5148 /len=2618 NM_006700 Hs.5148 NP_006691 /len=2618 NM_006700 /lg=5729827 /lg=Hs.5148 /len=2618 NM_006700 Hs.5148 NP_006691 /len=2618 NM_006700 /len=2618 NM_006700 /len=2618 NM_006700 /len=2618 NM_006700 /len=2618 NM_006700 /len=2618 NM_006700 /len=2618 NM_006700 /len=2618 NM_006700 /len=2618 NM_006700 /len=2618 NM_006718 /len=2618 NM_006	Figure 60 C	ont a.				
(FLN29), mRNA (/ds=(55,1803) /gb=NM_006700 /gi=5729827 /ug=Hs.5148 /len=2618 NM_006700 /gi=5729827 /ug=Hs.5148 /len=2618 NM_006700 /gi=5729827 /ug=Hs.5148 /len=2618 NM_006700 /gi=5729827 /ug=Hs.5148 /len=2618 NM_006700 /gi=5729825 /gi=27894292 /ug=Hs.75825 /gi=27894292 /ug=Hs.75825 /gi=27894292 /ug=Hs.75825 /gi=27894292 /ug=Hs.75825 /gi=3803206 /gi=3803206 /gi=3803206 /gi=3803206 /gi=3803206 /gi=3803206 /gi=3803206 /gi=3803206 /gi=3803206 /gi=3803206 /gi=5803206 /gi=5803206 /gi=5803206 /gi=5803206 /ug=Hs.271687 /ug=Hs.271687 /ug=Hs.271687 /gi=5803206 /ug=Hs.271687 /ug=Hs.271687 /ug=Hs.271687 /ug=Hs.271687 /ug=Hs.418083 /ug	fcrc2619	NM_006649	colon cancer antigen 16 (SDCCAG16), mRNA /cds=(29,2344) /gb=NM_006649 /gi=21361347 /ug=Hs.271926	NM_006649	Hs.271926	NP_006640
(FLN29), mRNA (/ds=(55,1803) /gb=NM_006700 /gi=5729827 /ug=Hs.5148 /len=2618 NM_006700 /gi=5729827 /ug=Hs.5148 /len=2618 NM_006700 /gi=5729827 /ug=Hs.5148 /len=2618 NM_006700 /gi=5729827 /ug=Hs.5148 /len=2618 NM_006700 /gi=5729825 /gi=27894292 /ug=Hs.75825 /gi=27894292 /ug=Hs.75825 /gi=27894292 /ug=Hs.75825 /gi=27894292 /ug=Hs.75825 /gi=3803206 /gi=3803206 /gi=3803206 /gi=3803206 /gi=3803206 /gi=3803206 /gi=3803206 /gi=3803206 /gi=3803206 /gi=3803206 /gi=5803206 /gi=5803206 /gi=5803206 /gi=5803206 /ug=Hs.271687 /ug=Hs.271687 /ug=Hs.271687 /gi=5803206 /ug=Hs.271687 /ug=Hs.271687 /ug=Hs.271687 /ug=Hs.271687 /ug=Hs.418083 /ug						
pleiomorphic adenoma gene-like 1 (PLAGL1), transcript variant 2, mRNA /cds=(2242,3633) /gb=NM_006718 /gi=27894292 /ug=Hs.75825 NM_002656; NM_006718 Hs.75825 NP_006709 immunodeficiency virus type I enhancer binding protein 2 (HIVEP2), mRNA /cds=(16,7518) /gb=NM_006734 /gi=19923373 /ug=Hs.75063 NM_006734 Hs.75063 NP_006725 NM_006734 /gi=91923373 /ug=Hs.75063 NM_006734 Hs.75063 NP_006725 NM_006734 /gi=91006734 /gi=91006734 /gi=91006734 /gi=91006734 /gi=91006734 /gi=91006734 /gi=91006734 /gi=91006734 /gi=91006734 /gi=91006734 /gi=91006734 /gi=91006735 /gi=9100			(FLN29), mRNA /cds=(55,1803) /gb=NM_006700 /gi=5729827			
gene-like 1 (PLAGL1), transcript variant 2, mRNA /cds=(2242,3633) /gb=NM_006718 /gi=27894292 /ug=Hs.75825 NM_006718 Hs.75825 NP_006709 immunodeficiency virus type I enhancer binding protein 2 (HIVEP2), mRNA /cds=(16,7518) /gb=NM_006734 /gi=19923373 /ug=Hs.75063 /len=9175 NM_006734 Hs.75063 NP_006725 retinol binding protein 4, plasma (RBP4), mRNA /cds=(89,688) /gb=NM_006744 /gi=8400727 /ug=Hs.418083 NP_006744 /gi=8400727 /ug=Hs.418083 NP_006735 NM_006744 /gi=8400727 /ug=Hs.418083 NP_006744 /gi=	fcrc2090	NM_006700			Hs.5148	NP_006691
virus type I enhancer binding protein 2 (HIVEP2), mRNA /cds=(16,7518) /gb=NM_006734 /gi=19923373 /ug=Hs.75063 /len=9175 NM_006734 Hs.75063 NP_006725 retinol binding protein 4, plasma (RBP4), mRNA /cds=(89,688) /gb=NM_006744 /gi=8400727 /ug=Hs.418083 /len=919 NM_006744 Hs.418083 NP_006735 U2(RNU2) small nuclear RNA auxillary factor 1 (U2AF1), mRNA /cds=(39,761) /gb=NM_006758 /gi=5803206 /ug=Hs.271687	seob1586	NM_006718	gene-like 1 (PLAGL1), transcript variant 2, mRNA /cds=(2242,3633) /gb=NM_006718 /gi=27894292 /ug=Hs.75825 /len=4816	NM_002656;	Hs.75825	NP_006709
Seob7015 NM_006734 /len=9175 NM_006734 Hs.75063 NP_006725			virus type I enhancer binding protein 2 (HIVEP2), mRNA /cds=(16,7518) /gb=NM_006734 /gi=19923373			
retinol binding protein 4, plasma (RBP4), mRNA /cds=(89,688) /gb=NM_006744 /gi=8400727 /ug=Hs.418083 /len=919 NM_006744 Hs.418083 NP_006735 U2(RNU2) small nuclear RNA auxillary factor 1 (U2AF1), mRNA /cds=(39,761) /gb=NM_006758 /gi=5803206 /ug=Hs.271687	seob7015	NM 006734	, –	NM 006734	Hs.75063	NP 006725
U2(RNU2) small nuclear RNA auxillary factor 1 (U2AF1), mRNA /cds=(39,761) /gb=NM_006758 /gi=5803206 /ug=Hs.271687			retinol binding protein 4, plasma (RBP4), mRNA /cds=(89,688) /gb=NM_006744 /gi=8400727 /ug=Hs.418083			000120
nuclear RNA auxillary factor 1 (U2AF1), mRNA /cds=(39,761) /gb=NM_006758 /gi=5803206 /ug=Hs.271687	ncr7792	NM_006744		NM_006744	Hs.418083	NP_006735
	fcr2607	NM 006758	nuclear RNA auxillary factor 1 (U2AF1), mRNA /cds=(39,761) /gb=NM_006758 /gi=5803206	NM_006758	Hs.271687	NP_006749

Figure 6b C	onta.		,		
		U2(RNU2) small			
		nuclear RNA auxillary			
		factor 1 (U2AF1),			
		mRNA /cds=(39,761)			
	1	/gb=NM_006758			
		/gi=5803206			
		/g=Hs.271687			
fcrb8901	NM_006758	/len=904	NIM 006750	Hs.271687	ND 000740
10100901		AFG3 ATPase family	NM_006758	IDS.27 1007	NP_006749
		•			
		gene 3-like 2 (yeast)			
		(AFG3L2), nuclear			
		gene encoding			
		mitochondrial protein,			
		mRNA			
		/cds=(114,2507)			
		/gb=NM_006796			
		/gi=5802969			
		/ug=Hs.29385			
fcrb7528	NM 006796	/len=2963	NM_006796	Hs.29385	NP 006787
		BTG family, member 3			
		(BTG3), mRNA			
		/cds=(155,1045)			
		/gb=NM_006806			
		/gi=21361363			
		•			
seoc2221	NIM ODGOOG	/ug=Hs.77311	NIM OCCOOC	11. 77044	ND 000707
Seoczzz I	NM_006806	/len=1511	NM_006806	Hs.77311	NP_006797
		for protein disulfide			
		isomerase-related			
		(PDIR), mRNA			
		/cds=(57,1616)			
		/gb=NM_006810			
		/gi=5803120			is
		/ug=Hs.76901			
miob6087	NM_006810	/len=1693	NM_006810	Hs.76901	NP_006801
		RAB40B, member			
		RAS oncogene family			
		(RAB40B), mRNA			
		/cds=(46,882)			
		/gb=NM_006822			
		/gi=5803162			
		/ug=Hs.302498			
ncrc5877	NM 006822	/len=1673	NM_006822	Hs.302498	NP 006813
110100077	11111_000022	cytoskeleton-	14141_000022	113.502450	INF_000013
	}	3 -	}		
		associated protein 4			
		(CKAP4), mRNA		-	
		/cds=(85,1893)			
		/gb=NM_006825			
		/gi=19920316			
		/ug=Hs.74368			
hfcr6370	NM 006825	/len=2913	NM_006825	Hs.74368	NP_006816

Figure 6b	Cont a.				
seoa5520	NM_006826	tyrosine 3- monooxygenase/trypto phan 5- monooxygenase activation protein, theta polypeptide (YWHAQ), mRNA /cds=(120,857) /gb=NM_006826 /gi=21464103 /ug=Hs.74405 /len=2166		Hs.74405	ND 006817
Se0a3320	14141_000626		14141_000020	INS.74405	NP_006817
seoa2819	NM_006827	transmembrane trafficking protein (TMP21), mRNA	NM_006827	Hs.74137	NP_006818
mine 2669	NIM OOGGGG	RNA helicase family (RNAH), mRNA /cds=(39,6647) /gb=NM_006828 /gi=24307916 /ug=Hs.48295	NIM 000000	11. 40005	ND 200040
mioa3668	NM_006828	/len=7315	NM_006828	Hs.48295	NP_006819
seoa6732	Z24725	mitogen inducible gene mig-2, complete CDS. /cds=(1,2165) /gb=Z24725 /gi=505032 /ug=Hs.75260 /len=3270	NM 006832	Hs.75260	NP 006823
ncr0144	NM_006860	RAB, member of RAS oncogene family-like 4 (RABL4), mRNA /cds=(364,921) /gb=NM_006860 /gi=9257237 /ug=Hs.50267 /len=1021	NM 006860	Hs.50267	NP 006851
		destrin (actin depolymerizing factor) (DSTN), mRNA /cds=(73,570) /gb=NM_006870 /gi=6466447 /ug=Hs.408576			
mioa0192	NM_006870	/len=1439	NM_006870	Hs.408576	NP_006861

Figure 6b Co	onta.				
		sterol-C5-desaturase			
		(ERG3 delta-5-			
		desaturase fungal)-like			
		(SC5DL), mRNA			
		/cds=(49,948)			
		/gb=NM_006918			
		/gi=10800413			1
		/ug=Hs.288031			
seoa9016	NM 006918	/len=2092	NM 006918	Hs.288031	NP_008849
00000010	11111_000010	splicing factor,	14111_000010	113.20001	141 _000043
		arginine/serine-rich 5			
		(SFRS5), mRNA			
		/cds=(219,542)			
		/gb=NM_006925			
		/gi=5902077			
		1 ~			
mara0420	NIM OCCOSE	/ug=Hs.166975	NIM OCCOSE	Un 400075	ND 000050
ncrc9428	NM_006925	/len=1865	NM_006925	Hs.166975	NP_008856
		nuclear pore complex			
		interacting protein			
		(NPIP), mRNA			
		/cds=(1,1053)			
		/gb=NM_006985			
		/gi=5902013			
		/ug=Hs.251928			
hfcr1964	NM_006985	/len=1070	NM_006985	Hs.251928	NP_008916
		chondromodulin I			
		precursor (CHM-I),			
		mRNA /cds=(1,1005)			
		/gb=NM_007015			
		/gi=5901931			
		/ug=Hs.97932			
hfcr0292	NM_007015	/len=1328	NM_007015	Hs.97932	NP_008946
		HIV-1 rev binding	Í		
		protein 2 (HRB2),			
		mRNA /cds=(30,1175)			
		/gb=NM_007043			
		/gi=21359979			
		/ug=Hs.154762			
ncr4194	NM_007043	/len=1527	NM_007043	Hs.154762	NP 008974
		clathrin, light	1		
		polypeptide (Lcb)			
		(CLTB), transcript			
1		variant brain, mRNA	ł		
		/cds=(173,862)			
		/gb=NM_007097			[
1		/gi=6005994			
1		/ug=Hs.380749	NM_001834;	1	
hfcr3615	NM_007097	/len=1134	. –	He 390740	ND 00000
111013013	ואואו_טטיטשי	Men-1194	NM_007097	Hs.380749	NP_009028

Figure 6b C	John G.				
seob7622	NM_007100	ATP synthase, H transporting, mitochondrial F0 complex, subunit e (ATP5I), mRNA /cds=(64,273) //gb=NM_007100 //gi=6005716 //ug=Hs.85539 /len=336	NM_007100	Hs.85539	NP_009031
ncrc4047	NM_007106	ubiquitin-like 3 (UBL3), mRNA /cds=(110,463) /gb=NM_007106 /gi=6005927 /ug=Hs.173091 /len=3323	NM_007106	Hs.173091	NP_009037
seoc2696	NM_007111	transcription factor Dp- 1 (TFDP1), mRNA /cds=(222,1454) /gb=NM_007111 /gi=21361419 /ug=Hs.79353 /len=2394	NM 007111	Hs.79353	NP 009042
miob6103	AK022561	cDNA FLJ12499 fis, clone NT2RM2001671, highly similar to Oryctolagus cuniculus sarcolemmal associated protein (SLAP1) mRNA		Hs.4007	NP_009090
mioc1122	NM_007266	XPA binding protein 1; putative ATP(GTP)- binding protein (NTPBP), mRNA /cds=(25,1149) /gb=NM_007266 /gi=14149628 /ug=Hs.18259 /len=1829	NM_007266	Hs.18259	NP_009197
seoa7212	NM_007270	FK506 binding protein 9, 63 kDa (FKBP9), mRNA /cds=(457,885) /gb=NM_007270 /gi=24307926 /ug=Hs.302749 /len=2517	NM_007270	Hs.302749	NP_009201

FK506 binding protein 9, 63 kDa (FKBP9), mRNA /cds=(457,885) /gb=NM_007270 /gi=24307926 /ug=Hs.302749 seoc0056 NM 007270 /len=2517 NM_007270 Hs.302749 NP_009201 FK506 binding protein 9, 63 kDa (FKBP9), mRNA /cds=(457,885) /gb=NM_007270 /gi=24307926 /ug=Hs.302749 fcrc2457 /len=2517 NM_007270 NM_007270 Hs.302749 NP 009201 GABA(A) receptorassociated protein (GABARAP), mRNA /cds=(105,458) /gb=NM 007278 /gi=6005763 seob2081 NM 007278 /ug=Hs.7719 /len=924 NM_007278 Hs.7719 NP 009209 synuclein, alpha (non A4 component of amyloid precursor) (SNCA), transcript variant NACP140, mRNA /cds=(47,469) /gb=NM 000345 /gi=6806896 /ug=Hs.76930 NM_000345; mioa9648 /len=1543 NM 000345 NM_007308 Hs.76930 NP_009292 MAD, mothers against decapentaplegic (Drosophila) interacting protein, receptor activation anchor (MADHIP), transcript variant 3, mRNA /cds=(439,4410) /gb=NM_004799 /gi=4759059 NM 004799; /ug=Hs.194716 NM_007323; NM_007324 ncrc1653 /len=4839 NM_004799 Hs.194716 NP_015563

Figure ob	Ouncu.		· · · · · · · · · · · · · · · · · · ·		····
mioa3572	NM_007361	nidogen 2 (osteonidogen) (NID2), mRNA /cds=(1,4131) /gb=NM_007361 /gi=6679055 /ug=Hs.82733 /len=4829	NM 007361	Hs.82733	NP 031387
		nuclear cap binding protein subunit 2, 20kDa (NCBP2), mRNA /cds=(27,497) /gb=NM_007362 /gi=19923386 /ug=Hs.240770	_		
seoa8993	NM_007362	/len=2120 phospholipase A2 receptor 1, 180kDa (PLA2R1), mRNA /cds=(207,4604) /gb=NM_007366 /gi=19923388 /ug=Hs.171945	NM_007362	Hs.240770	NP_031388
ncrb6261	NM_007366	/len=5633	NM_007366	Hs.171945	NP_031392
miod1707	J04806	Mus musculus osteopontin precursor, mRNA, complete cds Mus musculus troponin I, skeletal, fast 2		Mm.260317	NP_033289
miob4574	NM_009405	general transcription factor IIIC, polypeptide 3, 102kDa (GTF3C3), mRNA /cds=(94,2754) /gb=NM_012086 /gi=6912397 /ug=Hs.90847 /len=2961	NM_009405	Mm.39469	NP_033431
seob6064	NM_012096	adaptor protein containing pH domain, PTB domain and leucine zipper motif (APPL), mRNA /cds=(59,2188) /gb=NM_012096 /gi=6912241 /ug=Hs.27413 /len=5970	NM_012086	Hs.90847	NP_036218

Figure 6b Co	nitu.				
seob5223	NM_012098	angiopoietin-like 2 (ANGPTL2), mRNA /cds=(22,1503) /gb=NM_012098 /gi=6912235 /ug=Hs.8025 /len=1518	NM_012098	Hs.8025	NP_036230
miod0992	NM_012124	cysteine and histidine- rich domain (CHORD)- containing, zinc binding protein 1 (CHORDC1), mRNA /cds=(85,1083) /gb=NM_012124 /gi=6912303 /ug=Hs.22857 /len=2058	NM_012124	Hs.22857	NP 036256
		DEAD/H (Asp-Glu-Ala- Asp/His) box polypeptide 26 (DDX26), mRNA /cds=(477,3140) /gb=NM_012141 /gi=11024693 /ug=Hs.58570			
miob3591 fcrb2622	NM_012141 NM_012158	/len=3690 F-box and leucine-rich repeat protein 3A (FBXL3A), mRNA /cds=(298,1584) /gb=NM_012158 /gi=16306583 /ug=Hs.7540 /len=3489	NM_012141 NM_012158	Hs.58570 Hs.7540	NP_036273 NP_036290
ncr8538	NM_012158	F-box and leucine-rich repeat protein 3A (FBXL3A), mRNA /cds=(298,1584) /gb=NM_012158 /gi=16306583 /ug=Hs.7540 /len=3489	NM_012158	Hs.7540	NP_036290
ncrc9959	AF307332	meningioma- expressed antigen 5s splice variant mRNA, complete cds	 NM_012215	Hs.5734	NP_036347

Figure 60 C	one a.				
		SKI-interacting protein			
		(SNW1), mRNA			
		/cds=(28,1638)			
		/gb=NM_012245			
		/gi=18860912			
		/ug=Hs.79008			
fcrc6631	NM 012245	/len=2146	NM_012245	Hs.79008	NP_036377
10100001	11111_012240	phospholipase D3	14141_012245	113.73000	NF_030377
		(PLD3), mRNA			
		/cds=(488,1801)			
		/gb=NM_012268			
		/gi=7110640			
	l	/ug=Hs.74573			
fcr0706	NM_012268	/len=2131	NM_012268	Hs.74573	NP_036400
		mRNA for KIAA0987			
mioc2868	AB023204	protein, partial cds	NM_012307	Hs.103839	NP_036439
		F-box and leucine-rich			
		repeat protein 11			
		(FBXL11), mRNA	İ		
		/cds=(107,3595)			
		/gb=NM 012308			
ii	İ	/gi=16306579			
		/ug=Hs.219614			
miob8341	NM_012308	/len=6210	NM 012308	Hs.219614	NP 036440
1111000011	11111_012000	U6 snRNA-associated	14141_012000	113.213014	NF_030440
		Sm-like protein			
		(LSM5), mRNA			
		•			
		/cds=(1,276)			
		/gb=NM_012322			
		/gi=6912487			
		/ug=Hs.227280			
mioa6583	NM_012322	/len=749	NM_012322	Hs.227280	NP_036454
		G protein-binding			
		protein CRFG (CRFG),	1		
		mRNA /cds=(24,1925)			
		/gb=NM_012341			
		/gi=6912531			
		/ug=Hs.215766			
seoa4246	NM_012341	/len=2414	NM_012341	Hs.215766	NP 036473
	<u> </u>	rab3 GTPase-		1	1 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7
		activating protein, non-	1	1	
		catalytic subunit			
Ì	Ì	(150kD) (RAB3-			}
		GAP150), mRNA	1		
		/cds=(74,4255)			
		, ,			
	1	/gb=NM_012414			
		/gi=19923789			
		/ug=Hs.197289	l		
mioa3092	NM_012414	/len=5129	NM_012414	Hs.197289	NP_036546

Figure 6b C	ont a.				· · · · · · · · · · · · · · · · · · ·
ncrc6817	NM_013285	nucleolar GTPase (HUMAUANTIG), mRNA /cds=(80,2275) /gb=NM_013285 /gi=7019418 /ug=Hs.75528 /len=2331	NM_013285	Hs.75528	NP_037417
		NME7 (NME7), mRNA /cds=(93,1223)			
mioa8380	NM_013330	/gb=NM_013330 /gi=7242158 /ug=Hs.274479 /len=1475	NM 013330	Hs.274479	ND 027462
THIOAOSOO	NW_013330	hypothetical protein DKFZp586G0123 (DKFZp586G0123), mRNA /cds=(25,315) /gb=NM_013386 /gi=9558726 /ug=Hs.24713	NIVI_U13330	ITS.274479	NP_037462
miob9336	NM_013386	/len=1294	NM 013386	Hs.24713	NP 037518
		deiodinase, iodothyronine, type II (DIO2), transcript variant 1, mRNA /cds=(707,1528) /gb=NM_013989 /gi=7549802 /ug=Hs.154424	NM_000793;		
ncrc3049	NM_013989	/len=6735 deiodinase, iodothyronine, type II (DIO2), transcript variant 1, mRNA /cds=(707,1528) /gb=NM_013989 /gi=7549802 /ug=Hs.154424	NM_013989 NM_000793;	Hs.154424	NP_054644
seob1268	NM_013989	/len=6735	NM 013989	Hs.154424	NP 054644
seoa3164	NM 014028	HSPC019 protein (HSPC019), mRNA /cds=(58,444) /gb=NM_014028 /gi=7661737 /ug=Hs.163724 /len=2411	NM_014028	Hs.163724	
30000 104	114101_014020	//CII=24	11111 0 14020	Ji 18. 1007 24	NP_054747

Figure 6b Co	mra.				
		DKFZP586A0522			
İ		protein			
		(DKFZP586A0522),		İ	
		mRNA /cds=(21,755)			
		/gb=NM_014033			
		/gi=13378140			
	ľ	/ug=Hs.288771	ĺ		
ncrc0838	NM_014033	/len=1705	NM_014033	Hs.288771	NP_054752
	·	likely ortholog of			
		mouse hypoxia			i
		induced gene 1 (HIG1),	1		
		mRNA /cds=(93,374)			
	ļ	/gb=NM_014056			
		/gi=7661619			
seob5528	NM_014056	/ug=Hs.7917 /len=1362	NM_014056	Hs.7917	NP_054775
		HT001 protein			
		(HT001), mRNA			
		/cds=(242,1204)			
		/gb=NM_014065			
		/gi=7661837			
		/ug=Hs.279040			
seoa7223	NM_014065	/len=1402	NM_014065	Hs.279040	ND 054704
360a1223	14101_014003		14100	⊓5.2790 4 0	NP_054784
		nuclear receptor			
		coactivator 6 (NCOA6),			
		mRNA			
		/cds=(2755,8760)			
		/gb=NM_014071			
		/gi=7661975			
		/ug=Hs.159613			
seoa9997	NM_014071	/len=9301	NM_014071	Hs.159613	NP 054790
		trichorhinophalangeal			
		syndrome I (TRPS1),			
		mRNA			
		/cds=(639,4484)			
		/gb=NM_014112			
		/gi=7657658			
		/ug=Hs.26102			
seob4057	NM_014112	/len=10011	NM_014112	Hs.26102	NP 054831
		zinc-finger protein			- · · · · · · · · · · · · · · · · ·
		AY163807 (HSPC055),			
		mRNA			
Ì		/cds=(199,3114)		ł	·
	1	` '			
		/gb=NM_014153			
		/gi=27414496			
1		/ug=Hs.179898			
seob2148	NM_014153	/len=3859	NM_014153	Hs.179898	NP_054872

Figure 6b	Conta.				
sooh6296	NIM 014169	HSPC133 protein (HSPC133), mRNA /cds=(83,481) /gb=NM_014168 /gi=7661791 /ug=Hs.273063	NINA 04.4469	He 272062	ND 054007
seob6386	NM_014168	/len=963	NM_014168	Hs.273063	NP_054887
ncr3751	NM_014206	chromosome 11 open reading frame 10 (C11orf10), mRNA /cds=(56,295) /gb=NM_014206 /gi=7656933 /ug=Hs.90918 /len=418	NM_014206	Hs.90918	NP_055021
min 42500	NIM 04 4200	chromosome 11 open reading frame 10 (C11orf10), mRNA /cds=(56,295) /gb=NM_014206 /gi=7656933	NIM 044000		
miod3500	NM_014206	/ug=Hs.90918 /len=418	NM_014206	Hs.90918	NP_055021
f. 1 0000		transmembrane 4 superfamily member 1 (TM4SF1), mRNA /cds=(102,710) /gb=NM_014220 /gi=21265100 /ug=Hs.351316			
fcrb3963	NM_014220	/len=1583 transmembrane 4 superfamily member 1 (TM4SF1), mRNA /cds=(102,710) /gb=NM_014220 /gi=21265100 /ug=Hs.351316	NM_014220	Hs.351316	NP_055035
fcr2601	NM_014220	/len=1583	NM_014220	Hs.351316	NP 055035
		solute carrier family 25, member 13 (citrin) (SLC25A13), mRNA /cds=(138,2165) /gb=NM_014251 /gi=7657580			
mioa0461	NM_014251	/ug=Hs.9599 /len=3150	NM_014251	Hs.9599	NP_055066

Figure 6b	Contu.				
seob1187	NM_014280	DnaJ (Hsp40) subfamily C, member 8 (DNAJC8), mRNA /cds=(8,802) /gb=NM_014280 /gi=7657610 /ug=Hs.433540 /len=1525	NM_014280	Hs.433540	NP_055095
mioa2478	NM 014300	signal peptidase complex (18kD) (SPC18), mRNA /cds=(78,617) /gb=NM_014300 /gi=7657608 /ug=Hs.9534 /len=1105	NM 014300	Hs.9534	NP_055115
		Sec61 gamma (SEC61G), mRNA /cds=(91,297) /gb=NM_014302 /gi=14591933			
seoa1844	NM_014302	hypothetical protein (HSPC117), mRNA /cds=(76,1593) /gb=NM_014306 /gi=7657014 /ug=Hs.10729	NM_014302	Hs.9950	NP_055117
seob5054	NM_014306	/len=2005 kelch domain containing 2 (KLHDC2), mRNA /cds=(317,1537) /gb=NM_014315 /gi=7657300 /ug=Hs.20597	NM_014306	Hs.10729	NP_055121
ncr3404	NM_014315 NM_014319	integral inner nuclear membrane protein (MAN1), mRNA /cds=(7,2742) /gb=NM_014319 /gi=7706606 /ug=Hs.7256 /len=4703	NM_014315	Hs.20597	NP_055130

Figure 6b	Conta.	<u> </u>			
		coronin, actin binding			
		protein, 1C			
		(CORO1C), mRNA			
		/cds=(97,1521)			
		/gb=NM_014325			
		/gi=27477119			
		/ug=Hs.17377			
seoa6620	NM_014325	/len=3828	NM_014325	Hs.17377	NP_055140
30000020	14141_014020	coronin, actin binding	14141_014020	113.17077	
		protein, 1C			
		(CORO1C), mRNA			
		1,			
İ		/cds=(97,1521)			
<u> </u>		/gb=NM_014325			
		/gi=27477119			
1		/ug=Hs.17377			
ncr0340	NM_014325	/len=3828	NM_014325	Hs.17377	NP_055140
1					
		hypothetical protein,			
		estradiol-induced			
		(E2IG5), mRNA			
		/cds=(71,643)			
		/gb=NM_014367			
		/gi=21361426			
miod6781	NM_014367	/ug=Hs.5243 /len=1215	NM 014367	Hs.5243	NP 055182
-		ring finger protein 11			
		(RNF11), mRNA			
		/cds=(128,592)			
		/gb=NM_014372			
1		/gi=7657519			
		/g=Hs.96334			
miob3953	NM_014372	/len=2529	NM 014372	Hs.96334	NP_055187
1111003333	14101_014372	zinc finger protein	14372	П5.90334	NP_000101
		(ZNF-U69274), mRNA		Ì	
		/cds=(162,3323)			
		/gb=NM_014415			
		/gi=7657702			
:-b0740	NNA 044445	/ug=Hs.301956			
miob6713	NM_014415	/len=5052	NM_014415	Hs.301956	NP_055230
		stress-associated			
		endoplasmic reticulum	1		
1		protein 1; ribosome			
}		associated membrane	1	1	
		protein 4 (SERP1),	1		
		mRNA /cds=(316,516)	1		
		/gb=NM_014445	1		
		/gi=19923408	1		
		/ug=Hs.76698			
seob1008	NM_014445	/len=2488	NM_014445	Hs.76698	NP_055260
		cDNA FLJ36610 fis,			
hfcr2378	AK093929	clone TRACH2015987	1	Hs.76698	NP_055260
					

Figure 6b Cont'd. NP220 nuclear protein (NP220), mRNA /cds=(315,6251) /gb=NM_014497 /gi=21626467 /ug=Hs.169984 NM_014497 seob4145 NM_014497 /len=6570 Hs.169984 NP_055312 NP220 nuclear protein (NP220), mRNA /cds=(315,6251) /gb=NM 014497 /gi=21626467 /ug=Hs.169984 ncr2035 NM_014497 /len=6570 NM_014497 Hs.169984 NP_055312 mRNA; cDNA DKFZp434P2119 (from clone DKFZp434P2119); seoc0535 AL137543 partial cds NM_014547 Hs.22826 NP 055362 LATS, large tumor suppressor, 2 (Drosophila) (LATS2), mRNA /cds=(375,3641) /gb=NM_014572 /gi=18959199 /ug=Hs.432314 ncrc3313 NM 014572 /len=4098 NM_014572 Hs.432314 NP 055387 solute carrier family 11 (proton-coupled divalent metal ion transporters), member 3 (SLC11A3), mRNA /cds=(315,2030) /gb=NM 014585 /gi=19923794 ncrc3011 /ug=Hs.5944 /len=3333 NM_014585 NM_014585 Hs.5944 NP_055400 hect domain and RLD 3 (HERC3), mRNA /cds=(167,3319)/gb=NM_014606 /gi=7657151 /uq=Hs.35804 ncr1712 /len=4894 NM 014606 NM_014606 Hs.35804 NP_055421

Figure 6b	Conta.				
		basic leucine zipper	-		
		and W2 domains 1			
		(BZW1), mRNA			
		/cds=(81,1340)			
		/gb=NM_014670			
		/gi=7661849			
		/ug=Hs.155291			
ncrc5149	NM_014670	/len=2998	NM_014670	Hs.155291	NP_055485
		endoplasmic reticulum			
		stress-inducible,			
		ubiquitin-like domain			
		member 1			
	İ	(HERPUD1), mRNA			
		/cds=(96,1271)		Ĭ	
		/gb=NM_014685			
		/gi=7661869			
		/ug=Hs.146393			
ncrc4597	NM_014685	/len=1884	NM_014685	Hs.146393	NP_055500
		calsyntenin 3			
		(CLSTN3), mRNA			
		/cds=(539,3445)			
		/gb=NM_014718			
		/gi=7662267			
		/ug=Hs.107809			
hfcr6501	NM_014718	/len=4300	NM 014718	Hs.107809	NP 055533
111010301	14141_014710	ProSAPiP2 protein	14141_014710	113.107009	NF_000000
		(ProSAPiP2), mRNA			
		/cds=(850,2697)			
		/gb=NM_014726			
		/gi=7662301			
		/ug=Hs.94790			
fcrc0857	NM_014726	/len=4121	NM_014726	Hs.94790	NP_055541
		KIAA0164 gene			
		product (KIAA0164),			
1		mRNA			
		/cds=(254,3016)			
ļ		/gb=NM_014739			
					İ
		/gi=7661957			
4055		/ug=Hs.80338		l	
seoa1857	NM_014739	/len=5538	NM_014739	Hs.80338	NP_055554
		KIAA0102 gene	}		
		product (KIAA0102),	1		
		mRNA /cds=(308,679)	[
		/gb=NM_014752 ^			
1		/gi=7661907			
		/ug=Hs.77665			
mioa4552	NM_014752	/len=1370	NM_014752	Hs.77665	NP_055567
1111047002	14141_0 147.02	Men-1070	114181_014132	1113.77000	INF_000007

Figure 6b C	ont d.	144440054	, 		
		KIAA0254 gene			
		product (KIAA0254),			
		mRNA			
		/cds=(529,3507)			
		/gb=NM_014758			
		1 ° —			
		/gi=7662025			
i		/ug=Hs.76906			
fcr0609	NM_014758	/len=6049	NM_014758	Hs.76906	NP_055573
		translocase of outer		:	
		mitochondrial		Ì	
1		membrane 20 (yeast)			
		(KIAA0016), mRNA			
İ					
		/cds=(102,539)			
		/gb=NM_014765			
		/gi=7657256			
		/ug=Hs.75187			
seoa7078	NM_014765	/len=3259	NM_014765	Hs.75187	NP_055580
		translocase of outer	<u> </u>		
		mitochondrial			
		membrane 20 (yeast)			
		(KIAA0016), mRNA			
		1.			
	1	/cds=(102,539)			
		/gb=NM_014765			
1		/gi=7657256			
		/ug=Hs.75187			
fcrb1714	NM_014765	/len=3259	NM_014765	Hs.75187	NP 055580
		KIAA0441 gene			
		product (KIAA0441),			
		mRNA			
		/cds=(169,2262)			
		/gb=NM_014797			
1		/gi=7662127			
		/ug=Hs.32511			
seoa1080	NM_014797	/len=5597	NM_014797	Hs.32511	NP 055612
			<u> </u>		<u> </u>
		translocase of outer			
		mitochondrial			
		membrane 70 A			
		(yeast) (TOMM70A),			
		mRNA /cds=(92,1918)			
		/gb=NM_014820			
		/gi=7662672			
		/ug=Hs.21198			
ncrc5072	NM_014820	/len=4017	NM_014820	Hs.21198	NP_055635
	10020	1	1020	1.10.21100	1.1000000

Figure 6b C	onta.				
ncr0046	NM_014820	translocase of outer mitochondrial membrane 70 A (yeast) (TOMM70A), mRNA /cds=(92,1918) /gb=NM_014820 /gi=7662672 /ug=Hs.21198 /len=4017	NM 014820	Hs.21198	NP 055635
seob8660	NIM 014996	hypothetical protein YR-29 (YR-29), mRNA /cds=(85,867) /gb=NM_014886 /gi=21359901		LIa 9470	ND 055704
Seobooou	NM_014886	/ug=Hs.8170 /len=1105	NIVI_U 14886	Hs.8170	NP_055701
ncrc6382	NM_014929	KIAA0971 protein (KIAA0971), mRNA /cds=(59,2005) /gb=NM_014929 /gi=7662421 /ug=Hs.84429 /len=4999	NM_014929	Hs.84429	NP 055744
·		calsyntenin 1			
2004040	NIM 044044	(CLSTN1), mRNA /cds=(794,3739) /gb=NM_014944 /gi=7662373 /ug=Hs.29665			
ncr1640	NM_014944	/len=5219	NM_014944	Hs.29665	NP_055759
		KIAA0907 protein (KIAA0907), mRNA /cds=(27,1721) /gb=NM_014949 /gi=7662371 /ug=Hs.24656			
seob1385	NM_014949	/len=4500	NM_014949	Hs.24656	NP_055764
		dishevelled associated activator of morphogenesis 1 (DAAM1), mRNA /cds=(126,3362) /gb=NM_014992 /gi=21071076 /ug=Hs.197751			
mioc7444	NM_014992	/len=4256	NM_014992	Hs.197751	NP_055807

Figure 6b	Conta.				
		SMART/HDAC1			
		associated repressor	1		
		protein (SHARP),			
]		mRNA			
		/cds=(205,11199)			
		/gb=NM_015001			
		/gi=14790189		į.	
		/g=Hs.184245			
ncr3237	NM 015001	/len=12227	NIA 015001	Un 104045	ND 055040
11013237	14141_015001	pVHL-interacting	NM_015001	Hs.184245	NP_055816
		deubiquitinating			
		enzyme 1 (VDU1),			
		mRNA			
		/cds=(262,2997)			
		/gb=NM_015017			
		/gi=21489974	ļ		
		/ug=Hs.173694			
ncr2484	NM_015017	/len=4323	NM 015017	Hs.173694	NP 055832
		yl96f11.s1 Soares			
		infant brain 1NIB cDNA			
		clone IMAGE:45943 3'			
		similar to contains Alu			
		repetitive element;			
		mRNA sequence			
		/clone=IMAGE:45943			
		/clone_end=3'			
		/gb=H09059			
		/gi=873881			
		/ug=Hs.438854			
mioc2529	H09059	/len=494		Hs.438854	NP_055833
		KIAA1037 protein			
		(KIAA1037), mRNA			
		/cds=(399,2429)			
1		/gb=NM_015023)		
		/gi=22095348			
		/ug=Hs.172825			
seob8501	NM_015023	/len=4305	NM_015023	Hs.172825	NP_055838
	11111_010020	mRNA for KIAA0640	11111_013023	113.172023	INF_00000
	1	protein, partial cds.			
		1.			
		/cds=(1,1813)			
		/gb=AB014540			
		/gi=3327093			
		/ug=Hs.153026			
ncrb4439	AB014540	/len=4824	<u> </u>	Hs.153026	NP_055870

Figure 6b	Conta.				
		mRNA for KIAA0864			
		protein, partial cds.			
		/cds=(1,4210)			
		/gb=AB020671			
		/gi=20521679			
		/ug=Hs.433523			
fcrc3760	AB020671	/len=4872		Hs.433523	NP_055949
10.00.00	7.120200.	PHD finger protein 3		110:100020	
		(PHF3), mRNA			
		/cds=(28,6147)			•
		/gb=NM_015153			
ĺ		/gi=7662017			
		/g=7662017 /ug=Hs.78893			
miod7225	NIM 015152	/len=6948	NIM 045452	 70002	ND OFFOCO
1111007225	NM_015153	sulfatase SULF1	NM_015153	Hs.78893	NP_055968
		precursor, mRNA,			
		complete cds			
		/cds=(707,3322)			
<u> </u>		/gb=AF545571			
		/gi=28191289			
		/ug=Hs.70823			
seoc2506	AF545571	/len=5699	NM_015170	Hs.70823	NP_055985
		KIAA0874 protein			
		(KIAA0874), mRNA			
		/cds=(1,6189)			
		/gb=NM_015208			•
		/gi=14140237			
		/ug=Hs.27973			
miob2947	NM_015208	/len=6189	NM 015208	Hs.27973	NP 056023
		KIAA0433 protein			
		(KIAA0433), mRNA			
		/cds=(510,4241)			
		/gb=NM_015216			
		/gi=7662117			
		/ug=Hs.26179			
ncrc2472	NM_015216	/len=5814	NM_015216	Hs.26179	NP 056031
	11111_010210	7,011,001,7	0.102.10	113.20173	141 _00001
		kinesin family member			
		13B (KIF13B), mRNA			
		/cds=(38,5518)	1		
		/gb=NM_015254	1		
			!		
		/gi=13194196			
mich0E90	NIM 015054	/ug=Hs.15711 /len=8743	NINA 045054	115 45744	ND OFFICE
miob0589	NM_015254	//en=8743	NM_015254	Hs.15711	NP_056069

Figure 6b C	onta.				
miod5505	NM_015310	ADP-ribosylation factor guanine nucleotide factor 6 (EFA6R), mRNA /cds=(53,1657) /gb=NM_015310 /gi=7662395 /ug=Hs.6763 /len=6722 joined to JAZF1 (JJAZ1), mRNA /cds=(195,2414) /gb=NM_015355 /gi=15149469		Hs.6763	NP_056125
seoa1483	NM_015355	/ug=Hs.197803 /len=4441	NM_015355	Hs.197803	NP_056170
		hypothetical protein DJ328E19.C1.1 (DJ328E19.C1.1), mRNA /cds=(18,2783) /gb=NM_015383 /gi=7657016 /ug=Hs.218329			
miod3254	NM_015383	/len=3689	NM 015383	Hs.218329	NP 056198
		preimplantation protein 3 (PREI3), mRNA /cds=(14,598) /gb=NM_015387 /gi=7661623 /ug=Hs.107942			
ncrb6680	NM_015387	/len=2686	NM_015387	Hs.107942	NP_056202
miod7478	AB058721	mRNA for KIAA1818 protein, partial cds	NM 015409	Hs.306094	NP 056224
mioc6320	NM_015436	zinc finger protein 363 (ZNF363), mRNA /cds=(27,812) /gb=NM_015436 /gi=24308060 /ug=Hs.48297 /len=1543	 NM_015436	Hs.48297	NP_056251
seob4545	NM_015470	KIAA0857 protein (KIAA0857), mRNA /cds=(241,2202) /gb=NM_015470 /gi=24308074 /ug=Hs.24557 /len=4340	NM_015470	Hs.24557	NP_056285

Figure ob	Conta.	·			·
		DKFZP564G2022			
		protein			
		(DKFZP564G2022),			
		mRNA /cds=(43,1710)			
		/gb=NM_015497			
		/gi=13794264			
		/ug=Hs.16492			
miob2968	NM_015497	/len=2286	NM_015497	Hs.16492	NP 056312
		EGF-like-domain,		110.10102	141 _000012
		multiple 6 (EGFL6),			
		mRNA			
		/cds=(241,1902)			
		/gb=NM_015507			
		/gi=13124887			
		/g=13124667 /ug=Hs.12844			
forb1575	NIM 015507	/len=2398	NIM 045507	110 10011	ND OFCOO
fcrb1575	NM_015507		NM_015507	Hs.12844	NP_056322
		coactivator for steroid			
		receptors (COASTER),			
		mRNA			
		/cds=(226,3267)			
		/gb=NM_015555			
		/gi=20127147			
		/ug=Hs.172329			
miob6485	NM_015555	/len=4999	NM_015555	Hs.172329	NP_056370
		signal-induced			
		proliferation-associated			
		1 like 1 (KIAA0440),			
		mRNA			
		/cds=(349,5763)			
		/gb=NM_015556			
		/gi=7662125			
		/ug=Hs.172180			
seob7039	NM_015556	/len=6028	NM_015556	Hs.172180	NP 056371
		retinoic acid induced			
		14 (RAI14), mRNA			
		/cds=(112,3054)			
		/gb=NM_015577			
		/gi=13470085			
		/ug=Hs.15165			
seob5319	NM_015577	/len=4925	NM_015577	Hs.15165	NP_056392
				1.0.10100	111 _000002
		DKFZP434D1335	Ì	Ì	
		protein			
		(DKFZP434D1335),			
	1	mRNA /cds=(78,1469)			
		/gb=NM_015578			
		/gi=24308092			
miod5894	NM_015578	/ug=Hs.8258 /len=3389	NM 015579	Hs.8258	ND OFESOS
11110000004	TIAINI_0 1997 6	/ug-115.0200 /leff-3308	ס לככו ט_ואורן		NP_056393

Figure 6b Co	nta.				
		mRNA; cDNA DKFZp727l051 (from clone DKFZp727l051); partial cds /cds=(1,2099) /gb=AL117478			
fcrb7234	AL117478	/gi=5911952 /ug=Hs.239370 /len=2480	NM_015597	Hs.239370	NP_056412
		mRNA; cDNA DKFZp727l051 (from clone DKFZp727l051); partial cds /cds=(1,2099) /gb=AL117478			
fcrb6382	AL117478	/gi=5911952 /ug=Hs.239370 /len=2480	NM_015597	Hs.239370	NP 056412
mine 9402	NIM 045000	DKFZP586G011 protein (LAP1B), mRNA /cds=(56,1444) /gb=NM_015602 /gi=24308098 /ug=Hs.234265			
mioa8192 seob7419	NM_015602 BC028715	erythroid differentiation- related factor 1, mRNA (cDNA clone IMAGE:4838997), partial cds	NM_015602	Hs.234265 Hs.227209	NP_056417 NP_056423
seoa9792	AB036063	p53R2 mRNA for ribonucleotide reductase, complete cds. /cds=(245,1300) /gb=AB036063 /gi=7229085 /ug=Hs.94262 /len=4955		Hs.94262	NP_056528
seoa3108	NM_015933	hypothetical protein (HSPC016), mRNA /cds=(39,233) /gb=NM_015933 /gi=7705430 /ug=Hs.397853 /len=384	NM_015933	Hs.397853	NP_057017

Figure 6b (Sonta.				
		hypothetical protein			
		(HSPC016), mRNA			
		/cds=(39,233)			
	•	/gb=NM_015933			
		/gi=7705430			
		/ug=Hs.397853			
miob8825	NM_015933	/len=384	NM 015933	Hs.397853	NP 057017
1111000020	11111_010000	nucleolar protein	14141_010000	1113.007000	
		NOP5/NOP58	ľ		
		(NOP5/NOP58),			
		mRNA /cds=(1,1590)			
		/gb=NM_015934			
		/gi=7706253			ļ
		/ug=Hs.119908			
mioc8917	NM_015934	/len=1590	NM_015934	Hs.119908	NP_057018
		CGI-07 protein (CGI-			
		07), mRNA]	
		/cds=(124,1635)			
		/gb=NM_015938			
		/gi=19923795			
		/ug=Hs.181022			
ncrc0336	NM_015938	/len=2762	NM_015938	Hs.181022	NP_057022
		cDNA FLJ13498 fis,			
		clone PLACE1004550,			
		highly similar to CGI-20			
fcrb8225	AK023560	protein mRNA	NM 015949	Hs.107387	NP 057033
				1.0.10.00	111
		PTD013 protein			
		(PTD013), mRNA			
		/cds=(87,812)			
		/gb=NM_015952			
		/gi=7706269			
seoa5685	NM_015952	/ug=Hs.22679 /len=982	NIM 015052	Hs.22679	NP 057036
3000000	14141_010302	CGI-32 protein (CGI-	14141_013332	115.22079	NF_037030
]		32), mRNA			
		/cds=(103,924)			
		/gb=NM_015960			
		/gi=7705727			`
	NINA 045000	/ug=Hs.16606	045000		
seoc1402	NM_015960	/len=1323	NM_015960	Hs.16606	NP_057044
		and a start to the first			
	}	serologically defined	}	}	
		breast cancer antigen			
		84 (SDBCAG84),			
		mRNA /cds=(28,1179)			
		/gb=NM_015966			
		/gi=7706277			
		/ug=Hs.169992	}		
ncrc2484	NM_015966	/len=1337	NM_015966	Hs.169992	NP_057050

Figure 6b (John G.				
ncrb8063	NM 015966	serologically defined breast cancer antigen 84 (SDBCAG84), mRNA /cds=(28,1179) /gb=NM_015966 /gi=7706277 /ug=Hs.169992 /len=1337	NM_015966	Hs.169992	NP_057050
11010000	14.01_010000	cofactor required for	14111_010000	113.103332	141_037030
		Sp1 transcriptional activation, subunit 3, 130kDa (CRSP3), mRNA /cds=(120,4226) /gb=NM_004830 /gi=7019352			
		/ug=Hs.29679	NM_004830;		
ncrc2600	NM_004830	/len=5176	NM_015979	Hs.29679	NP_057063
		ubiquitin carboxyl- terminal hydrolase L5 (UCHL5), mRNA /cds=(132,1121) /gb=NM_015984 /gi=7706752 /ug=Hs.171581			
mioa6739	NM_015984	/len=1728	NM_015984	Hs.171581	NP_057068
	ر	CGI-48 protein (CGI- 48), mRNA /cds=(108,1673) /gb=NM_016001 /gi=7705764			
hfcr2708	NM_016001	/ug=Hs.6153 /len=1873	NM_016001	Hs.6153	NP_057085
		CGI-74 protein (CGI- 59), mRNA /cds=(1,1209) /gb=NM_016019 /gi=7706309			
seob1526	NM_016019	/ug=Hs.7194 /len=2296	NM_016019	Hs.7194	NP_057103
		retinol dehydrogenase 11 (all-trans and 9-cis) (RDH11), mRNA /cds=(41,997) /gb=NM_016026 /gi=20070271 /ug=Hs.179817			
seoa3847	NM_016026	/len=2538	NM_016026	Hs.179817	NP_057110

Figure 6b	Conta.				
		CGI-101 protein (F- LAN-1), mRNA /cds=(7,636) /gb=NM_016041 /gi=7705603 /ug=Hs.286131			
hfcr4007	NM_016041	/len=1123	NM_016041	Hs.286131	NP_057125
		chromosome 20 open reading frame 45 (C20orf45), mRNA /cds=(85,720) /gb=NM_016045 /gi=7705609			
seoa6226	NM_016045	/ug=Hs.3945 /len=2535 CGI-146 protein (PNAS-4), mRNA /cds=(59,640) /gb=NM_016076 /gi=7705641 /ug=Hs.42409		Hs.3945	NP_057129
miod5080	NM_016076	/len=1108	NM_016076	Hs.42409	NP_057160
miod2996	NM_016077	CGI-147 protein (CGI- 147), mRNA /cds=(128,667) /gb=NM_016077 /gi=7706350 /ug=Hs.12677 /len=806	NM_016077	Hs.12677	NP_057161
mino9452	NIM 046077	CGI-147 protein (CGI- 147), mRNA /cds=(128,667) /gb=NM_016077 /gi=7706350	NIM 046077	He 12077	ND 057404
mioc8153	NM_016077	/ug=Hs.12677 /len=806 CGI-148 protein (CGI- 148), mRNA /cds=(300,845) /gb=NM_016078 /gi=7705643 /ug=Hs.87295	NM_U16U//	Hs.12677	NP_057161
mioa6580	NM_016078	/len=2070	NM_016078	Hs.87295	NP_057162
ncr9044	AF125100	HSPC039 protein mRNA, complete cds /cds=(81,329) /gb=AF125100 /gi=5106995 /ug=Hs.406542 /len=1583	NM 016097	Hs.406542	NP 057181
ncr9044	AF125100		NM_016097	Hs.406542	NP_057181

Figure 60	Conta.				
		brain protein 44-like			
		(BRP44L), mRNA			
		/cds=(123,452)	Ī		
		/gb=NM_016098			
		/gi=7706368			
		/ug=Hs.108725			
ncrc9159	NM_016098	/len=988	NM_016098	Hs.108725	ND 057400
110109109	14141_010090	interleukin-1 receptor-	14W_0 10096	П5. 100725	NP_057182
		associated kinase 4			
		(IRAK4), mRNA			
		/cds=(50,1432)			
		/gb=NM_016123			
		/gi=7705840			
		/ug=Hs.142295			į
miob6228	NM_016123	/len=2817	NM_016123	Hs.142295	NP_057207
		INSIG-2 membrane			
		protein mRNA,			
ncrc1623	AF527632	complete cds	NM 016133	Hs.7089	NP_057217
		protein phosphatase		<u> </u>	
		methylesterase-1			
		(PMÉ-1), mRNA		}	
		/cds=(100,1260)			
		/gb=NM_016147			
		/gi=7706644			
		/g=Hs.63304			
seob6872	NM_016147	/len=2484	NIM 046447	115 62204	ND 057004
Seoboorz	NIVI_U 10 147		NM_016147	Hs.63304	NP_057231
		chromosome 1 open			
		reading frame 33			
		(C1orf33), mRNA			
		/cds=(32,751)			
		/gb=NM_016183			
		/gi=18490986			
		/ug=Hs.274201			
ncr5760	NM_016183	/len=1185	NM_016183	Hs.274201	NP_057267
		cleavage and			
		polyadenylation			
		specific factor 3,			
		73kDa (CPSF3),			
		mRNA /cds=(36,2090)			
		/gb=NM_016207	1		
		/gi=21314666	1		
		/g=21514000 /ug=Hs.16251	1		
fcr2860	NM_016207	/len=2286	NM 016207	He 16251	ND 057204
1012000	14141_010207	yeast Sec31p	NM_016207	Hs.16251	NP_057291
		1*			
		(KIAA0905), mRNA			
		/cds=(54,3716)			
		/gb=NM_014933			
		/gi=7662369	 .		
0.40-		/ug=Hs.70266	NM_014933;		
ncr0438	NM_014933	/len=4129	NM_016211	Hs.70266	NP_057295

Figure 6b C	John G.				
seob6000	NM_016217	hHDC for of Drosophila headcase (HDCL), mRNA /cds=(286,1917) /gb=NM_016217 /gi=7706434 /ug=Hs.6679 /len=5634		Hs.6679	NP_057301
		sorting nexin 9 (SNX9), mRNA /cds=(174,1961) /gb=NM_016224			
ncr9061	NM_016224	/gi=23111056 /ug=Hs.7905 /len=4200	NM 016224	Hs.7905	NP_057308
ncrb2053	NM_016227	chromosome 1 open reading frame 9 (C1orf9), mRNA /cds=(125,4342) /gb=NM_016227 /gi=7705321 /ug=Hs.108636 /len=5919	NM_014283; NM_016227	Hs.108636	NP_057311
fcrc3826	NM_016274	CK2 interacting protein 1; HQ0024c protein (CKIP-1), mRNA /cds=(285,1514) /gb=NM_016274 /gi=21361610 /ug=Hs.173380 /len=1633	NM 016274	Hs.173380	NP 057358
10103020	NIVI_010274	chromosome 15 open reading frame 15 (C15orf15), mRNA /cds=(144,635) /gb=NM_016304 /gi=18491027 /ug=Hs.284162	NIN_010274	115.173300	NF_05/336
seoa5121 mioc6997	NM_016304	/len=1487 DnaJ (Hsp40) subfamily B, member 11 (DNAJB11), mRNA /cds=(160,1236) /gb=NM_016306 /gi=25014110 /ug=Hs.278605 /len=1621	NM_016304 NM_016306	Hs.284162	NP_057388
	1.111_0.10000	1.011 1021	1.441_0.10000	113.270000	111 _007 030

Figure 60 (Jone d.				
. 4 4000		REV1-like (yeast) (REV1L), mRNA /cds=(213,3968) /gb=NM_016316 /gi=7706680 /ug=Hs.110347			
miob4333	NM_016316	/len=4276	NM_016316	Hs.110347	NP_057400
seob0096	NM_016322	RAB14, member RAS oncogene family (RAB14), mRNA /cds=(184,831) /gb=NM_016322 /gi=19923482 /ug=Hs.5807 /len=4106	NM_016322	Hs.5807	NP_057406
fcrb1457	NM_016322	RAB14, member RAS oncogene family (RAB14), mRNA /cds=(184,831) /gb=NM_016322 /gi=19923482 /ug=Hs.5807 /len=4106	NM_016322	Hs.5807	NP 057406
ncrc2172	AW292456	UI-H-BI2-agp-f-12-0- UI.s1 NCI_CGAP_Sub4 cDNA clone IMAGE:2725031 3', mRNA sequence /clone=IMAGE:272503 1 /clone_end=3' /gb=AW292456 /gi=6699092 /ug=Hs.437793 /len=745		Hs.437793	NP_057446
miod4184	NM_016403	hypothetical protein HSPC148 (HSPC148), mRNA /cds=(64,753) /gb=NM_016403 /gi=7705474 /ug=Hs.42743 /len=1046	NM_016403	Hs.42743	NP_057487
seob4928	NM_016441	cysteine-rich motor neuron 1 (CRIM1), mRNA /cds=(40,3150) /gb=NM_016441 /gi=10092638 /ug=Hs.19280 /len=5601	NM_016441	Hs.19280	NP_057525

Figure ob C	one a.				
miod1377	NM_016441	cysteine-rich motor neuron 1 (CRIM1), mRNA /cds=(40,3150) /gb=NM_016441 /gi=10092638 /ug=Hs.19280 /len=5601	NM 016441	Hs.19280	NP 057525
		hypothetical protein LOC51244 (LOC51244), mRNA /cds=(340,1233) /gb=NM_016474 /gi=24475969 /ug=Hs.158006			
miob0167	NM_016474	/len=1614	NM_016474	Hs.158006	NP_057558
miod7486	BC025306	clone IMAGE:4893383, mRNA, partial cds	NM_016488	Hs.281428	NP_057572
ncr3968	NM 016505	putative S1 RNA binding domain protein (PS1D), mRNA /cds=(137,862) /gb=NM_016505 /gi=21361575 /ug=Hs.54971 /len=1602	NM 016505	Hs.54971	NP 057589
hfcr5220	NM_016581	ECSIT (LOC51295), mRNA /cds=(78,1373) /gb=NM_016581 /gi=20149632 /ug=Hs.22199 /len=1668	 NM_016581	Hs.22199	NP 057665
seoa9729	NM_016587	chromobox 3 (HP1 gamma Drosophila) (CBX3), transcript variant 2, mRNA /cds=(152,703) /gb=NM_016587 /gi=20544150 /ug=Hs.406384 /len=1851	NM_007276; NM_016587	Hs.406384	NP_057671
fcrb7340	 NM_016594	FK506 binding protein 11, 19 kDa (FKBP11), mRNA /cds=(73,678) /gb=NM_016594 /gi=7706130 /ug=Hs.24048 /len=727		Hs.24048	NP_057678

Figure 6b	Contra.				
miob1134	NM_016608	ALEX1 protein (ALEX1), mRNA /cds=(372,1733) /gb=NM_016608 /gi=7706142 /ug=Hs.9728 /len=2141	NM_016608	Hs.9728	NP_057692
ncrc6332	NM_016618	hypothetical protein LOC51315 (LOC51315), mRNA /cds=(395,1174) /gb=NM_016618 /gi=7706155 /ug=Hs.5721 /len=1774	NM_016618	Hs.5721	NP_057702
miob3354	NM_016618	hypothetical protein LOC51315 (LOC51315), mRNA /cds=(395,1174) /gb=NM_016618 /gi=7706155 /ug=Hs.5721 /len=1774	NM 016618	Hs.5721	NP 057702
miod1323	NM 016627	hypothetical protein LOC51321 (LOC51321), mRNA /cds=(635,1195) /gb=NM_016627 /gi=7706167 /ug=Hs.268122 /len=1304	NM 016627	Hs.268122	NP 057711
		ARF protein (LOC51326), mRNA /cds=(88,489) /gb=NM_016632 /gi=7706177 /ug=Hs.264509			
ncr3148	NM_016632	/len=826 mitochondrial ribosomal protein S30 (MRPS30), mRNA /cds=(39,1358) /gb=NM_016640 /gi=16950598 /ug=Hs.28555	NM_016632	Hs.264509	NP_057716
seoa9724	NM_016640	/len=1482	NM_016640	Hs.28555	NP_057724

Cont'd.				
NM_006855	KDEL (Lys-Asp-Glu- Leu) endoplasmic reticulum protein retention receptor 3 (KDELR3), transcript variant 1, mRNA /cds=(157,801) /gb=NM_006855 /gi=8051612 /ug=Hs.250696 /len=1705	NM_006855; NM_016657	Hs.250696	NP_057839
NM_017444	chromatin accessibility complex 1 (CHRAC1), mRNA /cds=(196,591) /gb=NM_017444 /gi=24432041 /ug=Hs.279704 /len=2496	NM_017444	Hs.279704	NP_059140
	gn251 2 protein			
NM_017510	(HSGP25L2G), mRNA	NM_017510	Hs.279929	NP_059980
NM_017548	hypothetical protein H41 (H41), mRNA /cds=(324,1100) /gb=NM_017548 /gi=24475997 /ug=Hs.283690 /len=3346	NM_017548	Hs.283690	NP_060018
NM_017599	transmembrane protein vezatin (VEZATIN), mRNA /cds=(177,1886) /gb=NM_017599 /gi=19923537 /ug=Hs.24135 /len=3949	NM_017599	Hs.24135	NP_060069
NM 017606	hypothetical protein DKFZp434K1210 (DKFZp434K1210), mRNA /cds=(191,580) /gb=NM_017606 /gi=8922146 /ug=Hs.32352 /len=2133	NM 017606	Hs 32352	NP 060076
	NM_006855 NM_017444 NM_017510 NM_017548	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3 (KDELR3), transcript variant 1, mRNA /cds=(157,801) /gb=NM_006855 /gi=8051612 /ug=Hs.250696 MM_006855 /gi=8051612 /ug=Hs.250696 MM_006855 /gi=8051612 /ug=Hs.250696 MM_017444 /gi=24432041 /ug=Hs.279704 MM_017444 /gi=24432041 /ug=Hs.279704 MM_017510 Gp=NM_017548 /gi=2447597 /ug=Hs.283690 MM_017548 /gi=24475997 /ug=Hs.283690 MM_017548 /gi=24475997 /ug=Hs.283690 MM_017548 /gi=3346 Gransmembrane protein vezatin (VEZATIN), mRNA /cds=(177,1886) /gb=NM_017599 /gi=19923537 /ug=Hs.24135 /len=3949 Mypothetical protein DKFZp434K1210 (DKFZp434K1210 (DKFZp434K1210), mRNA /cds=(191,580) /gb=NM_017606 /gi=8922146 /ug=Hs.32352	KDEL (Lys-Asp-Glu- Leu) endoplasmic reticulum protein retention receptor 3 (KDELR3), transcript variant 1, mRNA /cds=(157,801) /gb=NM_006855 /gi=8051612 /ug=Hs.250696 NM_016657 Chromatin accessibility complex 1 (CHRAC1), mRNA /cds=(196,591) /gb=NM_017444 /gi=24432041 /ug=Hs.279704 /len=2496 NM_017510 Mypothetical protein H41 (H41), mRNA /cds=(324,1100) /gb=NM_017548 /gi=24475997 /ug=Hs.283690 NM_017548 Transmembrane protein vezatin (VEZATIN), mRNA /cds=(177,1886) /gb=NM_017599 /gi=19923537 /ug=Hs.24135 NM_017599 NM_017599 NM_017599 NM_017599 NM_017590 NM_017599 NM_017599 NM_017599 NM_017599 NM_017599 NM_017599 NM_017599 NM_017599 NM_017599 NM_017599 NM_017599 NM_017599 NM_017599 NM_017599 NM_017599 NM_017590	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3 (KDELR3), transcript variant 1, mRNA /cds=(157,801) /gb=NM_006855 /gi=8051612 /ug=Hs.250696 NM_016657 Hs.250696 NM_006855 /len=1705 NM_016657 Hs.250696 NM_016657 Hs.250696 NM_016657 Hs.250696 NM_016657 Hs.250696 NM_016657 Hs.250696 NM_016657 Hs.250696 NM_016657 Hs.250696 NM_016657 Hs.250696 NM_016657 Hs.250696 NM_016657 Hs.250696 NM_016657 Hs.250696 NM_016657 Hs.250696 NM_016657 Hs.250696 NM_017444 /gi=24432041 /ug=Hs.279704 NM_017444 /gi=24432041 /ug=Hs.279704 NM_017510 Hs.279704 NM_017510 Hs.279704 NM_017510 Hs.279704 NM_017510 Hs.279929 NM_017510 Hs.279929 NM_017510 Hs.279929 NM_017548 /gi=24475997 /ug=Hs.283690 NM_017548 Hs.283690 Hransmembrane protein vezatin (VEZATIN), mRNA /cds=(177,1886) /gb=NM_017599 /gi=19923537 /ug=Hs.24135 NM_017599 Hs.24135 NM_017599 /gi=3923461210 (DKFZP434K1210 (DKFZP434K1210), mRNA /cds=(191,580) /gb=NM_017606 /gi=8922146 /ug=Hs.32352

nt'd.				
NIM 047645	hypothetical protein FLJ20003 (FLJ20003), mRNA /cds=(31,1188) /gb=NM_017615 /gi=8923008 /ug=Hs.258798	NIM 047045	U. 050700	ND 000005
NIVI_U1/615	I	NM_01/615	HS.258798	NP_060085
AF246705	protein mRNA, partial cds	NM_017632	Hs.32922	NP_060102
NM_017691	rypothetical protein FLJ20156 (FLJ20156), mRNA /cds=(248,2305) /gb=NM_017691 /gi=8923153 /ug=Hs.12692 /len=2780	NM 017691	Hs.12692	NP 060161
	hypothetical protein FLJ20303 (FLJ20303), mRNA /cds=(86,1681) /gb=NM_017755 /gi=8923284 /ug=Hs.17138			
NM_017755	/len=2427	NM 017755	Hs.17138	NP 060225
NM_017761		NM_017761	Hs.7862	NP_060231
NM_017791	chromosome 14 open reading frame 58 (C14orf58), mRNA /cds=(325,1905) /gb=NM_017791 /gi=8923349 /ug=Hs.267566 /len=3614	NM_017791	Hs.267566	NP_060261
NM 017830	ovarian carcinoma immunoreactive antigen (OCIA), mRNA /cds=(168,905) /gb=NM_017830 /gi=8923426 /ug=Hs.132071 /len=1434	NM 017830	Hs.132071	NP_060300
	NM_017615 AF246705 NM_017691 NM_017755	hypothetical protein FLJ20003 (FLJ20003), mRNA /cds=(31,1188) /gb=NM_017615 /gi=8923008 /ug=Hs.258798 NM_017615 /len=1387 putative serine-rich protein mRNA, partial cds hypothetical protein FLJ20156 (FLJ20156), mRNA /cds=(248,2305) /gb=NM_017691 /gi=8923153 /ug=Hs.12692 NM_017691 hypothetical protein FLJ20303 (FLJ20303), mRNA /cds=(86,1681) /gb=NM_017755 /gi=8923284 /ug=Hs.17138 NM_017755 hypothetical protein FLJ20312 (FLJ20312), mRNA /cds=(384,803) /gb=NM_017761 /gi=20127576 /ug=Hs.7862 /len=2382 chromosome 14 open reading frame 58 (C14orf58), mRNA /cds=(325,1905) /gb=NM_017791 /gi=8923349 /ug=Hs.267566 NM_017791 varian carcinoma immoreactive antigen (OCIA), mRNA /cds=(168,905) /gb=NM_017830 /gi=8923426 /ug=Hs.132071	hypothetical protein FLJ20003 (FLJ20003), mRNA / cds=(31,1188) /gb=NM_017615 /gi=8923008 /ug=Hs.258798 NM_017615 Jen=1387	hypothetical protein FLJ2003 (FLJ2003), mRNA /cds=(31,1188) /gb=NM_017615 /gi=8923008 /lug=Hs.258798 /len=1387 putative serine-rich protein mRNA, partial cds hypothetical protein FLJ20156 (FLJ20156), mRNA /cds=(248,2305) /gb=NM_017691 /gi=8923153 /lug=Hs.12692 /len=2780 NM_017691 hypothetical protein FLJ20303 (FLJ20303), mRNA /cds=(86,1681) /gb=NM_017755 /gi=8923284 /lug=Hs.17138 /len=2427 NM_017755 NM_017761 /lyg=NM_017661 /gi=20127576 NM_017761 /lyg=Hs.7862 /len=2382 NM_017761 /lyg=Hs.7862 /len=2382 NM_017761 /lyg=Hs.7862 /len=2382 NM_017761 /lyg=Hs.7862 /len=2382 NM_017761 /lyg=Hs.7862 /len=2382 NM_017761 /lyg=Hs.7862 /len=2382 NM_017761 /lyg=Hs.7862 /len=2382 NM_017761 /lyg=Hs.7862 /len=2382 NM_017761 /lyg=Hs.267566 /lyg=Hs.267566 /lyg=Hs.267566 /lyg=S23349 /lyg=Hs.267566 /lyg=S23426 /lyg=Hs.132071

1.3	Conta.		,		
seoa4167	NM_017849	hypothetical protein FLJ20507 (FLJ20507), mRNA /cds=(258,974) /gb=NM_017849 /gi=8923465 /ug=Hs.202955 /len=4223	NM_017849	Hs.202955	NP_060319
	NN 047040	hypothetical protein FLJ20628 (FLJ20628), mRNA /cds=(23,1456) /gb=NM_017910 /gi=13435382 /ug=Hs.32356	NM 047040		
seoc0957	NM_017910	/len=1846	NM_017910	Hs.32356	NP_060380
		Hsp90-associating relative of Cdc37 (HARC), mRNA /cds=(100,1113) /gb=NM_017913 /gi=8923591 /ug=Hs.128646			
miod3325	NM_017913	/len=1542	NM_017913	Hs.128646	NP_060383
seob5880	AL834521	mRNA; cDNA DKFZp667F0310 (from clone DKFZp667F0310)	NM_017925	Hs.29032	NP 060395
mioc4782	NM_017943	F-box only protein 34 (FBXO34), mRNA /cds=(7,924) /gb=NM_017943 /gi=8923650 /ug=Hs.15467 /len=2006	NM_017943	Hs.15467	NP 060413
1111004702	14141_017343	71611-2000	14101 017 943	115.13407	NP_000413
 miob8286	AL832991	mRNA; cDNA DKFZp666K033 (from clone DKFZp666K033)	NM 017044	Ha 200700	ND 060444
		mitochondrial ribosomal protein L20 (MRPL20), nuclear gene encoding mitochondrial protein, mRNA /cds=(65,514) /gb=NM_017971 /gi=26638656 /ug=Hs.182698		Hs.300700	NP_060414
miod1030	NM_017971	/len=705	NM_017971	Hs.182698	NP_060441

Figure 6b C	ont a.				
ncrc0178	BC043393	Similar to hypothetical protein LOC208146, clone IMAGE:5498791, mRNA		Hs.318127	NP_060493
ncrc4402	NM_018032	LUC7-like (S. cerevisiae) (LUC7L), mRNA /cds=(89,1066) /gb=NM_018032 /gi=21359922 /ug=Hs.16803 /len=1542	NM_018032	Hs.16803	NP_060502
ncrc7169	NM_018047	hypothetical protein FLJ10290 (FLJ10290), mRNA /cds=(78,1340) /gb=NM_018047 /gi=8922327 /ug=Hs.25516 /len=2297	NM 018047	Hs.25516	NP 060517
1100	NIVI_018047	likely ortholog of mouse guanine nucleotide releasing protein x (GNRPX), mRNA /cds=(82,531) /gb=NM_018049 /gi=8922332 /ug=Hs.173739	NIVI_U18047	HS.25516	NP_060517
fcrb4270 seob7682	NM_018049 NM_018058	/len=1215 cartilage acidic protein 1 (CRTAC1), mRNA /cds=(319,1575) /gb=NM_018058 /gi=8922351 /ug=Hs.326444 /len=2178	NM_018049 NM_018058	Hs.173739 Hs.326444	NP_060519 NP_060528
seoa3761	NM_018061	hypothetical protein FLJ10330 (FLJ10330), mRNA /cds=(77,1717) /gb=NM_018061 /gi=8922357 /ug=Hs.342307 /len=3239	NM_018061	Hs.342307	NP_060531

Figure 6b (Sont d.				
		hypothetical protein FLJ10377 (FLJ10377), mRNA /cds=(116,2395) /gb=NM_018077 /gi=8922387			
		/ug=Hs.274263	<u> </u>		
fcrb8465	NM_018077	/len=2809	NM_018077	Hs.274263	NP_060547
mioc8471	NM_018115	hypothetical protein FLJ10498 (FLJ10498), mRNA /cds=(37,1920) /gb=NM_018115 /gi=8922466 /ug=Hs.109045 /len=2755	NM_018115	Hs. 109045	NP 060585
fcrb3896	NM_018184	hypothetical protein FLJ10702 (FLJ10702), mRNA /cds=(175,735) /gb=NM_018184 /gi=8922600 /ug=Hs.104222 /len=2944	NM_018184	Hs.104222	NP 060654
mioc3079	NM 018255	elongator protein 2 (ELP2), mRNA /cds=(11,2491) /gb=NM_018255 /gi=8922734 /ug=Hs.8739 /len=2494	NM 018255	Hs.8739	NP 060725
ncr2908	_ NM_018259	hypothetical protein FLJ10890 (FLJ10890), mRNA /cds=(29,3454) /gb=NM_018259 /gi=21361786 /ug=Hs.17283 /len=3533	NM_018259	Hs.17283	NP_060729
		chromosome 15 open reading frame 12 (C15orf12), nuclear gene encoding mitochondrial protein, mRNA /cds=(48,602) /gb=NM_018285 /gi=8922793			
mioc3139	NM_018285	/ug=Hs.6118 /len=1115 mRNA for KIAA1903	NM_018285	Hs.6118	NP_060755
miob7267	AB067490	protein, partial cds	NM_018353	Hs.89278	NP_060823

Figure 6b	Conta.				
ncrb0364	NM_018382	hypothetical protein FLJ11292 (FLJ11292), mRNA /cds=(151,615) /gb=NM_018382 /gi=8922980 /ug=Hs.272246 /len=1948	NM 018382	Hs.272246	NP 060852
fcrb9959	NM 018462	uncharacterized hematopoietic stem/progenitor cells protein MDS027 (MDS027), mRNA /cds=(21,248) /gb=NM_018462 /gi=27544938 /ug=Hs.421654 /len=888	NM 018462	Hs.421654	NP 060932
miod0807	NM_018464	uncharacterized hematopoietic stem/progenitor cells protein MDS029 (MDS029), mRNA /cds=(112,438) /gb=NM_018464 /gi=8923929 /ug=Hs.43549 /len=636	_	Hs.43549	NP_060934
miob3308	NM_018471	uncharacterized hypothalamus protein HT010 (HT010), mRNA /cds=(227,1420) /gb=NM_018471 /gi=8923807 /ug=Hs.6375 /len=2140	NM_018471	Hs.6375	NP_060941
ncr2695	NM_018480	uncharacterized hypothalamus protein HT007 (HT007), mRNA /cds=(228,887) /gb=NM_018480 /gi=8923801 /ug=Hs.24371 /len=1172	NM_018480	Hs.24371	NP_060950

Figure 6b	Conta.		· ·		
1		chondroitin sulfate			
		GalNAcT-2 (GALNACT	i		
		2), mRNA			
		/cds=(336,1964)			
		/gb=NM_018590			
		/gi=24429591			
		/ug=Hs.180758			
ncrb4182	NM_018590	/len=3745	NM 018590	Hs.180758	NP 061060
		ethanolamine kinase			
		(EKI1), mRNA			
		/cds=(90,1448)			
		/gb=NM_018638			
		/gi=21071078	1		
		/ug=Hs.120439			
mioc2290	NM_018638	/len=2221	NM_018638	Hs.120439	NP 061108
		mRNA for KIAA1247		7.0.120.00	111_001100
		protein, partial cds.			
		/cds=(286,2943)			
		/gb=AB033073			
		/gi=14133244			
		/gr 14100244 /ug=Hs.43857			
seob3220	AB033073	/len=4397	NM_018837	Hs.43857	NP 061325
00000220	715000010	Similar to G-protein	14101_010007	113.43007	NF_001323
		gamma-12 subunit,			
		clone MGC:14561			:
		IMAGE:4049838,			
seoc1318	BC005940	mRNA, complete cds		Hs.8107	ND 061220
30001010		EGF-containing fibulin-	7.5	115.0107	NP_061329
		like extracellular matrix			
		protein 1 (EFEMP1),			
		transcript variant 1,			
		mRNA			
		/cds=(150,1631)]	
		/gb=NM_004105			
		/gi=9665261			
		/g=9003201 /ug=Hs.76224	NM_004105;		
mioa5409	NM_004105	/len=2742	NM_018894	Hs.76224	NP 061489
1111040403	14141_004103	Gene 33/Mig-6 (MIG-	14141_010094	ПS.70224	NP_001469
		6), mRNA			
		/cds=(213,1601)			
		/gb=NM_018948			
		/gi=21314673			
		/g=21314673 /ug=Hs.11169			
mioa0626	NM 018948	/len=3099	NM 018948	Hs.11169	ND 064904
moaoozo	14141_010340	Gene 33/Mig-6 (MIG-	14141_010940	TS. 1 1 109	NP_061821
		6), mRNA			
		/cds=(213,1601)		1	
		/gb=NM_018948 /gi=21314673			
		/g=21314673 /ug=Hs.11169			
mioa6811	NIM 019049	1 -	NIM 049040	По 44460	ND 004004
IIIIOado I I	NM_018948	/len=3099	NM_018948	Hs.11169	NP_061821

Figure 6b Co	Titu.	10			
		Gene 33/Mig-6 (MIG-			
		6), mRNA			
		/cds=(213,1601)			
		/gb=NM_018948			
		/gi=21314673			
		/ug=Hs.11169			
miob7831	NM_018948	/len=3099	NM_018948	Hs.11169	NP_061821
		Gene 33/Mig-6 (MIG-			
		6), mRNA	<u> </u>		
		/cds=(213,1601)			
		/gb=NM_018948			
		/gi=21314673			
		/ug=Hs.11169			
mioc5197	NIM 019049	/len=3099	NM 040040	115 44400	ND 004004
1111003197	NM_018948	Gene 33/Mig-6 (MIG-	NM_018948	Hs.11169	NP_061821
		6), mRNA			
		/cds=(213,1601)			
İ		/gb=NM_018948			
		/gi=21314673			
		/ug=Hs.11169		· ·	
mioc7372	NM_018948	/len=3099	NM_018948	Hs.11169	NP_061821
		solute carrier family 38,			
		member 2 (SLC38A2),			
		mRNA			
		/cds=(352,1872)			
		/gb=NM_018976			
		/gi=21361601			
		/ug=Hs.298275			
miob4933	NM_018976	/len=4795	NM 018976	Hs.298275	NP 061849
		solute carrier family 38,			
		member 2 (SLC38A2),			
		mRNA			
		/cds=(352,1872)			
		/gb=NM_018976			
		/gi=21361601			
		/ug=Hs.298275			
seob4766	NM_018976	/len=4795	NM_018976	Hs.298275	ND 064940
36004700	14141_010310	solute carrier family 38,	141A1 0 109 1 0	113.2802/3	NP_061849
		member 2 (SLC38A2),			
		mRNA			
		/cds=(352,1872)			
		/gb=NM_018976			
}		/gi=21361601			
	l	/ug=Hs.298275			
seoc2050	NM_018976	/len=4795	NM_018976	Hs.298275	NP_061849

Figure 6b 0	Jonta.				
		solute carrier family 38, member 2 (SLC38A2), mRNA /cds=(352,1872) /gb=NM_018976 /gi=21361601			
		/ug=Hs.298275			
mioc1425	NM_018976	/len=4795	NM_018976	Hs.298275	NP_061849
ncr3604	BC013629	clone IMAGE:3445410, mRNA, partial cds		Hs.432900	NP_061852
miob7155	AB002342	mRNA for KIAA0344 gene, partial cds	NM_018979	Hs.432900	NP_061852
seoc0775	BC034698	Similar to RAB5 interacting protein 2, clone IMAGE:4508733, mRNA		Hs.62349	NP_061866
mioa0791	BC034698	Similar to RAB5 interacting protein 2, clone IMAGE:4508733, mRNA		Hs.62349	NP_061866
ncrb4000	XM_033181	strand-exchange protein 1 (SEP1), mRNA			NP_061874
mioa0535	NM_019026	putative membrane protein (LOC54499), mRNA /cds=(139,705) /gb=NM_019026 /gi=24308132 /ug=Hs.93832 /len=1186	NM_019026	Hs.93832	NP 061899
		amyloid beta (A4) precursor protein- binding, family B, member 1 interacting protein (APBB1IP), mRNA /cds=(88,2085) /gb=NM_019043 /gi=26665876 /ug=Hs.98874			
ncrc4247	NM_019043	/len=2423	NM_019043	Hs.98874	NP_061916
mioa4177	NM_019059	of Tom7 (S. cerevisiae) (TOM7), mRNA /cds=(94,261) /gb=NM_019059 /gi=9506858 /ug=Hs.112318 /len=487	NM_019059	Hs.112318	NP_061932

Figure ob	Contu.				
		-DNA 51 140007 5-			
	11/00/1/10	cDNA FLJ10287 fis,			
mioc2255	AK001149	clone HEMBB1001387	NM_019083	Hs.40337	NP_061956
		hypothetical protein			
		F23149_1 (PD2),			
		mRNA			
		/cds=(229,1824)			
		/gb=NM_019088			
		/gi=9506582			
		/ug=Hs.152894			
miob2671	NM_019088	/len=1966	NM_019088	Hs.152894	NP_061961
		S100 calcium binding			
		protein A4 (calcium			
		protein, calvasculin,			
		metastasin, murine			
:		placental (S100A4),			
		transcript variant 1,			
		mRNA /cds=(70,375)			
		/gb=NM_002961			
		/gi=9845514	NM_002961;		
ncrc9469	NM_002961	/ug=Hs.81256 /len=512	NM_019554	Hs.81256	NP_062427
		zinc finger protein 26			
	Ì	(KOX 20) (ZNF26),			
		mRNA			
		/cds=(699,1298)			
		/gb=NM_019591			
		/gi=11034838			
		/ug=Hs.26432			
mioc2961	NM_019591	/len=2385	NM_019591	Hs.26432	NP 062537
		Similar to CG6950		-	
		gene product, clone			
		MGC:5114			
		IMAGE:3453829,			
miod5008	BC000819	mRNA, complete cds		Hs.180378	NP_062556
-					
		SM-11044 binding			
		protein (SMBP), mRNA			
		/cds=(20,1780)			
		/gb=NM_020123			
		/gi=10047129			
seoc4093	NM_020123	/ug=Hs.8203 /len=3389	NM_020123	Hs.8203	NP_064508
-		lysophosphatidic acid			
		acyltransferase-delta			
		(LPAAT-delta), mRNA			
		/cds=(158,1294)			
	İ	/gb=NM_020133			
		/gi=9910391			
		/ug=Hs.353175			
ncrb6453	NM_020133	/len=1774	NM_020133	Hs.353175	NP_064518

Figure 6b C	onta.				
		hypothetical protein FLJ21827 (FLJ21827), mRNA /cds=(379,1446) /gb=NM_020153 /gi=21361819			
ncrb8224	NM 020152	/ug=Hs.334360 /len=1834	NIM 020152	110 224260	ND 004520
fcr4433	NM_020153	chromosome 11 hypothetical protein ORF3 (LOC56851), mRNA /cds=(14,742) /gb=NM_020154 /gi=9910345 /ug=Hs.4245 /len=1072	NM_020153	Hs.334360 Hs.4245	NP_064538
ncrc3856	NM_020192	GK003 protein (GK003), mRNA /cds=(10,690) /gb=NM_020192 /gi=21281666 /ug=Hs.83313 /len=901		Hs.83313	NP_064577
seob6229	NIM 020402	GK003 protein (GK003), mRNA /cds=(10,690) /gb=NM_020192 /gi=21281666	NIM 020400	III- 92242	ND 004577
ncr6344	NM_020192 NM_020199	/ug=Hs.83313 /len=901 HTGN29 protein (HTGN29), mRNA /cds=(205,1002) /gb=NM_020199 /gi=9910277 /ug=Hs.283437 /len=2371	NM_020199	Hs.83313 Hs.283437	NP_064577
ncrb3424	NM_020213	hypothetical protein from EUROIMAGE 1977056 (LOC56965), mRNA /cds=(609,1358) /gb=NM_020213 /gi=9910373 /ug=Hs.8694 /len=2359	NM_020213; NM_020214	Hs.8694	NP 064599

rigure ob	Oont a.				
seoc2923	NM 020215	hypothetical protein DKFZp761F2014 (DKFZp761F2014), mRNA /cds=(117,638) /gb=NM_020215 /gi=9910205 /ug=Hs.6434 /len=347		Hs.6434	NP 064600
	020210	hepatocellular carcinoma susceptibility protein (HCCA3), mRNA /cds=(53,847) /gb=NM_020232 /gi=22726188		110.0401	141 _004000
ncr3397	NM_020232	/ug=Hs.3726 /len=107 x 009 protein (MDS009), mRNA /cds=(127,534) /gb=NM_020234 /gi=9910425 /ug=Hs.64641	3 NM_020232	Hs.3726	NP_064617
ncrc9591	NM_020234	/len=1133 MOST2 protein (MOST2), mRNA /cds=(3461,3952) /gb=NM_020250 /gi=9910449 /ug=Hs.193920	NM_020234	Hs.64641	NP_064619
miob7274	NM_020250	/len=4750 I-kappa-B-interacting Ras-like protein 1 (KBRAS1), mRNA /cds=(1,579) /gb=NM_020345 /gi=9966808 /ug=Hs.173202	NM_020250	Hs.193920	NP_064635
ncr3587	NM_020345	/len=579 Similar to I-kappa-B-interacting Ras-like protein 1, clone MGC:20358 IMAGE:4549097,	NM_020345	Hs.173202	NP_065078
miod0956	BC012145	mRNA, complete cds	NM_001723;	Hs.173202	NP_065078
miob5873	AF165191	BPAG1n3 (BPAG1) mRNA, partial cds	NM_015548; NM_020388 NM_001723;	Hs.198689	NP_065121
mioc5308	AF165191	BPAG1n3 (BPAG1) mRNA, partial cds	NM_015548; NM_020388	Hs.198689	NP_065121

Figure 6b	Cont u.		,		·
		tumor endothelial			
		marker 7 precursor	[
		(TEM7), mRNA			
		/cds=(83,1585)			
		/gb=NM_020405			
		/gi=21361852			
		/ug=Hs.125036			
miod6773	NM_020405	/len=6140	NM 020405	Hs.125036	NP 065138
1111000770	14141_020400	hypothetical protein	14141_020403	115.123030	NP_000136
ļ		from clone 24796			
		(LOC57146), mRNA			
		/cds=(113,598)			
		/gb=NM_020422	1		
1		/gi=21361853			
1		/ug=Hs.27191			•
ncr5971	NM_020422	/len=1683	NM_020422	Hs.27191	NP_065155
		CTL2 gene, clone			
		MGC:41799			
		IMAGE:5268313,			
fcrb4974	BC040556	mRNA, complete cds	NM 020428	Hs.105509	NP 065161
		mRNA; cDNA			
		DKFZp434M2315			
-		(from clone			
l		DKFZp434M2315)			
fcrc0106	AL133060	(=BC012766.1)		Hs.180428	NP 065195
10/00/100	712100000	hypothetical protein	-	113.100420	NF_003193
		dJ122O8.2			
		(DJ122O8.2), mRNA			
		/cds=(34,300)			
		/gb=NM_020466			
		/gi=20070310			
		/ug=Hs.268115			
ncrb3445	NM_020466	/len=902	NM_020466	Hs.268115	NP_065199
		UDP-N-acetyl-alpha-D-			
		galactosamine:polypep			
		tide N-			
		acetylgalactosaminyltra		1	
		nsferase 1 (GalNAc-		1	
		T1) (GALNT1), mRNA			
		/cds=(32,1711)			
		/gb=NM_020474			
		/gi=13124890			
		/ug=Hs.80120			
ncrc3995	NM_020474	/len=3778	NM_020474	Hs.80120	NP_065207
110100000	114101_020474	Tuen-arra	1111VI_UZU4/4	JU9'00 150	

Figure 6b C	ontu.				
mioc3042	NM_020529	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha (NFKBIA), mRNA /cds=(95,1048) /gb=NM_020529 /gi=10092618 /ug=Hs.81328 /len=1550	NM_020529	Hs.81328	NP_065390
seoa6654	NM_020648	twisted gastrulation 1 (Drosophila) (TWSG1), mRNA /cds=(106,777) /gb=NM_020648 /gi=21314788 /ug=Hs.247302 /len=3693	NM_020648	Hs.247302	NP_065699
mioc6341	NM_020665	kidney-specific membrane protein (NX17), mRNA /cds=(261,929) /gb=NM_020665 /gi=21361864 /ug=Hs.129614 /len=1605	NM_020665	Hs.129614	NP_065716
fcrb6167	NM_020680	SCY1-like 1 (S. cerevisiae) (SCYL1), mRNA /cds=(40,2400) /gb=NM_020680 /gi=19923565 /ug=Hs.238839 /len=2580	NM_020680	Hs.238839	NP_065731
seob4734	NM_020685	HT021 (HT021), mRNA /cds=(145,531) /gb=NM_020685 /gi=10190735 /ug=Hs.47166 /len=797	NM_020685	Hs.47166	NP_065736
seoc5815	NM_020749	AT2 receptor- interacting protein 1 (ATIP1), mRNA /cds=(1,1311) /gb=NM_020749 /gi=21361871 /ug=Hs.7946 /len=3455	NM_020749	Hs.7946	NP_065800

likely ortholog of mouse tumor differentially expressed 1, like (TDE1L), mRNA /cds=(76,1437) /gb=NM 020755 /gi=24308212 /ug=Hs.146668 /len=3149 miob2941 NM_020755 NM_020755 Hs.146668 NP_065806 cDNA FLJ13577 fis, miod5775 AK023639 clone PLACE1008748 Hs.107287 NP 065870 zinc finger protein 291 (ZNF291), mRNA /cds=(38,4237) /gb=NM_020843 /gi=16507197 /ug=Hs.285848 mioa9709 NM 020843 /len=4703 NM_020843 Hs.285848 NP_065894 pleckstrin domain containing, family A (phosphoinositide binding specific) member 4 (PLEKHA4), mRNA /cds=(526,2865) /gb=NM_020904 /qi=10190743 /ug=Hs.9469 /len=3056 NM 020904 seoa3701 NM_020904 Hs.9469 NP_065955 mRNA for KIAA1609 protein, partial cds. /cds=(1,1423)/gb=AB046829 /gi=15425661 /ug=Hs.14449 fcrb1328 AB046829 /len=4683 Hs.14449 NP 065998 mesoderm induction early response 1 (MI-ER1), mRNA /cds=(234,1844) /gb=NM_020948 /gi=24308260 /ug=Hs.222746 ncrc2827 NM 020948 /len=4972 NM_020948 Hs.222746 NP 065999 ubiquitin C (UBC), mRNA /cds=(136,2193) /gb=NM_021009 /gi=20149305 /ug=Hs.183704 /len=2309 ncrc3596 NM_021009 NM 021009 Hs.183704 NP 066289

NADH dehydrogenase (ubiquinone) flavoprotein 3, 10kDa (NDUFV3), mRNA /cds=(575,1945) /gb=NM_021075 /gi=21361323 /ug=Hs.59745 /len=2023 NM_021075 Hs.59745 NP_066 Serine protease inhibitor, Kunitz type, 2 (SPINT2), mRNA /cds=(301,1059) /gb=NM_021102 NADE NAD NADE NADE NADE NADE NADE NADE NADE NADE NADE NADE NADE NADE NADE NADE NADE NADE NADE NADE	
serine protease inhibitor, Kunitz type, 2 (SPINT2), mRNA /cds=(301,1059)	553
inhibitor, Kunitz type, 2 (SPINT2), mRNA /cds=(301,1059)	223
/gi=10863908 /ug=Hs.31439	
fcrb4409 NM_021102 /len=1544 NM_021102 Hs.31439 NP_066	925
clone IMAGE:5265444, mRNA /gb=BC035161 /gi=23242943 ncr2700 BC035161 /ug=Hs.7278 /len=4402 Hs.7278 NP_066	940
eukaryotic translation elongation factor 1 beta 2 (EEF1B2), transcript variant 1, mRNA /cds=(236,913) /gb=NM_001959 /gi=16519564 /ug=Hs.421608 NM_001959; seob7649 NM 001959 /len=961 NM 021121 Hs.421608 NP 066	944
	744
eukaryotic translation elongation factor 1 beta 2 (EEF1B2), transcript variant 1, mRNA /cds=(236,913) /gb=NM_001959 /gi=16519564 /ug=Hs.421608 NM_001959;	
hfcr1189 NM_001959 /len=961 NM_021121 Hs.421608 NP_066	

pyrophosphatase (inorganic) (PP), nuclear gene encoding mitochondrial protein, mRNA /cds=(78,947) /gb=NM 021129 /gi=11056043 /ug=Hs.184011 /len=1282 seob4076 NM_021129 NM_021129 Hs.184011 NP_066952 peptidylprolyl isomerase A (cyclophilin A) (PPIA), mRNA /cds=(45,542) /gb=NM_021130 /gi=10863926 /ug=Hs.401787 ncrc1421 NM_021130 /len=753 NM 021130 Hs.401787 NP_066953 protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform (calcineurin A beta) (PPP3CB), mRNA /cds=(117,1691) /gb=NM_021132 /gi=11036639 /ug=Hs.151531 miob0636 NM 021132 /len=3079 NM 021132 Hs.151531 NP 066955 tumor necrosis factor, alpha-induced protein 1 (endothelial) (TNFAIP1), mRNA /cds=(212,1162) /gb=NM_021137 /gi=26051238 /ug=Hs.76090 ncrc1203 NM_021137 /len=3571 NM_021137 Hs.76090 NP_066960 likely ortholog of mouse another partner for ARF 1 (APA1), mRNA /cds=(183,1619) /gb=NM 021188 /gi=10863994 /ug=Hs.405945 ncrc6774 NM 021188 /len=2207 NM_021188 Hs.405945 NP 067011

chromosome 20 open reading frame 77 (C20orf77), mRNA /cds=(298,1278) /gb=NM_021215 /gi=22507393 /ug=Hs.27192 miod3743 NM 021215 /len=4219 NM_021215 Hs.27192 NP 067038 DC2 protein (DC2), mRNA /cds=(60,509) /gb=NM_021227 /gi=24308270 /ug=Hs.103180 fcrb5964 NM_021227 /len=1090 NM_021227 Hs.103180 NP 067050 KIAA0266 gene product (KIAA0266), mRNA /cds=(734,3034) /gb=NM 021645 /gi=11063982 /ug=Hs.127376 mioa9649 /len=5585 NM_021645 NM_021645 Hs.127376 NP_067677 mRNA for KIAA0626 seoc2477 AB014526 protein, complete cds NM_021647 Hs.178121 NP_067679 TGFB-induced factor 2 (TALE family homeobox) (TGIF2), mRNA /cds=(170,883) /gb=NM 021809 /gi=19923576 /ug=Hs.94785 fcrb1733 NM 021809 /len=3433 NM 021809 Hs.94785 NP_068581 of yeast long chain polyunsaturated fatty acid elongation enzyme 2 (HELO1), mRNA /cds=(345,1244) /gb=NM_021814 /qi=21361903 /ug=Hs.250175 seob1197 NM_021814 NM_021814 /len=3011 Hs.250175 NP_068586 hypothetical protein FLJ13149 (FLJ13149), mRNA /cds=(291,2585) /gb=NM_021826 /gi=11141902 /ug=Hs.112188 ncrb8203 NM_021826 /len=2836 NM_021826 Hs.112188 NP_068598

rigure ob C	Jone d.				
		hypothetical protein FLJ21839 (FLJ21839), mRNA /cds=(445,2619) /gb=NM_021831 /gi=19923577 /ug=Hs.433334			
seob7739	NM_021831	/len=3252	NM_021831	Hs.433334	NP_068603
seob9285	NM 021831	hypothetical protein FLJ21839 (FLJ21839), mRNA /cds=(445,2619) /gb=NM_021831 /gi=19923577 /ug=Hs.433334 /len=3252	NNA 004004		
SEOD9203	10101_021031	/ien=3252	NM_021831	Hs.433334	NP_068603
fcrb4383	NM_021939	FK506 binding protein 10, 65 kDa (FKBP10), mRNA /cds=(87,1835) /gb=NM_021939 /gi=21361894 /ug=Hs.3849 /len=2641	NM_021939	Hs.3849	NP_068758
		hypothetical protein FLJ22174 (FLJ22174), mRNA /cds=(1712,2173) /gb=NM_021945 /gi=24431990			
seoa2679	NM_021945	/ug=Hs.7734 /len=3326	NM_021945	Hs.7734	NP 068764
mioc0567	NM_021967	small EDRK-rich factor 1A (telomeric) (SERF1A), mRNA /cds=(184,516) /gb=NM_021967 /gi=11415045 /ug=Hs.32567 /len=1912	NM_021967	Hs.32567	NP_068802
miod6058	NM_021970	mitogen-activated protein kinase kinase 1 interacting protein 1 (MAP2K1IP1), mRNA /cds=(250,624) /gb=NM_021970 /gi=21614526 /ug=Hs.6361 /len=1416		Hs.6361	NP 068805

	Cont'd.				
ncrc0632	NM_021999	integral membrane protein 2B (ITM2B), mRNA /cds=(171,971) /gb=NM_021999 /gi=11527401 /ug=Hs.239625 /len=1843 mRNA for EGLN1	NM_021999	Hs.239625	NP_068839
fcrb9802	AJ310543	protein	NM_022051	Hs.6523	NP_071334
seob0569	NM_022333	TIA1 cytotoxic granule- associated RNA binding protein-like 1 (TIAL1), transcript variant 2, mRNA /cds=(158,955) /gb=NM_022333 /gi=13435393 /ug=Hs.182741 //en=1760	NM_003252; NM_022333	Hs.182741	NP 071728
		TIA1 cytotoxic granule- associated RNA binding protein-like 1 (TIAL1), transcript variant 2, mRNA /cds=(158,955) /gb=NM_022333 /gi=13435393 /ug=Hs.182741	NM_003252;		
fcrb1320	NM_022333	/len=1760	NM_022333	Hs.182741	NP_071728
		ubiquitin-conjugating enzyme E2 variant 1 (UBE2V1), transcript variant 2, mRNA /cds=(70,735) /gb=NM_003349 /gi=15718757 /ug=Hs.75875	NM_003349; NM_021988;		
seob6198	NM 003349	/len=2394	NM_022442	Hs.75875	NP 071887
seob3313	NM 003349	ubiquitin-conjugating enzyme E2 variant 1 (UBE2V1), transcript variant 2, mRNA /cds=(70,735) /gb=NM_003349 /gi=15718757 /ug=Hs.75875 /len=2394	NM_003349; NM_021988; NM_022442	Hs.75875	NP_071887

Figure 6b	Conta.			_	
mioc7763	NM_022488	autophagy Apg3p/Aut1p-like (APG3), mRNA /cds=(120,1064) /gb=NM_022488 /gi=19526772 /ug=Hs.26367 /len=1381 ribosomal protein S18 (RPS18), mRNA /cds=(46,504) /gb=NM_022551	NM_022488	Hs.26367	NP_071933
seob5044	NM_022551	/gi=14165467 /ug=Hs.275865 /len=549	NM_022551	Hs.275865	NP_072045
fcrc6570	NM_002890	RAS p21 protein activator (GTPase activating protein) 1 (RASA1), transcript variant 1, mRNA /cds=(119,3262) /gb=NM_002890 /gi=4506430 /ug=Hs.758 /len=4307	NM_002890; NM_022650	Hs.758	NP_072179
miod0355	NM_022735	golgi complex associated protein 1, 60kDa (GOCAP1), mRNA /cds=(56,1642) /gb=NM_022735 /gi=15826851 /ug=Hs.6831 /len=3598	NM 022735	Hs.6831	NP 073572
fcrb1729	NM_022735	golgi complex associated protein 1, 60kDa (GOCAP1), mRNA /cds=(56,1642) /gb=NM_022735 /gi=15826851 /ug=Hs.6831 /len=3598		Hs.6831	NP_073572
seob1955	AK091247	cDNA FLJ33928 fis, clone CTONG2017444		Hs.16603	NP_073592

I iguic ob o		· 			
		hypothetical protein			
		FLJ12892 (FLJ12892),			
		mRNA			
		/cds=(145,1929)			
		/gb=NM_022757			
		/gi=24308284			
		/ug=Hs.17731			
fcrb9909	NM_022757	/len=2987	NM 022757	Hs.17731	NP 073594
		FAD104 (FAD104),		\	
		mRNA /cds=(58,3672)			
		/gb=NM_022763			
		/gi=27477058			
		/ug=Hs.299883			
ncrc4267	NM_022763	/len=6894	NM_022763	Hs.299883	NP 073600
110104201	14141_022703	survival of motor	14141_022703	113.293003	NF_073000
		neuron 2, centromeric			
		(SMN2), transcript			
		variant d, mRNA			
		•			
		/cds=(164,1048)	NINA 047444		
		/gb=NM_017411	NM_017411;		
		/gi=13259525	NM_022875;		
5 5404		/ug=Hs.367729	NM_022876;		
fcrc5134	NM_017411	/len=1623	NM_022877	Hs.367729	NP_075015
seoa0114	X70326	MacMarcks mRNA	NM_023009	Hs.75061	NP_075385
		hypothetical protein			
		FLJ11021 similar to			
		splicing factor,			
		arginine/serine-rich 4			
		(FLJ11021), mRNA			
		/cds=(767,1375)			
		/gb=NM_023012	ļ		
		/gi=20127619			
		/ug=Hs.81648			
fcrc5169	NM_023012	/len=1878	NM_023012	Hs.81648	NP_075388
		hypothetical protein			
1		FLJ20989 (FLJ20989),			
1		mRNA /cds=(53,742)			
		/gb=NM_023080			
		/gi=12751496			
1		/ug=Hs.169615			
ncrb8607	NM_023080	/len=2643	NM_023080	Hs.169615	NP_075568
}		hypothetical protein			
		FLJ12389 similar to			
		acetoacetyl-CoA			
		synthetase			
		(FLJ12389), mRNA			
		/cds=(149,2167)			
		/gb=NM_023928			
		/gi=12965198			
1		/ug=Hs.239758			
ncrb8239	NM_023928	/len=3253	NM_023928	Hs.239758	NP_076417

Figure ob C	onea.				
miob7156	NM_001356	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3 (DDX3), transcript variant 2, mRNA /cds=(857,2845) /gb=NM_001356 /gi=13514812 /ug=Hs.380774 /len=5322	NM_001356; NM_024005	Hs.380774	NP_076829
mioa1473	NM_024010	methyltransferase reductase (MTRR), transcript variant 2, mRNA /cds=(31,2208) /gb=NM_024010 /gi=13325067 /ug=Hs.153792 /len=3291	NM_002454; NM_024010	Hs.153792	NP_076915
fcrc0835	NM_024038	hypothetical protein MGC2803 (MGC2803), mRNA /cds=(68,598) /gb=NM_024038 /gi=13128991 /ug=Hs.239894 /len=954	NM_024038	Hs.239894	NP_076943
mioc3206	NM 024041	hypothetical protein MGC3180 (MGC3180), mRNA /cds=(76,768) /gb=NM_024041 /gi=13128997 /ug=Hs.250570 /len=846	NM 024041	Hs.250570	NP 076946
mioc3316	NM_024045	nucleolar protein GU2 (GU2), mRNA /cds=(108,2321) /gb=NM_024045 /gi=13129005 /ug=Hs.7392 /len=2575		Hs.7392	NP_076950
seoc0619	NM_022902	solute carrier family 30 (zinc transporter), member 5 (SLC30A5), mRNA /cds=(202,2499) /gb=NM_022902 /gi=20070322 /ug=Hs.129445 /len=2952	NM_022902; NM_024055	Hs.129445	NP_076960

I iguic ob	Oontu.				
		ubiquitin-like 5 (UBL5),	1		
		mRNA /cds=(66,287)			
		/gb=NM_024292		İ	
		/gi=13236509			
mioa9033	NM_024292	/ug=Hs.13836 /len=41	3 NM_024292	Hs.13836	NP_077268
		Similar to v-maf			
		musculoaponeurotic			
		fibrosarcoma			
		oncogene family,			
		protein B (avian), clone			
		IMAGE:4470615,			
seoc7547	BC042615	mRNA, partial cds		Hs.7041	NP_077288
		c6.1A (C6.1A), mRNA			
		/cds=(3,953)			
		/gb=NM_024332			
		/gi=13236582			
seob1513	NM_024332	/ug=Hs.301927 /len=2846	NM 024332	Hs.301927	ND 077200
Seob 13 13	141VI_024332	//611-2040	14101_024332	IDS.30 1921	NP_077308
		cDNA FLJ39995 fis,			ļ
mioa0890	AK097314	cione STOMA2002141		Hs.102548	NP_077318
		Notch 2 (Drosophila)		.,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	
		(NOTCH2), mRNA			
		/cds=(257,7672)			
		/gb=NM_024408			
1		/gi=24041034			
		/ug=Hs.8121			
seoa7517	NM_024408	/len=11433	NM_024408	Hs.8121	NP_077719
1		p10-binding protein			
		(BITE), mRNA			
		/cds=(149,1942)			1
	[/gb=NM_024491			
		/gi=13346499	1		
00003245	NIM 024404	/ug=Hs.42315	NM 024404	115 40045	ND 077047
seoa3245	NM_024491	/len=2628 mRNA for KIAA1865	NM_024491	Hs.42315	NP_077817
		protein, partial cds.		1	
į		/cds=(622,2793)		1	
		/gb=AB058768		1	
		/gi=14017946		1	
Ì		/g=14017346 /ug=Hs.179260		1	
ncrc4757	AB058768	/len=3641		Hs.179260	NP_078772
	1= 555, 65	1		11.10.11.02.00	1141 _070772

Figure 6b Co	mu.				
		hypothetical protein MGC4701 (MGC4701), mRNA /cds=(149,1585) /gb=NM_024511 /gi=24308290			
seoc0778	NM_024511	/ug=Hs.421054 /len=1686	NM_024511	Hs.421054	NP_078787
mioc2828	NM_024524	hypothetical protein FLJ20986 (FLJ20986), mRNA /cds=(1758,3863) /gb=NM_024524 /gi=21362055 /ug=Hs.324507 /len=5226	NIM 024524	Hs.324507	ND 078800
fcrb3258		hypothetical protein FLJ22678 (FLJ22678), mRNA /cds=(188,2515) /gb=NM_024536 /gi=27545322	NM_024524		NP_078800
ICID3258	NM_024536	/ug=Hs.7718 /len=2965 cDNA FLJ23687 fis,	NM_024536	Hs.7718	NP_078812
ncr6426	AK074267	clone HEP10109		Hs.13222	NP_078836
ncrc5054	NM_024592	hypothetical protein FLJ13352 (FLJ13352), mRNA /cds=(97,1053) /gb=NM_024592 /gi=13375784 /ug=Hs.22972 /len=2271	NM_024592	Hs.22972	NP_078868
ncrc6825	NM 024635	hypothetical protein FLJ22643 (FLJ22643), mRNA /cds=(15,650) /gb=NM_024635 /gi=13375865 /ug=Hs.43579 /len=997	NM 024635	Hs.43579	NP 078011
fcrb6715	NM_024656	hypothetical protein FLJ22329 (FLJ22329), mRNA /cds=(36,767) /gb=NM_024656 /gi=13375904 /ug=Hs.367653 /len=2501	NM_024656	Hs.367653	NP_078911 NP_078932

Figure 60 Co	Jilea.	,			
seoa9494	NM_024713	hypothetical protein FLJ22557 (FLJ22557), mRNA /cds=(87,1001) /gb=NM_024713 /gi=13376012 /ug=Hs.106101 /len=2676	NM_024713	Hs.106101	NP_078989
		KIAA0643 protein (KIAA0643), mRNA /cds=(80,823) /gb=NM_024793 /gi=13435144 /ug=Hs.155995			
mioa8275	NM_024793	/len=2221 hypothetical protein FLJ23251 (FLJ23251), mRNA /cds=(235,1449) /gb=NM_024818 /gi=13376211 /ug=Hs.170737 /len=2132	NM_024793	Hs.155995	NP_079069 NP_079094
		hypothetical protein FLJ22662 (FLJ22662), mRNA /cds=(66,1586) /gb=NM_024829 /gi=13376231 /ug=Hs.178470	_		
ncrc7151	NM_024829 NM_024843	/len=1707 duodenal cytochrome b (FLJ23462), mRNA /cds=(74,934) /gb=NM_024843 /gi=19923602 /ug=Hs.31297 /len=4254	NM_024829 NM_024843	Hs.178470 Hs.31297	NP_079105 NP_079119
seoc0212	NM_025027	hypothetical protein FLJ14260 (FLJ14260), mRNA /cds=(431,1219) /gb=NM_025027 /gi=13430885 /ug=Hs.287629 /len=2441	NM 025027	Hs.287629	NP_079303
seoc2201	AB002306	mRNA for KIAA0308 gene, partial cds	NM_025134	Hs.8182	NP_079303

Contra.				
	likely ortholog of mouse Mak3p (S. cerevisiae) (MAK3P), mRNA /cds=(301,810) /gb=NM_025146 /gi=13376734 /ug=Hs.288932			·
NM_025146	/len=3576	NM_025146	Hs.288932	NP_079422
	hypothetical protein FLJ13386 (FLJ13386), mRNA /cds=(428,2539) /gb=NM_025180 /gi=22095366 /ug=Hs.300876			
NM_025180	/len=2770	NM_025180	Hs.300876	NP_079456
NM 025494	FLJ22843 (FLJ22843), mRNA /cds=(532,1287) /gb=NM_025184 /gi=13376775 /ug=Hs.301143	NINA 025194	11- 201142	ND 070400
NIVI_025184	//len=2291	NIVI_025184	HS.301143	NP_079460
AL832422	mRNA; cDNA DKFZp762K012 (from clone DKFZp762K012)		Hs.301651	NP_079465
NM 025190	(KIAA1641), mRNA /cds=(41,454) /gb=NM_025190 /gi=13449272 /ug=Hs.44566	NM 025190	Hs. 44566	NP_079466
	transcription termination factor-like protein (LOC80298), mRNA /cds=(341,1498) /gb=NM_025198 /gi=21314735			NP 079474
	NM_025146 NM_025180 NM_025184	likely ortholog of mouse Mak3p (S. cerevisiae) (MAK3P), mRNA /cds=(301,810) /gb=NM_025146 /gi=13376734 /ug=Hs.288932 /len=3576 hypothetical protein FLJ13386 (FLJ13386), mRNA /cds=(428,2539) /gb=NM_025180 /gi=22095366 /ug=Hs.300876 /len=2770 hypothetical protein FLJ22843 (FLJ22843), mRNA /cds=(532,1287) /gb=NM_025184 /gi=13376775 /ug=Hs.301143 /len=2291 mRNA; cDNA DKFZp762K012 (from clone DKFZp762K012) KIAA1641 protein (KIAA1641), mRNA /cds=(41,454) /gb=NM_025190 /gi=13449272 /ug=Hs.44566 NM_025190 /gi=13449272 /ug=Hs.44566 NM_025190 /len=2418 transcription termination factor-like protein (LOC80298), mRNA /cds=(341,1498) /gb=NM_025198 /gi=21314735	likely ortholog of mouse Mak3p (S. cerevisiae) (MAK3P), mRNA /cds=(301,810) /gb=NM_025146 /gi=13376734 /ug=Hs.288932 /len=3576 NM_025146 /hypothetical protein FLJ13386 (FLJ13386), mRNA /cds=(428,2539) /gb=NM_025180 /gi=22095366 /ug=Hs.300876 /len=2770 NM_025180 /gb=NM_025184 /gi=13376775 /ug=Hs.301143 /len=2291 NM_025184 /gi=13376775 /ug=Hs.301143 /len=2291 NM_025184 /gi=1349272 /ug=Hs.44566 /len=2418 NM_025190 /gi=13449272 /ug=Hs.44566 /len=2418 NM_025190 /gi=213449272 /ug=Hs.44566 /len=2418 NM_025190 /gb=NM_025198 /gi=21314735	likely ortholog of mouse Mak3p (S. cerevisiae) (MAK3P), mRNA /cds=(301,810) /gb=NM_025146 /gi=13376734 /ug=Hs.288932 /len=3576 NM_025146 Hs.288932 NM_025146 Hs.288932 /len=3576 NM_025146 Hs.288932 NM_025146 Hs.288932 NM_025146 Hs.288932 NM_025146 Hs.288932 NM_025146 Hs.288932 NM_025146 Hs.288932 NM_025146 Hs.288932 NM_025146 Hs.288932 NM_025146 Hs.288932 NM_025146 Hs.288932 NM_025146 Hs.288932 NM_025146 Hs.288932 NM_025146 NM_025146 NM_025146 NM_025146 NM_025146 NM_025148 NM_025148 NM_025148 NM_025148 NM_025148 NM_025148 NM_025148 NM_025148 NM_025148 NM_025148 NM_025148 NM_025149 NM_025148 NM_025149 NM_025148 NM_025149 NM_025149 NM_025149 NM_025148 NM_025149 NM_025148 NM_025148 NM_02

Figure 6b	Conta.		· · · · · · · · · · · · · · · · · · ·		
		hypothetical protein		*	
		PRO2730 (PRO2730),	1		
		mRNA	Ì		
		/cds=(1346,1759)			
		/gb=NM_025222			
		/gi=21361950	ļ		
		/ug=Hs.194110			
fcrb9018	NIM OSESSS	/len=2990	NIM ODEDDO	Hs.194110	ND 070400
10109010	NM_025222		NM_025222	<u>ПS. 1941 10</u>	NP_079498
		recombination protein			
		REC14 (REC14),			
		mRNA /cds=(77,994)			
		/gb=NM_025234			
		/gi=13376839			
		/ug=Hs.296242			
ncrc4663	NM_025234	/len=1205	NM_025234	Hs.296242	NP 079510
		DEAD/H (Asp-Glu-Ala-			
		Asp/His) box			
		polypeptide 9 (RNA			
		helicase A, nuclear			
		DNA helicase II;			
		_ ·			
		leukophysin) (DDX9),	1		
		transcript variant 1,			
		mRNA /cds=(81,3920)			
		/gb=NM_001357			
		/gi=13514819	1		
		/ug=Hs.74578	NM_001357;		
seoa2428	NM_001357	/len=4199	NM_030588	Hs.74578	NP_085077
		mRNA for KIAA1694			
		protein, partial cds.			
		/cds=(1,2275)			
		/gb=AB051481	1		
		/gi=12697932			
		/ug=Hs.19597			
seoa6432	AB051481	/len=4235	NM_030629	Hs.19597	NP 085132
33333702	7.0001701	mitogen-activated	1.1.11_000020	110.10001	141_000102
		protein kinase kinase 2			
		[-	İ		
		(MAP2K2), mRNA	1		
		/cds=(255,1457)			
		/gb=NM_030662			
1	I	/gi=21614527			
		/ug=Hs.72241			
fcr1020	NM_030662	/len=1759	NM_030662	Hs.72241	NP_109587
		1			
		t-complex 1 (TCP1),			
		mRNA /cds=(22,1692)			
		/gb=NM_030752		1	
		/gi=13540472			
seob0949	NM 030752	/ug=Hs.4112 /len=2019	NM 030752	Hs.4112	NP_110379
		p. = g	1300,02	1	

Figure 6b Co	Jile d.				
fcrb4413	NM_030755	thioredoxin domain- containing (TXNDC), mRNA /cds=(118,960) /gb=NM_030755 /gi=13559515 /ug=Hs.24766 /len=1112	NM_030755	Hs.24766	NP_110382
		basic helix-loop-helix domain containing, class B, 3 (BHLHB3), mRNA /cds=(135,1583) /gb=NM_030762 /gi=13540520			
miob4684	NM_030762	/ug=Hs.33829 /len=3641	NM 030762	Hs.33829	ND 440200
ncrb4385	AW298400	UI-H-BW0-ajj-h-09-0- UI.s1 NCI_CGAP_Sub6 cDNA clone IMAGE:2732033 3', mRNA sequence /clone=IMAGE:273203 3 /clone_end=3' /gb=AW298400 /gi=6704960 /ug=Hs.438172 /len=635		Hs.438172	NP_110389
ncrc9877	NM_030917	hypothetical protein DKFZp586K0717 (DKFZP586K0717), mRNA /cds=(168,1730) /gb=NM_030917 /gi=13569873 /ug=Hs.334812 /len=1914	NM_030917	Hs.334812	NP 112179
miob8080	NM_030920	leucine-rich acidic nuclear protein like (LANPL), mRNA /cds=(332,1138) /gb=NM_030920 /gi=23463320 /ug=Hs.71331 /len=3273	NM 030920	Hs.71331	NP 112182

Application of: Liew, et. al. Our Docket #: 4231/2042 Figure 6b Cont'd.

Figure 6b	Cont a.				
ł		similar to rat			
		tricarboxylate carrier-			
		like protein			
		(BA108L7.2), mRNA			
		/cds=(75,1040)			
		/gb=NM_030971			
		/gi=13569945			
		/ug=Hs.283844			
seoa2135	NM_030971	/len=2735	NM 030971	Hs.283844	NP_112233
00002100	1444_000071	RAB1B, member RAS	11111_000071	110.200011	111 _112200
		oncogene family			
		(RAB1B), mRNA	1		
		/cds=(48,653)			
		/gb=NM_030981			
		/gi=13569961			
four 4074	NINA 000004	/ug=Hs.300816	NINA 000004	11- 200040	ND 440040
fcrb4271	NM_030981	/len=1985	NM_030981	Hs.300816	NP_112243
		hatara sanaaya nyalaan			
		heterogeneous nuclear			
		ribonucleoprotein M			
		(HNRPM), transcript		1	
		variant 1, mRNA			
		/cds=(231,2423)			
		/gb=NM_005968			
		/gi=14141151			
		/ug=Hs.79024	NM_005968;		
hfcr2390	NM_005968	/len=2703	NM_031203	Hs.79024	NP_112480
		hypothetical protein			
1		DC50 (DC50), mRNA			
		/cds=(37,366)			
		/gb=NM_031210			
		/gi=24475712			
		/ug=Hs.324521			
mioa3018	NM_031210	/len=442	NM_031210	Hs.324521	NP_112487
		chromosome 20 open			
		reading frame 18			
		(C20orf18), transcript			
		variant 2, mRNA			
		/cds=(677,2179)			
		/gb=NM_031229	NM_006462;		
		/gi=14043035	NM_031227;		
		/ug=Hs.247280	NM_031228;		
ncrb3702	NM_031229	/len=2715	NM_031229	Hs.247280	NP_112506

Figure ob C	ont a.				
ncrc1740	NM_031243	heterogeneous nuclear ribonucleoprotein A2/B1 (HNRPA2B1), transcript variant B1, mRNA /cds=(170,1231) /gb=NM_031243 /gi=14043071 /ug=Hs.232400 /len=1780	NM_002137; NM_031243	Hs.232400	NP_112533
fcrb7098	NM_031298	hypothetical protein MGC2963 (MGC2963), mRNA /cds=(135,467) /gb=NM_031298 /gi=13775219 /ug=Hs.30011 /len=673		Hs.30011	NP_112588
fcrb1604	NM_031302	gycosyltransferase (LOC83468), mRNA /cds=(408,1457) /gb=NM_031302 /gi=21314737 /ug=Hs.159993 /len=1908	NM_031302	Hs.159993	NP_112592
ncrc5845	NM_031370	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa) (HNRPD), transcript variant 1, mRNA /cds=(286,1353) /gb=NM_031370 /gi=14110419 /ug=Hs.406404 /len=2197	NM_002138; NM_031369; NM_031370	Hs.406404	NP_112738
miob2192	NM_032174	hypothetical protein FLJ12770 (FLJ12770), mRNA /cds=(187,1113) /gb=NM_032174 /gi=21362029 /ug=Hs.321653 /len=2670	NM_032174	Hs.321653	NP_115550

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1 igure ob C					
ncrc2780	NM_032231	hypothetical protein FLJ22875 (FLJ22875), mRNA /cds=(152,634) /gb=NM_032231 /gi=15638951 /ug=Hs.406548 /len=1019	NM_032231	Hs.406548	NP_115607
		hypothetical protein DKFZp434I1916 (DKFZp434I1916), mRNA /cds=(144,563) /gb=NM_032245 /gi=14149959			
seob8807	NM 032245	/ug=Hs.334641 /len=800	NM 032245	Hs.334641	NP_115621
	NIM_002240	hypothetical protein DKFZp761J139 (DKFZp761J139), mRNA /cds=(3155,3970) /gb=NM_032280 /gi=14150026 /ug=Hs.15536	1441_002240		NF_113021
miod5190	NM_032280	/len=4635	NM_032280	Hs.15536	NP 115656
		hypothetical protein MGC13007 (MGC13007), mRNA /cds=(1099,1653) /gb=NM_032320 /gi=14150091 /ug=Hs.332382			
ncr8893	NM_032320	/len=2479 hypothetical protein MGC12458 (MGC12458), mRNA /cds=(30,518) /gb=NM_032328 /gi=14150107 /ug=Hs.330664	NM_032320	Hs.332382	NP_115696
mioa4782	NM_032328	/len=1026	NM_032328	Hs.330664	NP 115704
seoc4609	NM 032328	hypothetical protein MGC12458 (MGC12458), mRNA /cds=(30,518) /gb=NM_032328 /gi=14150107 /ug=Hs.330664 /len=1026	NM_032328	Hs.330664	
35007003	TI4IAI 025250	Men- 1020	INIVI_UUZUZO	JI 13.330004	NP_115704

Figure 6D	Contu.				_
		hypothetical protein			
		MGC12981			
		(MGC12981), mRNA			
		/cds=(225,767)			
		/gb=NM_032357 /gi=21362049			
		/gi=21302049 /ug=Hs.104203			
ncrb0653	NM_032357	/len=1644	NM 032357	Hs.104203	NP 115733
110100000	14141_032337	protocadherin gamma	14141_032337	HS. 104203	NF_110733
		subfamily C, 5			
		(PCDHGC5), transcript			
		variant 1, mRNA			
		/cds=(1,2835)			
		/gb=NM_018929	,		
		/gi=14277683			
		/ug=Hs.335001	NM_018929;		
fcrb4892	NM_018929	/len=4641	NM_032407	Hs.335001	NP_115783
		inner mitochondrial			
		membrane peptidase 2			
		like (IMMP2L), mRNA			
		/cds=(444,971)	Ì		
		/gb=NM_032549			
		/gi=14211844			
	NINE 000540	/ug=Hs.89576			
seob2337	NM_032549	/len=1540	NM_032549	Hs.89576	NP_115938
		hypothetical protein			
		FLJ20707 (FLJ20707),			
		mRNA /cds=(83,2173)			
		/gb=NM_032560			
		/gi=19923643			
		/ug=Hs.334657	NM 017936;		
ncrc4371	NM_032560	/len=2794	NM 032560	Hs.334657	NP 115949
-		V V V V V V V V V V V V V V V V V V V	<u> </u>		
		hypothetical protein			
		FLJ20707 (FLJ20707),			
		mRNA /cds=(83,2173)			
		/gb=NM_032560			
	[/gi=19923643			
f	NINA 000500	/ug=Hs.334657	NM_017936;		
fcrb1381	NM_032560	/len=2794	NM_032560	Hs.334657	NP_115949
}	}	lysyl oxidase-like 3			
		(LOXL3), mRNA			
	1.	/cds=(73,2334) /gb=NM_032603			
		/gi=22095373			
		/ug=Hs.334702			
fcrb5914	NM_032603	/len=3121	NM_032603	Hs.334702	NP_115992
L				1. 15.55 1. 52	1111 _ 1 10004

Figure 6b Co	ont'a.				
		ligand of numb-protein X (LNX), mRNA /cds=(236,2134) /gb=NM_032622 /gi=14249127 /ug=Hs.66295			
mioc8750	NM_032622	/len=3737	NM_032622	Hs.66295	NP_116011
hfor2659	NIM 006414	1-acylglycerol-3-phosphate O-acyltransferase 1 (lysophosphatidic acid acyltransferase, alpha) (AGPAT1), transcript variant 1, mRNA /cds=(319,1170) /gb=NM_006411 /gi=26787964 /ug=Hs.240534	NM_006411;	He 240524	
hfcr2658	NM_006411	/len=2242	NM_032741	Hs.240534	NP_116130
forth O.4.2.4	NIM 020040	hypothetical protein FLJ14800 (FLJ14800), mRNA /cds=(22,1350) /gb=NM_032840 /gi=14249553 /ug=Hs.62119	NNA 0000 40		
fcrb9134	NM_032840	/len=2568	NM_032840	Hs.62119	NP_116229
15h 4024	NIM 0000 40	hypothetical protein FLJ14834 (FLJ14834), mRNA /cds=(326,1237) /gb=NM_032849 /gi=21361885 /ug=Hs.62905			·
fcrb4231	NM_032849	/len=2342	NM_032849	Hs.62905	NP_116238
ncrc4384	NM_032870	SR rich protein (DKFZp564B0769), mRNA /cds=(33,2450) /gb=NM_032870 /gi=18699723 /ug=Hs.18368 /len=2663	NM_032870	Hs.18368	NP_116259
mioc8479	NM_032870	SR rich protein (DKFZp564B0769), mRNA /cds=(33,2450) /gb=NM_032870 /gi=18699723 /ug=Hs.18368 /len=2663	NM_032870	Hs.18368	NP_116259

rigure ob	Conta.				
		hypothetical protein			
		MGC13159			
		(MGC13159), mRNA			
		/cds=(592,1017)			
		/gb=NM_032927			
		/gi=14249719			
		/ug=Hs.12845			
mioc2997	NM_032927	/len=1759	NM_032927	Hs.12845	NP_116316
		CG016 (LOC88523),			
		mRNA			
		/cds=(323,2230)			
		/gb=NM_033111	Ì		
		/gi=14916464			
		/ug=Hs.112434			
miob7627	NM_033111	/len=2431	NM_033111	Hs.112434	NP_149102
		Similar to caldesmon			
		1, clone MGC:21352			
		IMAGE:4753285,	NM_004342;		
		mRNA, complete cds	NM_033138;		
		(=OK/SW-cl.14 mRNA,	NM_033139;		
		complete cds,	NM_033140;		
fcrb8060	BC040354	AB062484.1)	NM_033157	Hs.325474	NP 149347
		caldesmon 1 (CALD1),			
		transcript variant 1,			
		mRNA			
]		/cds=(230,2611)	NM_004342;		
		/gb=NM_033138	NM_033138;		
		/gi=15149460	NM_033139;		
		/ug=Hs.325474	NM_033140;		
mioc3127	NM_033138	/len=3610	NM_033157	Hs.325474	NP_149347
		ADP-ribosylation factor			
		domain protein 1,			
		64kDa (ARFD1),			
		transcript variant alpha,		İ	
		mRNA /cds=(23,1747)			
		/gb=NM_001656	NM_001656;		
		/gi=15208639	NM_033227;		
seob7404	NM_001656	1 •	NM_033228	Hs.792	NP 150231
		Mus musculus protein	-		
		phosphatase 1,	}		
		regulatory (inhibitor)			
		subunit 1C (Ppp1r1c),]		
mioa9492	NM_033264	mRNA	NM_033264	Mm.29963	NP_150289
		phosphatase 1, regulatory (inhibitor) subunit 1C (Ppp1r1c),	_	Hs.792 Mm.29963	NP_150231 NP_150289

Figure 6b Co	onta.				
		cyclin D-type binding-			
		protein 1 (CCNDBP1),	İ		
		transcript variant 1,			
		lmRNA			
		/cds=(158,1240)			
		/gb=NM_012142			
		/gi=16554565		1	
		, -	NINA 040440.		
.7000		/ug=Hs.36794	NM_012142;		
seoa7296	NM_012142	/len=1615	NM_037370	Hs.36794	NP_411241
		immediate early			
		response 3 (IER3),			
		transcript variant long,			
		mRNA /cds=(30,611)			
		/gb=NM_052815			
		/gi=16554596			
1		/ug=Hs.76095	NM_003897;		
miob6226	NM_052815	/len=1345	NM_052815	Hs.76095	NP 434702
	1.111_302010	hypothetical protein	1.311_002010	1.10.70000	141 _ 707102
		MGC4677 (MGC4677),			
	1	mRNA		1	
		/cds=(1337,1495)			
		/gb=NM_052871			
		/gi=16418372			
		/ug=Hs.432419			
hfcr2789	NM_052871	/len=1607	NM_052871	Hs.432419	NP 443103
		cyclin-dependent			
		kinase 4 (CDK4),			
		transcript variant 1,			
		mRNA			
		/cds=(228,1139)			
		/gb=NM_000075			
		/gi=16936531			
		/ug=Hs.95577	NM_000075;	ļ	
fcr2821	NM_000075	/len=1474	NM_052984	Hs.95577	NP_443710
1					
1					
		mitochondrial			
		ribosomal protein S33			
1		(MRPS33), nuclear			
1					
		•			
	}				-
			NIA 040074	1	
4404	NA 6466=:	1 🔍			
seoa1104	NM_016071	/ug=Hs.83006 /len=727	NM_053035	Hs.83006	NP_444263
		L			
		_ ·			
		Į,			
		(FUSIP1), transcript	NM_006625;		
ncrc3526	NM_006625	variant 1, mRNA	NM_054016	Hs.3530	NP_473357
seoa1104	NM_016071 NM_006625	1.	NM_006625;	Hs.83006 Hs.3530	NP_444263 NP_473357

Figure 6b	Conta.	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	,		
fcrb6890	NM_013354	CCR4-NOT transcription complex, subunit 7 (CNOT7), transcript variant 1, mRNA /cds=(340,1128) /gb=NM_013354 /gi=17978498 /ug=Hs.380963 /len=2653	NM_013354; NM_054026	Hs.380963	NP_473367
fcr2952	NM_058246	DnaJ (Hsp40) subfamily B, member 6 (DNAJB6), transcript variant 1, mRNA /cds=(156,1136) /gb=NM_058246 /gi=24234717 /ug=Hs.181195 /len=2495	NM_005494; NM_058246	Hs.181195	NP_490647
seob2974	NM_078467	cyclin-dependent kinase inhibitor 1A (p21, Cip1) (CDKN1A), transcript variant 2, mRNA /cds=(236,730) /gb=NM_078467 /gi=17978494 /ug=Hs.179665 /len=2281	NM_000389; NM_078467	Hs.179665	NP 510867
seob1801	NM_078469	BRCA2 and CDKN1A interacting protein (BCCIP), transcript variant C, mRNA /cds=(13,891) /gb=NM_078469 /gi=17402872 /ug=Hs.279862 /len=2338	NM_016567; NM_078468; NM_078469	Hs.279862	NP_510869
fcrb1834	NM_079425	myosin, light polypeptide 6, alkali, smooth muscle and non-muscle (MYL6), transcript variant 3, mRNA /cds=(41,514) /gb=NM_079425 /gi=17986263 /ug=Hs.77385 /len=717	NM_021019; NM_079423; NM_079424; NM_079425	Hs.77385	NP_524149

Figure ob Co	TIL G.	T-			
fcrb2208	NM_079425	myosin, light polypeptide 6, alkali, smooth muscle and non-muscle (MYL6), transcript variant 3, mRNA /cds=(41,514) /gb=NM_079425 /gi=17986263 /ug=Hs.77385 /len=717	NM_021019; NM_079423; NM_079424; NM_079425	Hs.77385	NP_524149
ncrc4135	NM_079425	myosin, light polypeptide 6, alkali, smooth muscle and non-muscle (MYL6), transcript variant 3, mRNA /cds=(41,514) /gb=NM_079425 /gi=17986263 /ug=Hs.77385 /len=717	NM_021019; NM_079423; NM_079424; NM_079425	Hs.77385	NP_524149
ncrc0097	NM_079425	myosin, light polypeptide 6, alkali, smooth muscle and non-muscle (MYL6), transcript variant 3, mRNA /cds=(41,514) /gb=NM_079425 /gi=17986263 /ug=Hs.77385 /len=717	NM_021019; NM_079423; NM_079424; NM_079425	Hs.77385	NP 524149
fcr3053	NM_080425	GNAS complex locus (GNAS), transcript variant 3, mRNA /cds=(1,2730) /gb=NM_080425 /gi=18426897 /ug=Hs.374523 /len=3091	NM_000516; NM_016592; NM_080425; NM_080426		NP_536351
miob2855	NM_080425	GNAS complex locus (GNAS), transcript variant 3, mRNA /cds=(1,2730) /gb=NM_080425 /gi=18426897 /ug=Hs.374523 /len=3091	NM_000516; NM_016592; NM_080425; NM_080426	Hs.374523	NP_536351

rigule ob C	- Citta:				
fcre1745	BQ066467	AGENCOURT_686105 7 NIH_MGC_99 cDNA clone IMAGE:5931113 5', mRNA sequence /clone=IMAGE:593111 3 /clone_end=5' /gb=BQ066467 /gi=19895513 /ug=Hs.446485 /len=1029		Hs.446485	NP_536351
		UPF2 regulator of nonsense transcripts (yeast) (UPF2), transcript variant 1, mRNA /cds=(130,3948) /gb=NM_080599	NIM 045542:		
hfcr5865	NM_080599	/gi=18375675 /ug=Hs.3862 /len=5223	NM_015542;	Hs.3862	NP 542166
		similar to RIKEN cDNA 5730528L13 gene (MGC17337), mRNA /cds=(68,895) /gb=NM_080655 /gi=18087818 /ug=Hs.78531			
mioc5103	NM_080655	/len=1175 chromosome 20 open reading frame 108 (C20orf108), mRNA /cds=(41,619) /gb=NM_080821 /gi=18201877 /ug=Hs.352413	NM_080655	Hs.78531	NP_542386
miod4449	NM_080821	/len=3026 collectin sub-family member 12 (COLEC12), transcript variant II, mRNA /cds=(172,2040) /gb=NM_030781 /gi=18641357 /ug=Hs.29423	NM_080821 NM_030781;	Hs.352413	NP_543011
mioa9189	NM_030781	/len=4685	NM_130386	Hs.29423	NP_569057

Figure 6b Co	ont a.				
		KIAA1966 protein			
		(KIAA1966), mRNA			
		/cds=(492,2468)			
		1			
		/gb=NM_133370			
		/gi=21166354			
		/ug=Hs.158184			
mioa6147	NM_133370	/len=3248	NM_133370	Hs.158184	NP 588611
		RAD50 (S. cerevisiae)			
		(RAD50), transcript			
		variant 1, mRNA			
ļ		· ·			
	1	/cds=(388,4326)			
		/gb=NM_005732			
		/gi=19924128			
		/ug=Hs.41587	NM_005732;		
ncrc1811	NM 005732	/len=5891	NM 133482	Hs.41587	NP 597816
	 	CD109 (CD109),			
		mRNA			
		.			
		/cds=(113,4450)			
		/gb=NM_133493			
		/gi=19424129			
		/ug=Hs.55964			
seob4451	NM_133493	/len=5883	NM 133493	Hs.55964	NP 598000
		decorin (DCN),	1444_100100	110.00001	141 _000000
		transcript variant A1,			
		mRNA	NM_001920;		
		/cds=(200,1279)	NM_133503;		
		/gb=NM_001920	NM_133504;		
		/gi=19743844	NM_133505;		
		/ug=Hs.433989	NM_133506;		
ncrc2119	NM 001920	/len=1751	NM_133507	Hs.433989	NP 598014
110102110	1411_001020	clone MGC:3081	100007	113.400000	147_330014
	D000000	IMAGE:3347416,			<u>. </u>
seoa2654	BC000626	mRNA, complete cds	NM_015227	Hs.22982	NP_598368
		SOCS box-containing			
		WD protein SWiP-1]
		(WSB1), transcript			
		variant 3, mRNA			
		/cds=(317,1051)	1	1	
		, , ,			
		/gb=NM_134264			
		/gi=20143909	NM_015626;		
		/ug=Hs.187991	NM_134264;		
mioa6731	NM_134264	/len=4243	NM_134265	Hs.187991	NP_599027
	† 	Rattus norvegicus	<u> </u>		
		calcium-independent	1		
		•		1	
		alpha-latrotoxin			
		receptor 2 (Cirl2),		L	
seob5379	NM_134408	mRNA	NM_134408	Rn.12089	NP_599235

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rigule on	Conta.			·	
		hypothetical protein			
		BC009518			
		(LOC90799), mRNA			
		/cds=(59,2524)			
		/gb=NM_138363			İ
				Ì	
		/gi=19923898			
		/ug=Hs.135265			
ncrb8585	NM_138363	/len=2705	NM_138363	Hs.135265	NP_612372
		DNIA EL 126960 50			
		cDNA FLJ36860 fis,			
		clone ASTRO2015295.			
		/gb=AK094179			
		/gi=21753186			
		/ug=Hs.352406			
fcrc2852	AK094179	/len=2882		Hs.352406	NP_612398
		golgi associated,			
		gamma adaptin ear			
		containing, ARF			
		binding protein 3			
		(GGA3), transcript			
		variant long, mRNA			
		/cds=(10,2181)			
		/gb=NM_138619			
		1 -			
		/gi=20336266	NINA 04 4004		
, ,,,,,		/ug=Hs.87726	NM_014001;		
fcr2220	NM_138619	/len=3860	NM_138619	Hs.87726	NP_619525
		beta-site APP-cleaving			
		enzyme (BACE),			
		transcript variant a,			
		mRNA			
		/cds=(447,1952)			
		/gb=NM_012104	NM_012104;		
		/gi=21040369	NM_138971;		
		/ug=Hs.49349	NM_138972;		
ncrb5060	NM 012104	/len=5832	NM_138973	Hs.49349	NP 620429
		mRNA for presenilin-	1	110.10010	141_020420
		like protein 4 (PSL4			
mioc9262	AJ345030	gene)	NM_139015	Hs.21143	NP_620584
1111000202	7,004000	- gene)	14W_139013	П5.21143	INP_020304
1		mitogen-activated			
		protein kinase-	1		
		activated protein	1		
		kinase 5 (MAPKAPK5),	1		
1					<u> </u>
1		transcript variant 2,			
		mRNA			
		/cds=(260,1681)			
		/gb=NM_139078			
]		/gi=21237767	1		
	1	/ug=Hs.30327	NM_003668;		
ncr2717	NM_139078	/len=2066	NM_139078	Hs.30327	NP_620777
		cDNA: FLJ22554 fis,			
seoc2213	AK026207	clone HSI01092		Hs.93842	NP_631903

Figure 6b Co	T	·		,	·
fcrb4802	NM_139207	nucleosome assembly protein 1-like 1 (NAP1L1), transcript variant 1, mRNA /cds=(125,1300) /gb=NM_139207 /gi=21327707 /ug=Hs.302649 /len=3582	NM_004537; NM_139207	Hs.302649	NP_631946
	<u> </u>		-		
		tetratricopeptide repeat domain 8 (TTC8), mRNA /cds=(53,1648) /gb=NM_144596 /gi=21389382 /ug=Hs.55158			
mioc0107	NM_144596	/len=2241	NM_144596	Hs.55158	NP_653197
		A kinase (PRKA) anchor protein 13 (AKAP13), transcript variant 2, mRNA /cds=(214,8655) /gb=NM_007200 /gi=21493028 /ug=Hs.301946	NM_006738;		
ncr3976	NM_007200	//ug=Hs.301946 //len=10156	NM_007200; NM_144767	Hs.301946	NP_658913
f		apolipoprotein A-I binding protein (APOA1BP), mRNA /cds=(28,894) /gb=NM_144772 /gi=21426826 /ug=Hs.374850			
ncrc3276	NM_144772	/len=1120	NM_144772	Hs.374850	NP_658985
	_	muscleblind-like protein MBLL39 (MBLL39), transcript variant 1, mRNA /cds=(782,1885) /gb=NM_144778 /gi=21464124 /ug=Hs.283609	NM_005757;		
mioa4883	NM_144778	/len=4665	NM_144778	Hs.283609	NP 659002
seob9435	NM_145040	protein kinase C, delta binding protein (PRKCDBP), mRNA /cds=(35,820) /gb=NM_145040 /gi=21450786 /ug=Hs.431979 /len=1053	NM_145040	Hs.431979	NP_659477

Figure	6b	Cont'd.

Figure 6b	Cont a.				
		non-SMC (structural	,		
1		maintenance of			
		chromosomes)			
		element 1 protein			
		(NSE1), mRNA			
		/cds=(24,794)			
		/gb=NM_145080			
		/gi=21489972			
		/ug=Hs.284295			
ncr3197	NM 145080	/len=992	NM_145080	Hs.284295	NP_659547
		non-SMC (structural			
		maintenance of			
	ì	chromosomes)			
		element 1 protein			
		(NSE1), mRNA			
		/cds=(24,794)			
		/gb=NM_145080			
		/gi=21489972			
		/ug=Hs.284295			
seoa3106	NM_145080	/len=992	NM 145080	Hs.284295	NP_659547
30000100	14141_143000	similar to hypothetical	143000	115.204293	NF_009041
		protein BC014127			
ncrc9280	NM_145283	(LOC158046), mRNA	NM 145283	Un 200216	ND ccoanc
110109200	140200	(LOC 158046), INKINA	140203	Hs.309216	NP_660326
		hyronino 3			
		tyrosine 3-			
		monooxygenase/trypto			
		phan 5-			
		monooxygenase			
		activation protein, zeta			
}		polypeptide (YWHAZ),			
		transcript variant 2,			
	İ	mRNA /cds=(127,864)			
		/gb=NM_145690			
		/gi=21735624			
		/ug=Hs.75103	NM_003406;		
seoa1427	NM_145690	/len=2876	NM_145690	Hs.75103	NP_663723
		likely ortholog of rat V-			
		1 protein (V-1), mRNA		İ	
Į		/cds=(229,585)			
		/gb=NM_145808			
		/gi=21956644			
		/ug=Hs.21321			
miob7373	NM_145808	/len=3770	NM_145808	Hs.21321	NP_665807
		annexin A11			7
		(ANXA11), transcript			
		variant c, mRNA			
		/cds=(484,2001)			
		/gb=NM_145869			
		/gi=22165432	NM_001157;		
		/ug=Hs.75510	NM_145868;		
ncr0663	NM_145869	/len=2731	NM_145869	Hs.75510	NP_665876
		1	1	1.15.75516	1.41 _000070

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Figure ob C	Ont G.				
		prefoldin 5 (PFDN5),			
		transcript variant 1,			
		mRNA /cds=(36,500)			
		/gb=NM_002624			
		/gi=22202632	NM_002624;		
		/ug=Hs.288856	NM_145896;		
seob9820	NM_002624	/len=661	NM_145897	Hs.288856	NP 665904
		A kinase (PRKA)			
		anchor protein 2		ł	
		(AKAP2), transcript		İ	
		variant 1, mRNA		1	
		/cds=(181,3492)			
		/gb=NM_007203			
		/gi=22325354			
		/ug=Hs.42322	NM_007203;		
miob4055	NM_007203	/len=7522	NM_147150	Hs.42322	NP_671492
		intersectin 2 (ITSN2),			111 _07 1702
		transcript variant 1,			
		mRNA			
		/cds=(242,5332)			
		/gb=NM_006277			
		/gi=22325384	NM_006277;		
		/ug=Hs.166184	NM 019595;		
mioc7471	NM_006277	/len=6092	NM_147152	Hs.166184	NP 671494
	1111_000277	7.011 0002	147 102	113.100104	141 _07 1434
		Similar to hypothetical			
		protein MGC30540,			
		clone MGC:17342			
		IMAGE:4342258,			
		mRNA, complete cds			
		/cds=(216,1457)			
		/gb=BC042899			
		/gi=27552863			
		/ug=Hs.153716			
miob5855	BC042899	/len=3028	NM 147156	Hs.153716	ND 671510
111000000	150072033	sorting nexin 6 (SNX6),	141/ 150	113.133710	NP_671512
		transcript variant 1,			:
		mRNA			
		/cds=(498,1370)			
		1			
		/gb=NM_021249			
		/gi=23111048	NIM COACAC		1
50007442	NM 024240	/ug=Hs.284291	NM_021249;	11- 204004	ND 000440
seoa7443	NM_021249	/len=3041	NM_152233	Hs.284291	NP_689419

Figure 6b	Conta.				
seob6572	NM_152255	proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7), transcript variant 2, mRNA /cds=(116,616) /gb=NM_152255 /gi=23110947 /ug=Hs.233952 /len=1069 hypothetical protein MGC17943 (MGC17943), mRNA /cds=(214,564)		Hs.233952	NP_689468
		/gb=NM_152261			
1		/gi=22748614			
	NINA 450004	/ug=Hs.106390	150004		
miod6560	NM_152261	/len=3167 hypothetical protein	NM_152261	Hs.106390	NP_689474
		FLJ30656 (FLJ30656), mRNA /cds=(52,639) /gb=NM_152344 /gi=22748746 /ug=Hs.349887			
fcrc6043	NM_152344	/len=2212	NM_152344	Hs.349887	NP_689557
		hypothetical protein MGC33602 (MGC33602), mRNA /cds=(140,748) /gb=NM_152391 /gi=22748836 /ug=Hs.274415			
seob5632	NM_152391	/len=1790	NM_152391	Hs.274415	NP_689604
		hypothetical protein DKFZp564C236 (DKFZp564C236), mRNA /cds=(1590,2003) /gb=NM_152392 /gi=22748838 /ug=Hs.378856			
miob7550	NM_152392	/len=2161	NM_152392	Hs.378856	NP_689605
mioc7570	NM_152392	hypothetical protein DKFZp564C236 (DKFZp564C236), mRNA /cds=(1590,2003) /gb=NM_152392 /gi=22748838 /ug=Hs.378856 /len=2161	NM_152392	Hs.378856	ND 690605
	11111_102032	//Ci1 - 2 10 1	192092	1113.370000	NP_689605

Figure ob Co	1				
miod2886	NM_152520	hypothetical protein FLJ25270 (FLJ25270), mRNA /cds=(244,1353) /gb=NM_152520 /gi=22749086 /ug=Hs.6295 /len=2493 hypothetical protein FLJ35725 (FLJ35725), mRNA /cds=(201,1298) /gb=NM_152544 /gi=22749134	NM_152520	Hs.6295	NP_689733
		/ug=Hs.380632	1		
hfcr2389	NM_152544	/len=1851	NM_152544	Hs.380632	NP_689757
		hypothetical protein MGC26996 (MGC26996), mRNA /cds=(344,1171) /gb=NM_152553 /gi=22749144 /ug=Hs.307526			
seoc4762	NM_152553	/len=1804	NM_152553	Hs.307526	NP 689766
		hypothetical protein MGC24103 (MGC24103), mRNA /cds=(445,549) /gb=NM_152576 /gi=22749194 /ug=Hs.287447			
ncrc4508	NM_152576	/len=1767	NM_152576	Hs.287447	NP_689789
ncrc5648	NM_152862	actin related protein 2/3 complex, subunit 2, 34kDa (ARPC2), transcript variant 1, mRNA /cds=(113,1015) /gb=NM_152862 /gi=23238210 /ug=Hs.83583 /len=1462	NM_005731; NM_152862	Hs.83583	NP_690601
ncrc0849	NM_152306	ubiquitin-like, containing PHD and RING finger domains 2 (URF2), transcript variant 1, mRNA /cds=(341,1852) /gb=NM_152306 /gi=23312361 /ug=Hs.348602 /len=3720	NM_152306; NM_152896	Hs.348602	NP 690856

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Figure 6b	Conta.				
		glycosyltransferase AD	-		·
		017 (AD-017),			
		transcript variant 1,			
		mRNA			
		/cds=(140,1255)			
		/gb=NM_152932			
İ		/gi=23510345			
		/ug=Hs.283737	NM_018446;		
seob0426	NM_152932	/len=1635	NM_152932	Hs.283737	ND 600000
36000420	14141_132332	tumor necrosis factor	14141_132932	П5.203/3/	NP_690909
		(ligand) superfamily,			
		member 12			
		(TNFSF12), transcript			
		variant 2, mRNA			
		/cds=(97,501)			
		/gb=NM_153012			
		/gi=23510440			
		/ug=Hs.26401	NM_003809;		
seob4030	NM_153012	/len=1642	NM_153012	Hs.26401	NP_694557
		cDNA FLJ25221 fis,	"		
miod3983	AK057950	clone STM00723	NM_153013	Hs.81907	NP_694558
		myotubularin related			
		protein 3 (MTMR3),			
		transcript variant 3,			
		mRNA			
		/cds=(288,3884)			
		/gb=NM_021090			
		/gi=23510385	NM_021090;		
		/ug=Hs.63302	NM_153050;		
fcrc5713	NM_021090	/len=5963	NM_153051	Hs.63302	NP 694691
		hypothetical protein			
		MGC35048			
		(MGC35048), mRNA			
		/cds=(700,1563)			
		/gb=NM_153208			
		/gi=23397455			
		/g=Hs.367493			
miod1924	NM 153208	/len=2603	NM 153208	Un 267402	ND 604040
111100 1324	133200		199200	Hs.367493	NP_694940
		hypothetical protein MGC21981			
		I			
		(MGC21981), mRNA			
	1	/cds=(66,764)			
		/gb=NM_153267	}	}	
	1	/gi=23397567			
	1,100	/ug=Hs.131987	 		
miod1814	NM_153267	/len=1727	NM_153267	Hs.131987	NP_694999

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Figure 6b (John G.				
ncr9587	NM_003334	ubiquitin-activating enzyme E1 (A1S9T and BN75 temperature sensitivity complementing) (UBE1), transcript variant 1, mRNA /cds=(130,3306) /gb=NM_003334 /gi=23510337 /ug=Hs.2055 /len=3504	NM_003334; NM 153280	Hs.2055	NP_695012
fcrb3843	BC028002	clone IMAGE:5212110, mRNA /gb=BC028002 /gi=24081066 /ug=Hs.386507 /len=2415		Hs.386507	NP_699204
seoa4598	NM_153425	TNFRSF1A-associated via death domain (TRADD), transcript variant 2, mRNA /cds=(731,1489) /gb=NM_153425 /gi=24234725 /ug=Hs.89862 /len=1959	NM_003789; NM_153425	Hs.89862	NP_700474
miob8816	NM_004516	interleukin enhancer binding factor 3, 90kDa (ILF3), transcript variant 2, mRNA	_	Hs.256583	NP_703194
miob8578	NM_153638	pantothenate kinase 2 (Hallervorden-Spatz syndrome) (PANK2), transcript variant 1, mRNA /cds=(56,1399) /gb=NM_153638 /gi=24430170 /ug=Hs.286212 /len=1959	NM_024960; NM_153637; NM_153638; NM_153639; NM_153640; NM_153641	Hs.286212	NP_705905
fcrb7833	NM_153649	tropomyosin 3 (TPM3), mRNA /cds=(52,798) /gb=NM_153649 /gi=24119202 /ug=Hs.85844 /len=2089	NM_152263; NM_153649	Hs.85844	NP_705935

I igule ob	Oont a.		, 		
mioc2021	NM_153649	tropomyosin 3 (TPM3), mRNA /cds=(52,798) /gb=NM_153649 /gi=24119202 /ug=Hs.85844 /len=2089	NM_152263; NM_153649	Hs.85844	NP 705935
1111002021	TVIVI_133049		10101_103049	П5.00044	INP_705935
fcrb3739	NM_018951	homeo box A10 (HOXA10), transcript variant 1, mRNA /cds=(50,1231) /gb=NM_018951 /gi=24497548 /ug=Hs.110637 /len=2618	NM_018951; NM_153715	Hs.110637	NP 714926
10100700	14141_010931	tm68a09.x1	14141_1557-15	ns. 110031	NP_/ 14920
ncrc0807	Al498805	NCI_CGAP_Brn25 cDNA clone IMAGE:2163256 3', mRNA sequence /clone=IMAGE:216325 6 /clone_end=3' /gb=Al498805 /gi=4390787 /ug=Hs.436349 /len=460		Hs.436349	NP_722550
ncr1218	NM_170662	Cas-Br-M (murine) ecotropic retroviral transforming sequence b (CBLB), mRNA	NM_170662		, NP_733762
miob3898	NM_006930	S-phase kinase- associated protein 1A (p19A) (SKP1A), transcript variant 1, mRNA /cds=(140,622) /gb=NM_006930 /gi=25777710 /ug=Hs.171626 /len=2172	NM_006930; NM_170679	Hs.171626	NP_733779
seoa1739	NM_006930	S-phase kinase- associated protein 1A (p19A) (SKP1A), transcript variant 1, mRNA /cds=(140,622) /gb=NM_006930 /gi=25777710 /ug=Hs.171626 /len=2172	NM_006930; NM_170679	Hs.171626	NP_733779

Figure 6b C	onta.				
ncrc3358	NM 006930	S-phase kinase- associated protein 1A (p19A) (SKP1A), transcript variant 1, mRNA /cds=(140,622) /gb=NM_006930 /gi=25777710 /ug=Hs.171626 /len=2172	NM_006930; NM_170679	Hs.171626	NP 733779
		lamin A/C (LMNA), transcript variant 1, mRNA /cds=(213,2207) /gb=NM_170707 /gi=27436945 /ug=Hs.377973	NM_005572; NM_170707;		
fcrb2162	NM_170707	/len=3181 selenoprotein H (SELH), mRNA /cds=(243,611) /gb=NM_170746 /gi=25014108 /ug=Hs.290874	NM_170708	Hs.377973	NP_733822
ncrb0303	NM_170746	/len=834 adenylate kinase 2 (AK2), nuclear gene encoding mitochondrial protein, transcript variant AK2B, mRNA /cds=(43,741) /gb=NM_013411 /gi=26665888 /ug=Hs.294008	NM_001625; NM_013411;	Hs.290874	NP_734467
miob3249	NM_013411	/len=2146 ATP-binding cassette, sub-family A (ABC1), member 5 (ABCA5), transcript variant 1, mRNA /cds=(1219,6147) /gb=NM_018672 /gi=27262623 /ug=Hs.180513	NM_172199 NM_018672;	Hs.294008	NP_751949
ncrc9736	NM_018672	/len=7044	NM_172232	Hs.180513	NP_758424

Figure 6b Co	JILU.	<u> </u>			,
		nuclear receptor			
		subfamily 4, group A,			
		member 2 (NR4A2),			
		transcript variant 1,			
		mRNA			
		/cds=(336,2132)			
		/gb=NM_006186	NM_006186;		
		1 ×			
		/gi=27894347	NM_173171;		
1		/ug=Hs.82120	NM_173172;		
miod7367	NM_006186	/len=3447	NM_173173	Hs.82120	NP_775265
		nuclear DNA-binding			
		protein (C1D),			
		transcript variant 1,			
		mRNA /cds=(64,489)			
		/gb=NM_006333			
		/gi=27894371			
		/ug=Hs.15164	NM_006333;		
seoc4316	NM_006333	/len=1200	NM 173177	Hs.15164	NP 775269
		SNF1-like kinase	1		
		(SNF1LK), mRNA			
		/cds=(98,2449)			
				,	
		/gb=NM_173354			
		/gi=27597093			
	l	/ug=Hs.380991			
fcrb4375	NM_173354	/len=4726	NM_173354	Hs.380991	NP_775490
		hypothetical protein			
		LOC115286			
		(LOC115286), mRNA			
		/cds=(189,740)			
		/gb=NM_173471			
		/gi=27735034			
		/ug=Hs.379386			
ncrb8220	NM_173471	/len=1873	NM_173471	Hs.379386	NP 775742
		hypothetical protein	 		
		LOC123803			
		(LOC123803), mRNA			
		/cds=(15,947)			
		/gb=NM_173474			
		/gi=27735048			
		1 ~			
mich2067	NINA 470474	/ug=Hs.351573	NINA 470474	Un 254572	 ND 775745
miob2067	NM_173474	/len=1146	NM_173474	Hs.351573	NP_775745
		mucosa associated			
}		lymphoid tissue	}	}	}
		lymphoma			
	-	translocation gene 1			
		(MALT1), transcript			
		variant 1, mRNA			
		/cds=(259,2733)			
		/gb=NM_006785			
		/gi=27886564			ļ
		/ug=Hs.180566	NM_006785;		l
ncrb3373	NM_006785	/len=5029	NM_173844	Hs.180566	NP_776216
		1		,	

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Figure 6b	Contra.				
seoc4356	NM_173852	keratinocytes associated protein 2 (KCP2), mRNA /cds=(1,489) /gb=NM_173852 /gi=27777660 /ug=Hs.374854 /len=489	NM_173852	Hs.374854	NP_776251
mioa4628	NM_002816	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12 (PSMD12), mRNA /cds=(44,1414) /gb=NM_002816 /gi=4506220 /ug=Hs.4295 /len=3548	NM_002816; NM_174871	Hs.4295	NP_777360
miod0468	BC042754	Similar to low density lipoprotein receptor- related protein 2, clone IMAGE:4828259, mRNA, partial cds /cds=(1,1059) /gb=BC042754 /gi=27769271 /ug=Hs.205865 /len=3814	NM_174902	Hs.205865	NP_777562
miod5984	BC028585	hypothetical gene supported by AK000174; AK055070; AK055612, clone IMAGE:4836971, mRNA		Hs.374538	NP_777569
seob7613	NM_004349	core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related (CBFA2T1), transcript variant 1, mRNA /cds=(412,2145) /gb=NM_004349 /gi=28329413 /ug=Hs.31551 /len=3463	NM_004349; NM_175634; NM_175635; NM_175636	Hs.31551	NP_783554

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Figure 6b	Conta.				
seoa3885 seoa1559	AK090822 AB011108	cDNA FLJ33503 fis, clone BRAMY2004521. /cds=(367,750) /gb=AK090822 /gi=21749052 /ug=Hs.356719 /len=2339 hypothetical protein (KIAA0536) chromosome 20 open reading frame 178,	NM_175893 NM_003913; NM_176800	Hs.356719 Hs.198891	NP_787089 NP_789770
seoc2470	BC033859	clone MGC:45387 IMAGE:5173394, mRNA, complete cds	NM_176812	Hs.352579	NP_789782
seob7547	NM 014599	melanoma antigen, family D, 2 (MAGED2), mRNA /cds=(97,1917) /gb=NM_014599 /gi=21264316 /ug=Hs.4943 /len=2077	NM_014599; NM 177433	Hs.4943	NP 803182
		armadillo repeat protein ALEX2 (ALEX2), mRNA /cds=(458,2356) /gb=NM_014782 /gi=21361239 /ug=Hs.48924			711 _000102
fcrc1974	NM_014782	/len=2788 protein phosphatase 2A, regulatory subunit B' (PR 53) (PPP2R4), mRNA /cds=(190,1161) /gb=NM_021131 /gi=10880986 /ug=Hs.400740	NM_177949 NM_021131; NM_178000; NM_178001; NM_178002;	Hs.48924	NP_808818
fcrb3476	NM_021131	/len=2661 clone MGC:16435 IMAGE:3946253, mRNA, complete cds /cds=(137,1471) /gb=BC013374 /gi=15426525 /ug=Hs.179661	NM_178003	Hs.400740	NP_821070
seob5640	BC013374	/len=2519 solute carrier family 35, member B2	NM_178014	Hs.179661	NP_821133
fcrb7780	NM_178148	(SLC35B2), mRNA	NM_178148		NP_835361

Figure on Co	nicu.	T	 -		
fcrb8973	NM_030789	histocompatibility (minor) 13 (HM13), mRNA /cds=(86,1219) /gb=NM_030789 /gi=23308606 /ug=Hs.386538 /len=1584	NM_030789	Hs.386538	NP_848697
ncrc4320	NM_015339	activity-dependent neuroprotector (ADNP), mRNA /cds=(346,3654) /gb=NM_015339 /gi=12229216 /ug=Hs.3657 /len=4713	NM_015339	Hs.3657	NP_852107
hfcr2890	NM 144601	chemokine-like factor super family 3 (CKLFSF3), mRNA /cds=(527,1075) /gb=NM_144601 /gi=21389400 /ug=Hs.7773 /len=2318	NM 144601	Hs.7773	NP 853533
seob6131	NM_002916	replication factor C (activator 1) 4, 37kDa (RFC4), mRNA /cds=(284,1375) /gb=NM_002916 /gi=4506490 /ug=Hs.35120 /len=1446	NM_002916	Hs.35120	NP_853551
ncrc7040	NM_012094	peroxiredoxin 5 (PRDX5), mRNA /cds=(37,681) /gb=NM_012094 /gi=6912237 /ug=Hs.31731 /len=805	NM_012094	Hs.31731	NP_857635
mioc4994	AK026583	cDNA: FLJ22930 fis, clone KAT07255. /gb=AK026583 /gi=10439467 /ug=Hs.90790 /len=1600		Hs.90790	NP_858042

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Figure 6b C	Cont'd.				
seob7409	NM_006534	nuclear receptor coactivator 3 (NCOA3), mRNA /cds=(184,4422) /gb=NM_006534 /gi=5729725 /ug=Hs.225977 /len=6754 O-linked N- acetylglucosamine (GlcNAc) transferase (UDP-N-	NM_006534	Hs.225977	NP_858045
ncrc5688	NM_003605	acetylglucosamine:poly peptide-N- acetylglucosaminyl transferase) (OGT), mRNA /cds=(2040,4802) /gb=NM_003605 /gi=6006036 /ug=Hs.100293 /len=5733	NM_003605	Hs.100293	NP_858059
fcrc0631	AL834355	mRNA; cDNA DKFZp547F237 (from clone DKFZp547F237); complete cds (=AK024813.1)		Hs.6820	NP_859049
ncrc7016	NM_012381	origin recognition complex, subunit 3-like (yeast) (ORC3L), mRNA /cds=(27,2162) /gb=NM_012381 /gi=6912561 /ug=Hs.74420 /len=2510	NM_012381	Hs.74420	NP_862820
fcrb5313	NM_002654	pyruvate kinase, muscle (PKM2), mRNA /cds=(110,1705) /gb=NM_002654 /gi=4505838 /ug=Hs.198281 /len=2287	NM_002654	Hs.198281	NP_872271

Figure 6b Co	nitu.				
		UI-E-CQ1-act-a-04-0-			
		UI.s1 UI-E-CQ1 cDNA			
		clone UI-E-CQ1-act-a-			
		04-0-UI 3', mRNA			
		sequence /clone=UI-E-			
		CQ1-act-a-04-0-UI			
		/clone_end=3'			
		/gb=BU727332			
	-	/gi=23648099			
		/ug=Hs.116567			
mioa1163	BU727332	/len=1621		Hs.116567	NP_872297
		synaptophysin-like			
		protein (SYPL), mRNA			
		/cds=(34,813)			
		/gb=NM_006754			
		/gi=5803184			
	1	/ug=Hs.80919			
seoa5090	NM_006754	//len=2130	NIM 006754	LL 90010	ND 074204
36043030	TVIVI_000/34	/ICII-213U	NM_006754	Hs.80919	NP_874384
		NADU dahudaanaa			
		NADH dehydrogenase			
		(ubiquinone) 1 beta			
ľ		subcomplex, 6, 17kDa			
		(NDUFB6), mRNA			
		/cds=(104,490)			
		/gb=NM_002493			
		/gi=20149518			
		/ug=Hs.109646			
seob7229	NM_002493	/len=733	NM 002493	Hs.109646	NP_877416
				1101100010	
		myeloid cell leukemia			
		sequence 1 (BCL2-			
1					
		related) (MCL1),			
		mRNA /cds=(64,1116)			
		/gb=NM_021960			
1		/gi=19923213			
		/ug=Hs.86386			
seob4039	NM_021960	/len=3953	NM_021960	Hs.86386	NP_877495
		activating transcription			
		factor 4 (tax-			
		responsive enhancer			
		element B67) (ATF4),			
		mRNA			
		/cds=(882,1937)			
1				ļ	
		/gb=NM_001675			
		/gi=4502264			
, 5470		/ug=Hs.181243			
fcr5176	NM_001675	/len=2015	NM_001675	Hs.181243	NP_877962

Figure 6b C	zoni a.				
		scavenger receptor class A, member 3 (SCARA3), mRNA			
		/cds=(142,1962)			
		/gb=NM_016240			
		/gi=7705335			
		/ug=Hs.128856			
fcrb5840	NM 016240	/len=3636	NM 016240	Hs.128856	NP_878185
101000-10	14141_010240	vesicle transport-	14101_010240	113.120000	141_070100
1		related protein			
		(RA410), mRNA			
		/cds=(8,1930)			
		/gb=NM_016106			
		/gi=7706370			
		/ug=Hs.27023	NM_016106;		
mioa1055	NM_016106	/len=2149	NM 016163	Hs.27023	NP 878255
		eukaryotic translation			
		initiation factor 5			
		(EIF5), mRNA		1	
		/cds=(469,1764)			
		/gb=NM_001969			
		/gi=21361336			
		/ug=Hs.433702			
mioa1708	NM_001969	/len=3899	NM_001969	Hs.433702	NP 892116
		vacuolar protein sorting 28 (yeast) (VPS28), mRNA /cds=(62,727) /gb=NM_016208 /gi=7705884 /ug=Hs.339697			
fcr0018	NM_016208	/len=928	NM_016208	Hs.339697	NP_898880
seob6510	NM 000211	prion protein (p27-30) (Creutzfeld-Jakob disease, Gerstmann- Strausler-Scheinker syndrome, fatal familial insomnia) (PRNP), mRNA /cds=(50,811) /gb=NM_000311 /gi=4506112 /ug=Hs.74621 /len=2415		He 74624	ND 808002
seob6510	NM_000311	microsomal epoxide	NM_000311	Hs.74621	NP_898902
		hydrolase (EPHX1)			
miod0533	AF253417	gene, complete cds	NM_000120		NP_000111
		adenylosuccinate			1.1000111
seoa5679	X66503	synthetase mRNA	NM_001126		NP_001117

Application of: Liew, et. al. Our Docket #: 4231/2042 Figure 6b Cont'd.

Figure 6b	Conta.				
mioa1077	NM_018212	enabled (Drosophila) (ENAH), mRNA /cds=(77,646) /gb=NM_018212 /gi=8922657 /ug=Hs.14838 /len=2943	NM_018212	Hs.14838	NP_060682
fcrb8910	NM_006083	IK cytokine, down- regulator of HLA II (IK), mRNA /cds=(112,1785) /gb=NM_006083 /gi=11038650 /ug=Hs.8024 /len=1785	NM_006083	Hs.8024	NP_006074
mioa4677	AJ010770	hyperion gene, exons 1 50	NM_005751; NM_147166; NM_147171; NM_147185		NP_005742; NP_671695; NP_671700; NP_671714
fcr4024	AF058293	D-dopachrome tautomerase (=U49785; Y11151)	NM_001355		NP_001346
seob3386	AB017563	IGSF4 gene, exon 10 and complete cds	NM_014333		NP_055148
ncrc1032	NM_147185	A kinase (PRKA) anchor protein (yotiao) 9 (AKAP9), transcript variant 3, mRNA	NM_005751; NM_147166; NM_147171; NM_147185		NP_005742; NP_671695; NP_671700; NP_671714
ncr3139	AF038042	BRCA1-associated RING domain protein (BARD1) gene, exons 10, 11 and complete cds	NM_000465		NP_000456
seob6096	NM_002223	inositol 1,4,5- triphosphate receptor, type 2 (ITPR2), mRNA	NM_002223		NP_002214
mioc5061	NM_000489	alpha thalassemia/mental retardation syndrome X linked (RAD54 S. cerevisiae) (ATRX), transcript variant 1, mRNA	NM_000489; NM_138270; NM_138271		NP_000480; NP_612114; NP_612115

Figure	6h	Col	nt'd
INGUIC	\mathbf{v}		III U.

r igure ob Co		hypothetical protein FLJ31034 (FLJ31034), mRNA /cds=(598,1023) /gb=NM_152724 /gi=22749438 /ug=Hs.351342			
seob8489	NM_152724	_	NM_152724	Hs.351342	NP_689937

	FIGURE 6c: OA stage specific markers for Marked OA only					
Common						
name	Genbank	Description	RefSeq	UniGene	Rep_prot	
name	Genbank	acetyl-Coenzyme A acetyltransferase 1 (acetoacetyl Coenzyme A thiolase) (ACAT1), nuclear gene encoding mitochondrial protein, mRNA /cds=(77,1360) /gb=NM_000019 /gi=4557236	Rerseq	UniGene	Rep_prot	
		/ug=Hs.37				
mioc9900	NM_000019	/len=1518	NM_000019	Hs.37	NP 000010	
ncrb5699	NM 000064	complement component 3 (C3), mRNA /cds=(61,5052) /gb=NM_000064 /gi=4557384 /ug=Hs.284394 /len=5067	NM 000064	Hs.284394	NP 000055	
fcr0459	NM 000088	collagen, type I, alpha 1 (COL1A1), mRNA /cds=(120,4514) /gb=NM_000088 /gi=14719826 /ug=Hs.172928 /len=5921	NM 000088	Hs.172928	NP 000079	
fcrc5190	NM 000093	collagen, type V, alpha 1 (COL5A1), mRNA /cds=(383,5899) /gb=NM_000093 /gi=16554578 /ug=Hs.146428 /len=6496	NM 000093	Hs.146428	NP_000079	

Application of: Liew, et. al. Our Docket #: 4231/2042 Figure 6c Cont'd.

7.194.00	c Conta.	T		 	, , , , , , , , , , , , , , , , , , ,
1		nuclear receptor			
	1	subfamily 3, group			
	1	C, member 1			
		(glucocorticoid			
		receptor) (NR3C1),			
		mRNA			
ŀ		/cds=(133,2466)			
		/gb=NM_000176			
		/gi=4504132		1	
		/ug=Hs.75772	•	1	
seob2139	NM 000176	/len=4788	NM 000176	Hs.75772	NP_000167
		glutathione			
		synthetase (GSS),			
		mRNA			
		/cds=(41,1465)			
		/gb=NM_000178			
		/gi=4504168			
		/ug=Hs.82327			
fcr7019	NM 000178	/len=1856	NM_000178	Hs.82327	NP 000169
				1.0.02027	111 _000100
		Kallmann syndrome			ļ
		1 sequence (KAL1),			i
	İ	mRNA			
		/cds=(151,2193)		,	
		/gb=NM_000216			
		/gi=4557682			
•	İ	/ug=Hs.89591			
seoa2854	NM 000216	/len=6314	NM 000216	Hs.89591	NP 000207
100002001	14111_000210	phosphorylase	11111_000210	113.00001	141_000207
		kinase, beta			
		(PHKB), mRNA			
ļ		/cds=(25,3306)			
		/gb=NM_000293			
		/gi=4505782			
		/ug=Hs.78060			
fcrb6099	NM 000293	/len=4284	NM_000293	Hs.78060	NP_000284
10100033	14141_000293	polycystic kidney	14101_000283	11 13.7 0000	INF_UUU204
	1	disease 2			
		(autosomal			
		dominant) (PKD2),			
		mRNA			
		/cds=(67,2973)			
	Ì	/gb=NM_000297		Ì	
		/gi=4505834			
mioh1115	NM 000207	/ug=Hs.82001 /len=5057	NIM OCCOO	LL 02004	ND 000000
miob1115	NM_000297	men=5057	NM_000297	Hs.82001	NP_000288

Figure 6	Contu.				
		steroid sulfatase			
	1	(microsomal),			
	Ĭ	arylsulfatase C,			
		isozyme S (STS),			
1		mRNA]		
		/cds=(221,1972)	İ		
		/gb=NM_000351			
	1				
		/gi=13162281			
		/ug=Hs.79876	l	l	
mioc4557	NM_000351	/len=6520	NM_000351	Hs.79876	NP_000342
		secreted			
		phosphoprotein 1			
		(osteopontin, bone			
	ł	sialoprotein I, early			
	1	T-lymphocyte			
		activation 1)			
		(SPP1), mRNA			
		/cds=(88,990)			
		/gb=NM_000582		į	
		/gi=4759165			
İ		/ug=Hs.313			
fcrb7178	NM 000582	/len=1524	NM 000582	Hs.313	NP 000573
10107 170	14101_000002	NAD(P)H	14141_000302	113.515	NF_000373
		dehydrogenase,			
		quinone 1 (NQO1),			
		mRNA			
		/cds=(51,875)			
		/gb=NM_000903			
		/gi=4505414			
		/ug=Hs.406515			
ncrb0513	NM_000903	/len=2447	NM_000903	Hs.406515	NP_000894
		ribosomal protein			
		L4 (RPL4), mRNA			
		/cds=(57,1340)		ĺ	
		/gb=NM_000968			
		/gi=16579884			
		/ug=Hs.286	Ī		
ncrc9867	NM_000968	/len=1449	NM 000968	Hs.286	NP 000959
		ribosomal protein			
		L4 (RPL4), mRNA			
		/cds=(57,1340)			
		/gb=NM_000968			
		/gi=16579884			
		/ug=Hs.286		Ì	
seob7575	NM 000968	/len=1449	NM 000968	Hs.286	NP 000959
25001010	Li111 000300	1/1011-1773	TI4161_000900	Li 19.200	[เมน"กกกลอล

Figure 6	T CONT. U.	Tu . "	T	Γ	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,
		ribosomal protein			
		L37a (RPL37A),			
	1	mRNA			
		/cds=(36,314)			
		/gb=NM_000998			
		/gi=16306561			
		/ug=Hs.296290			
fcrb5272	NM 000998	/len=392	NM 000998	Hs.296290	NP_000989
	1 =	ribosomal protein			
		L36a-like			
	<u> </u>	1			
		(RPL36AL), mRNA			
		/cds=(95,415)			
		/gb=NM_001001			
		/gi=16306559			
İ		/ug=Hs.419465			
ncr0847	NM 001001	/len=537	NM_001001	Hs.419465	NP_000992
1.0.0017		ribosomal protein	00 100 1	1.70 10-100	111 _000002
1	1				
1		S8 (RPS8), mRNA		ľ	
		/cds=(24,650)			
		/gb=NM_001012			
		/gi=4506742			
1		/ug=Hs.399720			
seob5579	NM_001012	/len=705	NM 001012	Hs.399720	NP 001003
30000070	14141_001012	ATP-binding	14141_001012	113.333720	NF_001003
		cassette, sub-family			
		F (GCN20),			
		member 1			
		(ABCF1), mRNA			
İ		/cds=(95,2518)			
		/gb=NM_001090			
		/gi=10947134	,		
	!	/ug=Hs.9573			
seob9734	NM_001090	/len=3141	NM_001090	Hs.9573	NP_001081
ľ					
1		casein kinase 1,			
1		gamma 2			
		(CSNK1G2), mRNA			
		1,			
1		/cds=(54,1301)			
1		/gb=NM_001319			
		/gi=21314777			
		/ug=Hs.181390			
fcr1462	NM_001319	/len=2446	NM 001319	Hs.181390	NP 001310
		dynein,			
1	1	cytoplasmic,			
	1	lintermediate			
		I -			
		polypeptide 2			
		(DNCI2), mRNA			
1		/cds=(166,2082)			
1		/gb=NM_001378			
		/gi=24307878			
		/ug=Hs.66881			
coob6494	NIM 004370		NINA 004270	Un 66004	 ND 004000
seob6484	NM_001378	/len=2602	NM_001378	Hs.66881	NP_001369

1369
1000
1395
1437
1448
1530

1.90.00	Conta.		<u> </u>		
fcrb2913	NM 001555	immunoglobulin superfamily, member 1 (IGSF1), mRNA /cds=(81,4091) /gb=NM_001555 /gi=4504624 /ug=Hs.22111 /len=4381	NM 001555	Hs.22111	NP 001546
10102913	14141_001333	S-	14141_001555	NS.22111	NP_001546
		adenosylmethionine decarboxylase 1 (AMD1), mRNA /cds=(321,1325) /gb=NM_001634 /gi=5209326 /ug=Hs.262476			
hfcr4444	NM_001634	/len=3414	NM_001634	Hs.262476	NP 001625
fcrc0416	NM 001685	ATP synthase, H transporting, mitochondrial F0 complex, subunit F6 (ATP5J), nuclear gene encoding mitochondrial protein, mRNA /cds=(693,1019) /gb=NM_001685 /gi=19913429 /ug=Hs.73851 /len=1178	NM 001685	Hs.73851	NP 001676
	14M001000	AU RNA binding protein/enoyl-Coenzyme A hydratase (AUH), nuclear gene encoding mitochondrial protein, mRNA /cds=(5,1024) /gb=NM_001698 /gi=4502326 /ug=Hs.81886	14M_001000	113.70001	141 _001070
fcrb8509	NM_001698	•	NM_001698	Hs.81886	NP_001689

c Cont'd.				
NM 001792	N-cadherin (neuronal) (CDH2), mRNA /cds=(206,2926) /gb=NM_001792 /gi=14589888 /ug=Hs.161	NM 001792	He 161	NP 001783
14141_001792	11011-4122	NIVI_001792	IDS. 10 I	NP_001783
NIM 001855	mRNA /cds=(166,4332) /gb=NM_001855 /gi=18641349 /ug=Hs.83164		He 92464	NID 004946
NIVI_001855		NM_001855	HS.83164	NP_001846
NIM 004004	oxidase subunit IV isoform 1 (COX4I1), nuclear gene encoding mitochondrial protein, mRNA /cds=(165,674) /gb=NM_001861 /gi=17017985 /ug=Hs.433419	NM 004004		
NM_001861		NM_001861	Hs.433419	NP_001852
	oxidase subunit VIIa polypeptide 1 (muscle) (COX7A1), nuclear gene encoding mitochondrial protein, mRNA /cds=(463,702) /gb=NM_001864 /gi=18105034			
NM 001864	_	NM 001864	Hs 421621	NP 001855
	carboxypeptidase E (CPE), mRNA /cds=(291,1721) /gb=NM_001873 /gi=4503008 /ug=Hs.75360			NP_001864
	NM_001855 NM_001861 NM_001864	(neuronal) (CDH2), mRNA /cds=(206,2926) /gb=NM_001792 /gi=14589888 /ug=Hs.161 /len=4122 collagen, type XV, alpha 1 (COL15A1), mRNA /cds=(166,4332) /gb=NM_001855 /gi=18641349 /ug=Hs.83164 /NM_001855 /len=5222 cytochrome c oxidase subunit IV isoform 1 (COX4I1), nuclear gene encoding mitochondrial protein, mRNA /cds=(165,674) /gb=NM_001861 /gi=17017985 /ug=Hs.433419 /NM_001861 /len=802 cytochrome c oxidase subunit VIIa polypeptide 1 (muscle) (COX7A1), nuclear gene encoding mitochondrial protein, mRNA /cds=(463,702) /gb=NM_001864 /gi=18105034 /ug=Hs.421621 /len=783 carboxypeptidase E (CPE), mRNA /cds=(291,1721) /gb=NM_001873 /gi=4503008 /ug=Hs.75360	N-cadherin (neuronal) (CDH2), mRNA	N-cadherin (neuronal) (CDH2), mRNA /cds=(206,2926) /gb=NM_001792 /gi=14589888 //g=Hs.161 NM_001792 /len=4122 NM_001792 collagen, type XV, alpha 1 (COL15A1), mRNA /cds=(166,4332) /gb=NM_001855 /gi=18641349 /ug=Hs.83164 NM_001855 /len=5222 NM_001855 cytochrome c oxidase subunit IV isoform 1 (COX4I1), nuclear gene encoding mitochondrial protein, mRNA /cds=(165,674) /gb=NM_001861 /gi=17017985 /ug=Hs.433419 NM_001861 /len=802 NM_001861 /len=802 Cytochrome c oxidase subunit VIIa polypeptide 1 (muscle) (COX7A1), nuclear gene encoding mitochondrial protein, mRNA /cds=(463,702) /gb=NM_001864 /gi=18105034 /ug=Hs.421621 /len=783 NM_001864 /len=784 NM_001864 /len=784 NM_001864 /len=784 NM_001864

Figure 60	Conta.				
		damage-specific			
		DNA binding			
1	İ	protein 1, 127kDa			1
1		(DDB1), mRNA		1	
ŀ		/cds=(110,3532)			
}		/gb=NM_001923			
		_	,		
		/gi=13435358			
	l	/ug=Hs.108327		l	
seob6680	NM_001923	/len=4221	NM_001923	Hs.108327	NP_001914
	1	dermatopontin,			
		clone MGC:45278			
		IMAGE:5176855,			
		mRNA, complete			
seob8260	BC033736	cds		Hs.80552	NP 001928
		E2F transcription		-	
		factor 5, p130-		1	
		binding (E2F5),			
		mRNA			
		/cds=(35,1075)			
		/gb=NM_001951			
		/gi=12669916			
l		/ug=Hs.2331			
seob9960	NM_001951	/len=1752	NM_001951	Hs.2331	NP 001942
		early growth	_		
		response 1			
		(EGR1), mRNA			1
		/cds=(271,1902)			
		/gb=NM_001964			
		/gi=4503492			
		/ug=Hs.326035		l	
bfcw0492	NM_001964	/len=3132	NM_001964	Hs.326035	NP_001955
		fibroblast growth	İ	1	
		factor 2 (basic) ·		1	
		(FGF2), mRNA]	
		/cds=(302,934)		1	
		/gb=NM_002006			
		/gi=15451897			
		/ug=Hs.284244			
seob5260	NM_002006	/len=6802	NM 002006	Hs.284244	NP 001997
36003200	14101_002000		14101_002000	1113.204244	1145_001991
		flightless I			
		(Drosophila) (FLII),			
		mRNA			
}		/cds=(52,3861)		}	
		/gb=NM_002018			
1		/gi=22547155		1	
		/ug=Hs.83849			
hfcr1140	NM_002018	/len=4176	NM_002018	Hs.83849	NP_002009
		1	1502510	1	1

Figure 60	Contu.				
		farnesyltransferase,			
		CAAX box, alpha			
		(FNTA), mRNA		Į	
		/cds=(7,1146)			
		/gb=NM_002027			
		/gi=4503770			
		/ug=Hs.356463			
mioc1963	NM_002027	/len=1644	NM_002027	Hs.356463	NP_002018
		ferritin, heavy	,		
		polypeptide 1			
		(FTH1), mRNA			
		/cds=(92,664)			
		/gb=NM_002032			
		/gi=4503794			
		/ug=Hs.418650			
fcrb4599	NM_002032	/len=801	NM_002032	Hs.418650	NP 002023
		follicular lymphoma			
		variant			
		translocation 1			
		(FVT1), mRNA			
		/cds=(108,1106)			
		/gb=NM_002035			
		/gi=4503816			
		/ug=Hs.74050			
seoa1901	NM 002035	/len=2272	NM 002035	Hs.74050	NP 002026
ncrb4472	NM_002065	glutamate-ammonia ligase (glutamine synthase) (GLUL), mRNA /cds=(461,1582) /gb=NM_002065 /gi=21361767 /ug=Hs.170171 /len=3137	NM_002065	Hs.170171	NP_002056
		potassium channel,			
		subfamily K, member 1			
		(KCNK1), mRNA			
		/cds=(183,1193)			
		/gb=NM_002245			
		/gi=15451900			
		/ug=Hs.79351			
ncrb2247	NM_002245	/len=1901	NM 002245	Hs.79351	NP 002236
10102241	1111_002270	mutS 3 (E. coli)	1111_002240	13.7 333 1	141 _002200
		(MSH3), mRNA			
		/cds=(17,3403)			
		/gb=NM_002439			
		/gi=4505248			
		/ug=Hs.42674			
seoc0384	NM_002439	/len=4374	NM_002439	Hs.42674	NP_002430
		1		<u> </u>	

Figure 60	CONT. U.				,
		myosin light chain 1			
		slow a (MLC1SA),			
		mRNA			
		/cds=(48,674)			
		/gb=NM_002475			
		/gi=17986280			
		/ug=Hs.90318			
hfcr5003	NM 002475	/len=778	NM 002475	Hs.90318	NP 002466
		protein	_		
		phosphatase 1,			
		regulatory (inhibitor)			
		subunit 12À			
		(PPP1R12A),			
		mRNA			
		/cds=(1,3093)			
		/gb=NM_002480			
		/gi=4505316			
		/ug=Hs.16533			
seob2966	NM_002480	/len=4613	NM_002480	Hs.16533	NP 002471
		non-metastatic cells			
		2, protein (NM23B)		Į.	
		expressed in			
		(NME2), nuclear			
		gene encoding			
		mitochondrial			
		protein, mRNA			
		/cds=(73,531)			
		/gb=NM_002512			
		/gi=4505408			
		/ug=Hs.433416			
ncr0176	NM 002512	/len=670	NM 002512	Hs.433416	NP_002503
11010110	14111_002012	paralemmin	14111_002012	1110.100110	111 _002000
1		(PALM), mRNA			
		/cds=(146,1309)			
		/gb=NM_002579			
		/gi=4557041			
		/ug=Hs.78482			
fcr2908	NM_002579	/len=2823	NM 002579	Hs.78482	NP 002570
1012300	1411_002073	phosphodiesterase	1411_002070	110.70402	141 _002070
	ļ	4B, cAMP-specific			
		(phosphodiesterase			
		E4 dunce			
		Drosophila)	Ì	Ì	
		(PDE4B), mRNA			
		/cds=(766,2460)			
		/gb=NM_002600			
1		/gi=4505662		ĺ	
		/ug=Hs.188			
ncrb0897	NM 002600	/len=4068	NM_002600	Hs.188	NP 002591
TICIDO091	11111 002000	MCH-7000	114141_002000	p 13. 100	1141- 002381

	Conta.				
mioa1657	NM 002715	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform (PPP2CA), mRNA /cds=(210,1139) /gb=NM_002715 /gi=4506016 /ug=Hs.91773 /len=2181	NM_002715	Hs.91773	NP_002706
	3027 10	protein	141 002110	. 10.0 1770	141 _002100
		phosphatase 6, catalytic subunit (PPP6C), mRNA /cds=(69,986) /gb=NM_002721 /gi=20127429 /ug=Hs.356739			
hfcr0470	NM_002721	•	NM 002721	Hs.356739	NP_002712
fcrb3629	NM_002736	protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B), mRNA /cds=(167,1423) /gb=NM_002736 /gi=4506064 /ug=Hs.77439 /len=3259	NM_002736	Hs.77439	NP_002727
10120020	11111_002700	phosphoribosyl	11111_002700	110.77 400	141 _002121
seoc4856	NM_002765	pyrophosphate synthetase 2 (PRPS2), mRNA /cds=(61,1017) /gb=NM_002765 /gi=4506128 /ug=Hs.2910 /len=2457	NM_002765	Hs.2910	NP_002756
mioa8804	NM 002793	proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1), mRNA /cds=(48,773) /gb=NM_002793 /gi=22538462 /ug=Hs.407981 /len=872	NM 002793	Hs.407981	NP 002784

1 19410 00	Conta.	Т			,
hfcr1324	NM_002811	proteasome (prosome, macropain) 26S subunit, non- ATPase, 7 (Mov34 (PSMD7), mRNA /cds=(128,1102) /gb=NM_002811 /gi=25777614 /ug=Hs.155543 /len=1673	NM_002811	Hs.155543	NP_002802
seob1172	NM 002857	peroxisomal farnesylated protein (PXF), mRNA /cds=(11,910) /gb=NM_002857 /gi=4506338 /ug=Hs.168670 /len=3662	NM 002857	Hs.168670	NP 002848
Seod 1172	NIVI_002857	RAB5B, member	NN_002857	ns. 100070	NP_002848
fcrc1601	BC050558	RAS oncogene family, clone IMAGE:6191566, mRNA, partial cds			NP 002859
seoa9409	NM 002937	ribonuclease, RNase A family, 4 (RNASE4), mRNA /cds=(173,616) /gb=NM_002937 /gi=20070170 /ug=Hs.283749 /len=1414	NM 002937	Hs.283749	NP 002928
		replication protein A1, 70kDa (RPA1), mRNA /cds=(44,1894) /gb=NM_002945 /gi=20070171 /ug=Hs.84318			
ncrb4843	NM_002945	/len=2824	NM_002945	Hs.84318	NP_002936

syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan) (SDC2), mRNA /cds=(460,1065) /gb=NM_002998 /gi=27804306 /ug=Hs.1501 hfcr2554 /len=2172 NM 002998 NM 002998 Hs.1501 NP 002989 succinate dehydrogenase complex, subunit C, integral membrane protein, 15kDa (SDHC), nuclear gene encoding mitochondrial protein, mRNA /cds=(27,536)/gb=NM 003001 /gi=9257243 /ug=Hs.433982 fcrc3497 NM_003001 /len=1315 NM_003001 Hs.433982 NP 002992 mRNA for MEGF5. seoa8906 AB011538 partial cds NM 003062 Hs.57929 NP_003053 clone IMAGE:4821017, ncrc3172 BC034956 mRNA Hs.77196 NP_003118 Sjogren syndrome antigen B (autoantigen La) (SSB), mRNA /cds=(73,1299)/gb=NM 003142 /gi=10835066 /ug=Hs.83715 fcr4414 NM_003142 NM 003142 /len=1619 Hs.83715 NP_003133 syntaxin 5A (STX5A), mRNA /cds=(27,932)/gb=NM 003164 /gi=4507292 /ug=Hs.302300 fcrb8872 NM 003164 /len=1507 NP_003155 NM 003164 Hs.302300

Figure of	c Cont'd.				<u> </u>
		tubulin-specific			·
		chaperone e			
		(TBCE), mRNA			
		/cds=(81,1664)			
		/gb=NM_003193			
		/gi=6006029			
		/ug=Hs.343564			
mioc8840	NM 003193	/len=1882	NM_003193	Hs.343564	NP 003184
1111000040	14141_000190	toll-like receptor 3	14141_005195	115.545504	147_003104
		1			
		(TLR3), mRNA			
		/cds=(102,2816)			
		/gb=NM_003265			
		/gi=19718735			
		/ug=Hs.29499			
ncrc6925	NM_003265	/len=3057	NM_003265	Hs.29499	NP_003256
		tumor protein,			
		translationally-			
		controlled 1 (TPT1),		1	
		mRNA			
		/cds=(95,613)			
	<u> </u>	/gb=NM_003295			
		/gi=4507668			
		/ug=Hs.401448			
ncrc4323	NM_003295	/len=830	NM_003295	Hs.401448	NP_003286
110104323	14101_003293	tumor suppressing	14101_003233	113.401440	141 _003200
1		subtransferable			
		candidate 1			
		(TSSC1), mRNA			
		/cds=(152,1315)			
		/gb=NM_003310			
		/gi=4507702			
		/ug=Hs.4992			
hfcr2808	NM_003310	/len=1705	NM_003310	Hs.4992	NP_003301
		UDP-glucose		-	
		dehydrogenase			
1		(UGDH), mRNA		1	
		/cds=(79,1563)	1	1	
		/gb=NM_003359			
		/gi=4507812			
		/ug=Hs.28309	1		
mioa1608	NM 003359	/len=2950	NM 003359	Hs.28309	NP 003350
	1.111_000000	vimentin (VIM),			
1		mRNA	1		
		/cds=(123,1523)	[1
		/gb=NM 003380			
		/gi=4507894			
	Ì	-			
2220056	NIM OCCOOL	/ug=Hs.297753	NIM OCCOR	Un 207752	ND 002274
seoa0256	NM_003380	/len=1851	NM_003380	Hs.297753	NP_003371
		ZFX mRNA for put.			
1.6.4045	V50700	transcription	NIN	007.	ND 000404
hfcr1848	X59739	activator, isoform 2	[NM_003410	Hs.2074	NP_003401

1 19470 01	Conta.	· · · · · · · · · · · · · · · · · · ·			
ncrc7043	NM_003418	zinc finger protein 9 (a cellular retroviral nucleic acid binding protein) (ZNF9), mRNA /cds=(103,636) /gb=NM_003418 /gi=4827070 /ug=Hs.2110 /len=1500	NM_003418	Hs.2110	NP 003409
		leucine zipper			
fcr3528	AF062089	protein Fip3p (=AF074382 IkB kinase gamma subunit)	NM 003639	Hs.43505	NP 003630
		inhibitor of kappa light polypeptide gene enhancer in B- cells, kinase complex-associated protein (IKBKAP), mRNA /cds=(304,4302) /gb=NM_003640 /gi=4504628 /ug=Hs.31323			
ncr8843	NM_003640	/len=4803	NM_003640	Hs.31323	NP_003631
seoa7086	NM_003750	eukaryotic translation initiation factor 3, subunit 10 theta, 150/170kDa (EIF3S10), mRNA /cds=(114,4262) /gb=NM_003750 /gi=4503508 /ug=Hs.154796 /len=5256	NM_003750	Hs.154796	NP_003741
ncrb1337	NM_003753	eukaryotic translation initiation factor 3, subunit 7 zeta, 66/67kDa (EIF3S7), mRNA /cds=(372,2018) /gb=NM_003753 /gi=23238220 /ug=Hs.55682 /len=2169	NM_003753	Hs.55682	NP_003744

rigule oc	John G.	Lat., 121 - 2	ı		
		delta-like 1			
		(Drosophila)			
		(DLK1), mRNA			
		/cds=(163,1314)			
		/gb=NM_003836			
		/gi=21361079			
		/ug=Hs.169228			
fcr2541	NM 003836	/len=1556	NM 003836	Hs.169228	NP 003827
1012041	14111_000000	glycogenin 2	14111_000000	113.100220	141 _000027
		(GYG2), mRNA			
		1.			
		/cds=(284,1789)			
		/gb=NM_003918			
		/gi=5453673			
		/ug=Hs.380757			
fcr4878	NM_003918	/len=3267	NM_003918	Hs.380757	NP_003909
		protein regulator of			<u> </u>
		cytokinesis 1			
		(PRC1), mRNA			
		/cds=(79,1941)	1		
		/gb=NM 003981			1
		/gi=4506038			
İ		/ug=Hs.344037	ŀ		
hfcr1428	NM_003981	/len=3044	NM 003981	Hs.344037	NP 003972
11101 1420	14111_000001	G protein pathway	11111_000001	110.011007	111_000072
	1	suppressor 1			
		(GPS1), mRNA			
		1, ,,			
		/cds=(21,1523)			l
		/gb=NM_004127			
		/gi=13435380			
		/ug=Hs.268530			
fcrb2356	NM_004127	/len=1866	NM_004127	Hs.268530	NP_004118
		myosin IXB			
		(MYO9B), mRNA]
		/cds=(1,6069)			
		/gb=NM_004145			
		/gi=4758749			
		/ug=Hs.159629			
fcr1337	NM 004145	/len=6069	NM 004145	Hs.159629	NP 004136
13, 133,	1.411_004140	developmentally			
		regulated GTP			
		binding protein 1			
		_ ·			
		(DRG1), mRNA			
Ì		/cds=(66,1169)	}	•	1
	1	/gb=NM_004147			
		/gi=4758795			
		/ug=Hs.115242			
seob2336	NM_004147	/len=1383	NM_004147	Hs.115242	NP_004138

Figure of	Cont'd.				
		mRNA; cDNA			
		DKFZp761F0118			
		(from clone			
		DKFZp761F0118)			
		/cds=(1,6490)			
		/gb=AL831917			
		/gi=21732430			
		/ug=Hs.6685			
seoa6724	AL831917	/len=7334		Hs.6685	NP 004232
00000121	71200 10 11			110.000	111 _00 1202
		U5 snRNP-specific			
		•			
		protein, 116 kD (U5-			
		116KD), mRNA			
		/cds=(61,2979)			
		/gb=NM_004247			
		/gi=4759279			
		/ug=Hs.151787			
mioa7299	NM 004247	/len=3784	NM 004247	Hs.151787	NP 004238
		peptidase			
	ļ	(mitochondrial			
		,			
ļ		processing) beta			
		(PMPCB), mRNA			
1		/cds=(14,1483)			
		/gb=NM_004279			
		/gi=4758733			
		/ug=Hs.184211			
mioa1303	NM 004279	/len=1771	NM 004279	Hs.184211	NP 004270
		BCL2/adenovirus	_		
Ì		E1B 19kDa			
		interacting protein 2			
		(BNIP2), mRNA			
		1,			
		/cds=(212,1156)			
		/gb=NM_004330			
		/gi=4757855			
		/ug=Hs.155596			
mioc5692	NM_004330	/len=2382	NM_004330	Hs.155596	NP_004321
	1	desmoplakin (DPI,			
		DPII) (DSP), mRNA			
	1	/cds=(280,8895)			
	1		1		
1	1	/gb=NM_004415			
	1	/gi=4758199			
1	}	/ug=Hs.349499	}	}	}
ncr7839	NM_004415	/len=9588	NM_004415	Hs.349499	NP_004406
		glutamyl-prolyl-			
	ŀ	tRNA synthetase			
		(EPRS), mRNA			
	[/cds=(59,4381)			
		/gb=NM_004446	ļ		
		, -			
		/gi=4758293			
1000		/ug=Hs.55921		55004	
ncr1699	NM_004446	/len=4586	NM_004446	Hs.55921	NP_004437

Figure 6	Conta.				
		enhancer of			
		rudimentary			
		(Drosophila) (ERH),			
}		mRNA			
		/cds=(72,386)			
		/gb=NM_004450			
		/gi=4758301			
		/ug=Hs.433413			
mioa2965	NM 004450	/len=815	NM 004450	11- 400440	ND 004444
111042905	14101_004450		10101_004450	Hs.433413	NP_004441
		ubiquitin specific			
	ļ	protease 6 (Tre-2			
	ĺ	oncogene) (USP6),			
		mRNA			
		/cds=(1697,4057)			
		/gb=NM_004505			
}		/gi=4758563			
		/ug=Hs.111065			
seoa2467	NM_004505	/len=7878	NM_004505	Hs.111065	NP_004496
		NADH			
		dehydrogenase			
		(ubiquinone) Fe-S		1	
İ		protein 3, 30kDa			
		(NADH-coenzyme			
		Q reductase)			
		(NDUFS3), mRNA			
}		/cds=(13,807)			
ł		/gb=NM_004551			
		/gi=4758787			
		/ug=Hs.429506			
mioa6913	NM 004551	/len=899	NM 004551	Un 420506	ND 004E40
1111040913	14141_004551	nuclear factor of	14141_004551	Hs.429506	NP_004542
ļ					
		activated T-cells,			
		cytoplasmic,			
		calcineurin-			
		dependent 4			
		(NFATC4), mRNA			
		/cds=(294,3002)			
		/gb=NM_004554			
		/gi=27886562			
		/ug=Hs.77810			
hfcr5956	NM_004554	/len=3399	NM_004554	Hs.77810	NP_004545
		splicing factor 1			
}		(SF1), mRNA]
		/cds=(383,2254)			
		/gb=NM_004630			
		/gi=4759339			
		/ug=Hs.180677			
mioa1370	NM_004630	/len=3131	NM_004630	Hs.180677	NP_004621
		cDNA FLJ33043		1	
		fis, clone		1	
seoc2955	AK057605	THYMU2000440		Hs.193145	NP_004645
		1	·	15 55 . 75	100-0-0

Figure 60	Conta.				
		RAB11A, member			
		RAS oncogene			
		family (RAB11A),			
		mRNA			
		/cds=(104,754)			
		/gb=NM_004663			
		/gi=20149549			
		/ug=Hs.75618			
miod1389	NM_004663	/len=2474	NM_004663	Hs.75618	NP_004654
		splicing factor,			
		arginine/serine-rich			
		2, interacting			
		protein (SFRS2IP),			
		mRNA			
		1			
		/cds=(1211,4657)			
		/gb=NM_004719			
		/gi=4759171			
		/ug=Hs.51957			
ncr5046	NM_004719	/len=5307	NM_004719	Hs.51957	NP_004710
		ATP-binding			
		cassette, sub-family			
		G (WHITE),			
		member 2			
	!				
		(ABCG2), mRNA			
		/cds=(205,2172)			
		/gb=NM_004827			
		/gi=4757849			
		/ug=Hs.194720			
mioc4923	NM 004827	/len=2719	NM 004827	Hs.194720	NP 004818
		NHP2 non-histone	_		
		chromosome			
		protein 2-like 1 (S.			
		l			
		cerevisiae)			
		(NHP2L1), mRNA			
		/cds=(95,481)			
		/gb=NM_005008			
		/gi=4826859			
		/ug=Hs.182255			
seoa9916	NM 005008	/len=1475	NM 005008	Hs.182255	NP 004999
		` · · · · · · · · · · · · · · · · · · ·	_ :: <u>_</u> : :		
		thyroid hormone			
		receptor-associated	ł		
		protein, 240 kDa			
Ì			ì		
		subunit (TRAP240),			
		mRNA			
		/cds=(78,6602)			
		/gb=NM_005121			
		/gi=4827043			
		/ug=Hs.11861			
ncrc3256	NM_005121	/len=7389	NM_005121	Hs.11861	NP_005112
		•			

Figure 6	Conta.	 		····	
		heat shock 70kDa protein 1A			
	į	(HSPA1A), mRNA			
		/cds=(198,2123)			
		/gb=NM_005345			
		/gi=26787973			
mioa8899	NM 005345	/ug=Hs.75452 /len=2383	NM OOES45	Ua 75450	ND 005000
111000099	14141_003343	/lef1-2363	NM_005345	Hs.75452	NP_005336
		solute carrier family			
		20 (phosphate			
		transporter),			
		member 1			
		(SLC20A1), mRNA			
		/cds=(371,2410)			
		/gb=NM_005415			
		/gi=7382462			
b0204	NINA 005445	/ug=Hs.78452	NINA 005445	11- 70450	ND 005400
seob8301	NM_005415	/len=3220 chromosome 6	NM_005415	Hs.78452	NP_005406
		open reading frame			
		11 (C6orf11),			
		mRNA			
		/cds=(54,1886)			
		/gb=NM_005452			
		/gi=14550417			
		/ug=Hs.17930			
fcrc4551	NM_005452	/len=2074	NM_005452	Hs.17930	NP_005443
		phosphatidylinositol			
		glycan, class K			
		(PIGK), mRNA			
		/cds=(25,1212)			
		/gb=NM_005482			
		/gi=23199982 /ug=Hs.62187			
fcrb2637	NM_005482	/len=1897	NM_005482	Hs.62187	NP_005473
10102007	1411_000402	SMC4 structural	14141_000402	113.02.107	NF_003473
		maintenance of			
		chromosomes 4-			
-		like 1 (yeast)			
		(SMC4L1), mRNA			
		/cds=(233,4099)			
}		/gb=NM_005496			
		/gi=21361251			
, , , , , , ,		/ug=Hs.50758			
seob5523	NM_005496	/len=5261	NM_005496	Hs.50758	NP_005487

	c Conta.				
seoc2904	NM_005499	SUMO-1 activating enzyme subunit 2 (UBA2), mRNA /cds=(26,1948) /gb=NM_005499 /gi=4885648 /ug=Hs.4311 /len=2617	NM_005499	Hs.4311	NP_005490
36002904	14101_000499	//6/1-201/	[14141_000 4 88	115.4311	NF_005490
		ah42f05.s1 Soares_testis_NHT cDNA clone 1292193 3' similar to P54687 BRANCHED- CHAIN AMINO ACID AMINOTRANSFER ASE, CYTOSOLIC ;, mRNA sequence /clone=1292193 /clone_end=3' /gb=AA705851 /gi=2715769 /ug=Hs.443872			
ncrc7188	AA705851	/len=412	:	Hs.443872	NP 005495
		major histocompatibility complex, class I, B (HLA-B), mRNA /cds=(11,1099) /gb=NM_005514 /gi=21327676 /ug=Hs.77961	NIM 005544		
fcrb4784	NM_005514	/len=1310	NM_005514	Hs.77961	NP_005505
norb6946	NM 005536	inositol(myo)-1(or 4)- monophosphatase 1 (IMPA1), mRNA /cds=(99,932) /gb=NM_005536 /gi=8393607 /ug=Hs.171776 /len=2349	NM 005536	Hs.171776	NP_005527
ncrb6846	TI4IAI_009990	/ICH-2043	LIAINI_000000	p 15. 17 17 70	INF_0000Z1

MADS box transcription enhancer factor 2, polypeptide A (myocyte enhancer factor 22), polypeptide A (myocyte enhancer factor 2A) (MEF2A), mRNA /ods=(415,1938) /gb=NM_005587 /gi=5031906 /ug=Hs.182280 MM_005587 /gi=5031906 /ug=Hs.182280 MM_005587 Hs.182280 NP_005578 MM_005595 MM_005597 MM_0055	94.00	Conta.	·	·		
polypeptide- associated complex alpha polypeptide (NACA), mRNA /cds=(26,673) /gb=NM_005594 /gi=5031930 /ug=Hs.32916 /len=797 NM_005594 Hs.32916 NP_005585 splicing factor, arginine/serine-rich 4 (SFRS4), mRNA /cds=(107,1591) /gb=NM_005626 /gi=21361281 /ug=Hs.76122 /len=2167 NM_005626 Hs.76122 NP_005617 solute carrier family 1 (neutral amino acid transporter), member 5 (SLC1A5), mRNA /cds=(591,2216) /gb=NM_005628 /gi=5032092 /ug=Hs.183556 /len=2856 NM_005628 Hs.183556 NP_005619 factor 2 (SERF2), mRNA /cds=(1023,1319) /gb=NM_005770 /gi=21361286 /ug=Hs.380718	miob3595	NM_005587	transcription enhancer factor 2, polypeptide A (myocyte enhancer factor 2A) (MEF2A), mRNA /cds=(415,1938) /gb=NM_005587 /gi=5031906 /ug=Hs.182280	NM_005587	Hs.182280	NP_005578
arginine/serine-rich 4 (SFRS4), mRNA /cds=(107,1591) /gb=NM_005626 /gi=21361281 /ug=Hs.76122 hfcr6573 NM_005626 /len=2167 NM_005626 NM_005626 NM_005626 NM_005626 NM_005626 NM_005626 NM_005626 NM_005628 /gi=5032092 /ug=Hs.183556 fcrc1607 NM_005628 NM_005628 /gi=5032092 /ug=Hs.183556 NM_005628	ncrc2607	NM 005594	polypeptide- associated complex alpha polypeptide (NACA), mRNA /cds=(26,673) /gb=NM_005594 /gi=5031930 /ug=Hs.32916		Hs.32916	NP 005585
solute carrier family 1 (neutral amino acid transporter), member 5 (SLC1A5), mRNA /cds=(591,2216) /gb=NM_005628 /gi=5032092 /ug=Hs.183556 fcrc1607 NM_005628 /len=2856 NM_005628 Hs.183556 NP_005619 small EDRK-rich factor 2 (SERF2), mRNA /cds=(1023,1319) /gb=NM_005770 /gi=21361286 /ug=Hs.380718			splicing factor, arginine/serine-rich 4 (SFRS4), mRNA /cds=(107,1591) /gb=NM_005626 /gi=21361281 /ug=Hs.76122			
small EDRK-rich factor 2 (SERF2), mRNA /cds=(1023,1319) /gb=NM_005770 /gi=21361286 /ug=Hs.380718		_	solute carrier family 1 (neutral amino acid transporter), member 5 (SLC1A5), mRNA /cds=(591,2216) /gb=NM_005628 /gi=5032092 /ug=Hs.183556			
fcr2530 NM 005770 /len=1408 NM 005770 Hs.380718 NP 005761			small EDRK-rich factor 2 (SERF2), mRNA /cds=(1023,1319) /gb=NM_005770 /gi=21361286 /ug=Hs.380718			

Figure 60	Conta.			,	· · · · · · · · · · · · · · · · · · ·
		serine/arginine			
		repetitive matrix 1			
		(SRRM1), mRNA			
	}	/cds=(6,2468)			
i		/gb=NM_005839			
		/gi=5032118			
		/ug=Hs.18192			
forb 7751	NIM ODEODO	/len=3698	NM 005839	Hs.18192	ND 005000
fcrb7751	NM_005839	1	14141_002638	ITS. 10 192	NP_005830
		proliferation-		ł	
		associated 2G4,			
		38kDa (PA2G4),			
		mRNA			
		/cds=(98,1282)			
		/gb=NM_006191			
		/gi=5453841			
	i	/ug=Hs.374491			
fcrc6248	NM 006191	/len=1697	NM 006191	Hs.374491	NP 006182
		ubiquinol-			
		cytochrome c			
		reductase binding			
		protein (UQCRB),			
		1'			
		mRNA			
		/cds=(54,389)			
		/gb=NM_006294			
		/gi=20070231			
		/ug=Hs.131255			
fcrb1720	NM_006294	/len=965	NM_006294	Hs.131255	NP_006285
		progesterone-			
		induced blocking			
1		factor 1 (PIBF1),			
		mRNA `			
		/cds=(1,2277)		ļ	
		/gb=NM_006346			
]		/gi=5453889			
		1 -			
1011	NINA 000040	/ug=Hs.43913	NINA DOCCARO	110 42042	ND 000007
seoa1611	NM_006346	/len=2277	NM_006346	Hs.43913	NP_006337
		dual-specificity			
	1	tyrosine-(Y)-			
		phosphorylation			
		regulated kinase 2			
		(DYRK2), transcript			
	1	variant 2, mRNA	ļ		
		/cds=(161,1966)			
		/gb=NM_006482			
		/gi=5922003			
		/ug=Hs.173135	NM 003583;		
forb3110	NIM 006492	/len=3615		Uc 172125	ND ODGATO
fcrb3119	NM_006482	Me11-30 13	NM_006482	Hs.173135	NP_006473

rigule 0	c Cont'd.				
		t-complex-			
		associated-testis-			
	•	expressed 1-like 1			
		(TCTEL1), mRNA			
		/cds=(1,342)			
		1 ' '	1		
		/gb=NM_006519		İ	
		/gi=5730084			
		/ug=Hs.266940			
seob3455	NM_006519	/len=713	NM 006519	Hs.266940	NP 006510
	†	HBS1-like (S.	† -		
		cerevisiae)			
		(HBS1L), mRNA			
		/cds=(194,2248)			
1		/gb=NM_006620			
Ì		/gi=24431963			
		/ug=Hs.221040			
miod0526	NM_006620	/len=7163	NM_006620	Hs.221040	NP_006611
		MLL septin-like			
		fusion (MSF),			
		mRNA			
		/cds=(258,1964)			
		/gb=NM_006640			
		1 -			
		/gi=19923366			
l		/ug=Hs.181002			
hfcr4423	NM_006640	/len=3929	NM_006640	Hs.181002	NP_006631
		mannosidase,			
		alpha, class 1A,		1	
		member 2			
1		(MAN1A2), mRNA			
		/cds=(521,2446)	1		
		/gb=NM_006699			
		/gi=5729912		1	
		1 ~			
	NA COCCOO	/ug=Hs.367638	NINA 000000	11- 007000	ND 000000
mioa1392	NM_006699	/len=2792	NM_006699	Hs.367638	NP_006690
		troponin T3,			
		skeletal, fast	1		
		(TNNT3), mRNA			
		/cds=(13,789)]		
}		/gb=NM_006757	1		
		/gi=5803202			
		/ug=Hs.73454			
fcrb5996	NM 006757	/len=1000	NM 006757	Hs.73454	NP 006748
	† · · · · · · · · · · · · · · · · · · ·	DEAD/H (Asp-Glu-		1	
		Ala-Asp/His) box			
1		polypeptide 18 (Myc	1		
1			Ί	1	
1		regulated)]
1		(DDX18), mRNA			
1		/cds=(72,2084)			
1		/gb=NM_006773			
		/gi=13787205			
		/ug=Hs.100555			
miob9470	NM_006773	/len=2753	NM_006773	Hs.100555	NP_006764
			·		

Figure 60	, conta.				
	1	chromosome 1			
		open reading frame			
ļ		29 (C1orf29),			
		mRNA			
1		/cds=(242,1483)			
		/gb=NM_006820			
		/gi=5803026			
ļ		/ug=Hs.75470			
ncrb8569	NM_006820	/len=2058	NM_006820	Hs.75470	NP_006811
		zinc finger protein			
		24 (KOX 17)			
1		(ZNF24), mRNA			
		/cds=(165,1271)			
		/gb=NM_006965			
		/gi=5902161			
		/ug=Hs.183593			
seob5012	NM_006965	/len=2513	NM_006965	Hs.183593	NP_008896
		a disintegrin-like			
		and			
1		metalloprotease			
		(reprolysin type)			
		with			
ŀ					
ł		thrombospondin			
	Ì	type 1 motif, 1			
		(ADAMTS1),			
		mRNA			
		/cds=(294,3146)			
		/gb=NM_006988			
		/gi=11038653			
		/ug=Hs.8230			
nor7672	NIM OOGOOO	/len=4459	NIM ODEOGO	U 0220	ND 000010
ncr7672	NM_006988	Į.	NM_006988	Hs.8230	NP_008919
		transforming, acidic			
ļ		coiled-coil]		
·		containing protein 2			
		(TACC2), mRNA			
		/cds=(87,3167)			
		/gb=NM_006997			
		/gi=11119413			
	Ì	1 -			
f	NINA 000007	/ug=Hs.272023	NINA 000007	LL- 070000	LUD AGGGGG
fcrb2452	NM_006997	/len=3686	NM_006997	Hs.272023	NP_008928
		ubiquitin-like 3			
		(UBL3), mRNA			
	}	/cds=(110,463)	}		
		/gb=NM_007106			
		/gi=6005927			
		/ug=Hs.173091			
ncr3419	NM 007106	/len=3323	NM_007106	Hs.173091	NP_009037
11010419	[141VI_007 100	1/10/1-0020	[141VI_00/100	1113.173081	ไเสน"กกลกว (

Figure 60	Contu.				
	1	tumor necrosis			
		factor, alpha-		ļ	
		induced protein 6			
		(TNFAIP6), mRNA			
		/cds=(77,910)			
		/gb=NM_007115		1	
		1 -		İ	
		/gi=26051242			
İ		/ug=Hs.29352			
mioa5836	NM_007115	/len=1440	NM_007115	Hs.29352	NP_009046
		Ig superfamily			
1		protein (Z39IG),			
		mRNA			
		/cds=(46,1245)			
ŀ		/gb=NM_007268			
		/gi=6005957			
		_			
1055		/ug=Hs.8904			NID COSTO
ncr1055	NM_007268	/len=1787	NM_007268	Hs.8904	NP_009199
		transcription			
		termination factor,			
		RNA polymerase I			
		(TTF1), mRNA			
		/cds=(45,2705)			
		/gb=NM_007344			
		/gi=6678454			
		1 •]	
	l	/ug=Hs.54780			
ncrb2027	NM_007344	/len=2847	NM_007344	Hs.54780	NP_031370
		nidogen 2		1	
		(osteonidogen)			
		(NID2), mRNA			
		/cds=(1,4131)			
		/gb=NM_007361			
		/gi=6679055			
		/ug=Hs.82733		ļ	
2221406	NIM 007204	1 •	NINA 007004	112 00700	ND 004007
seoa1496	NM_007361	/len=4829	NM_007361	Hs.82733	NP_031387
		soc-2 suppressor of]
		clear (C. elegans)			
	İ	(SHOC2), mRNA			
		/cds=(278,2026)			
		/gb=NM_007373			
		/gi=6677944			
		/ug=Hs.104315			
min-2500	NIM COZOZO	1 -	NINA COZOZO	Un 104345	ND 034300
mioc3590	NM_007373	/len=3872	NM_007373	Hs.104315	NP_031399
		Mus musculus			
		neuron specific			
		gene family			
		member 1, mRNA			
		(cDNA clone] .
		MGC:11446			
		IMAGE:3603440),		!	
seoc7694	BC008272	complete cds	NM_010942	Mm.7414	NP 035072
36001034	150000212	Icombiere cas	1141VI_0 1034Z	[1VIII. / 4 14	[NF_033012

1 19410 00	Conta.				
ncrc5363	NM 012201	golgi apparatus protein 1 (GLG1), mRNA /cds=(27,3560) /gb=NM_012201 /gi=6912389 /ug=Hs.78979 /len=3909	NM 012201	Hs.78979	NP 036333
ncressos	14141_012201		14141_012201	HS.76979	INP_030333
		meningioma expressed antigen 5 (hyaluronidase) (MGEA5), mRNA /cds=(396,3146) /gb=NM_012215 /gi=11024697 /ug=Hs.5734			
fcrb5122	NM_012215	/len=5147	NM_012215	Hs.5734	NP 036347
mioa1058	NM 012257	HMG-box containing protein 1 (HBP1), mRNA /cds=(187,1731) /gb=NM_012257 /gi=21361410 /ug=Hs.10882 /len=2857	NM 012257	Hs.10882	NP 036389
	_	U6 snRNA- associated Sm-like protein (LSM5), mRNA /cds=(1,276) /gb=NM_012322 /gi=6912487 /ug=Hs.227280	_		
fcrb9390	NM_012322	/len=749 likely ortholog of	NM_012322	Hs.227280	NP_036454
		mouse acyl- Coenzyme A thioesterase 2, mitochondrial (ACATE2), mRNA /cds=(148,1368) /gb=NM_012332 /gi=6912517 /ug=Hs.18625			
mioc6385	NM_012332	/len=1954	NM_012332	Hs.18625	NP_036464

Figure 6	c Conta.				
		c-myc binding			
		protein (MYCBP),]		
		mRNA			
		/cds=(39,350)			
		/gb=NM 012333			
		/gi=8850230			
		/ug=Hs.78221			
fcrc0148	NM 012333	/len=2070	NM 012333	Hs.78221	NP 036465
10100140	14141_012000	transmembrane 4	14141_012000	113.70221	141_030403
		superfamily			
		-			
		member tetraspan			
		NET-7 (NET-7),			
		mRNA	ļ	1	
		/cds=(122,1006)			
1		/gb=NM_012339			
1		/gi=21264576			
		/ug=Hs.95583			
fcrc3288	NM_012339	/len=1727	NM_012339	Hs.95583	NP_036471
		muscle specific	Î		
		gene (M9), mRNA			
ļ	Ì	/cds=(172,828)			
		/gb=NM_013234			
		/gi=10801344			
		/ug=Hs.283781			
ncrc2273	NM_013234	/len=911	NM 013234	Hs.283781	NP_037366
110102210	, <u>_</u> 0 , 020 ,	DKFZP586A0522			
		protein			
		(DKFZP586A0522),			
1		mRNA		ļ	
		/cds=(21,755)			
		1 ' '			
		/gb=NM_014033			
		/gi=13378140			
l		/ug=Hs.288771			
mioc6374	NM_014033	/len=1705	NM_014033	Hs.288771	NP_054752
		signal peptidase			1
		12kDa (SPC12),			
		mRNA			
		/cds=(169,444)			
		/gb=NM_014041			
		/gi=7661745			
		/ug=Hs.11125			
fcrb8467	NM 014041	/len=798	NM_014041	Hs.11125	NP_054760
			<u> </u>		
		PRO0659 protein	1		
		(PRO0659), mRNA	1		
		/cds=(60,584)			
		/gb=NM_014138			
		/gi=7662583			
		/ug=Hs.6451			
fcrb3618	NM_014138	/len=1416	NM_014138	Hs.6451	NP 054857
[[CLD20.10	TIMINI_0 14 130	Men-1410	1141VI_U 14 130	Ji 15.040 I	DAL 004001

I iguic o	C Conta.				
		cDNA: FLJ21950			
		fis, clone			
fcrc5593	AK025603	HEP04949	NM 014181	Hs.372208	NP 054900
		of Yeast RRP4			
		(ribosomal RNA			
		processing 4), 3'-5'-			
		exoribonuclease			
4500	NINA 04 4005		NINA 04 4005	11- 044070	ND 055400
ncr4539	NM_014285	(RRP4), mRNA	NM_014285	Hs.211973	NP_055100
		zinc finger protein			
		(ZF5128), mRNA			
		/cds=(95,1756)			
		/gb=NM_014347			
		/gi=7657692			
		/ug=Hs.296365			
ncr3511	NM 014347	/len=3000	NM 014347	Hs.296365	NP 055162
	<u> </u>	transmembrane 4			
		superfamily			
		member tetraspan			1
		NET-6 (NET-6),			
İ		mRNA			
ì		/cds=(207,821)			
		/gb=NM_014399			
		/gi=21264573			
		/ug=Hs.284243			
hfcr1163	NM_014399	/len=1875	NM_014399	Hs.284243	NP_055214
		brain and			
		nasopharyngeal			
		carcinoma			
		susceptibility			
		protein (NSG-X),			
		mRNA			
		/cds=(186,518)			
		/gb=NM_014411			
		/gi=14149650			
		/ug=Hs.26937		11. 00007	ND 055000
miob9024	NM_014411	/len=1897	NM_014411	Hs.26937	NP_055226
		putative breast			
		adenocarcinoma			
		marker (32kD) (BC-			
		2), mRNA	ļ		
		/cds=(130,798)	1		
		/gb=NM_014453	1		
	[/gi=7656921	1		
		/ug=Hs.12107			
seoa7608	NM 014453	/len=903	NM_014453	Hs.12107	NP 055268
	1	1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		1	1

<u>Figure oc</u>	Cont'd.				
		FGF receptor activating protein 1 (FRAG1), mRNA /cds=(129,1076) /gb=NM_014489 /gi=7657101 /ug=Hs.133968			
seob9292	NM_014489	/len=2040	NM_014489	Hs.133968	NP_055304
seoc6779	NM_014500	HIV TAT specific factor 1 (HTATSF1), mRNA /cds=(183,2450) /gb=NM_014500 /gi=21361436 /ug=Hs.171595 /len=2785	NM_014500	Hs.171595	NP_055315
seob1770	NM_014608	cytoplasmic FMR1 interacting protein 1 (CYFIP1), mRNA /cds=(53,3814) /gb=NM_014608 /gi=24307968 /ug=Hs.77257 /len=4394	NM_014608	Hs.77257	NP_055423
miob3420	NM_014669	KIAA0095 gene product (KIAA0095), mRNA /cds=(67,2526) /gb=NM_014669 /gi=7661901 /ug=Hs.155314 /len=2681	NM_014669	Hs.155314	NP_055484
ncr5651	NM_014739	KIAA0164 gene product (KIAA0164), mRNA /cds=(254,3016) /gb=NM_014739 /gi=7661957 /ug=Hs.80338 /len=5538	NM_014739	Hs.80338	NP_055554
ncrc5813	NM_014764	DAZ associated protein 2 (DAZAP2), mRNA /cds=(70,576) /gb=NM_014764 /gi=7661885 /ug=Hs.75416 /len=1897	NM_014764	Hs.75416	NP_055579

	y conta.	, , , , , , , , , , , , , , , , , , , 	,	, , , , , , , , , , , , , , , , , , , 	,
7400	NN 044774	KIAA0494 gene product (KIAA0494), mRNA /cds=(978,2465) /gb=NM_014774 /gi=7662159 /ug=Hs.62515		U. 00545	ND OFFERD
ncr7136	NM_014774	/len=5766	NM_014774	Hs.62515	NP_055589
		RB1-inducible coiled-coil 1 (RB1CC1), mRNA /cds=(516,5291) /gb=NM_014781 /gi=7661991 /ug=Hs.50421			
seoa4070	NM 014781	/len=6614	NM 014781	Hs.50421	NP_055596
		C-type lectin BIMLEC precursor (BIMLEC), mRNA /cds=(12,710) /gb=NM_014880 /gi=26892292 /ug=Hs.2441			
seoa8443	NM_014880	/len=1033	NM_014880	Hs.2441	NP_055695
ncrc3700	D87466	mRNA for KIAA0276 gene, partial cds. /cds=(1,932) /gb=D87466 /gi=1665816 /ug=Hs.240112 /len=4185		Hs.240112	ND 055020
110103700	D07400			IDS.240112	NP_055930
fcrb4706	D31888	KIAA0071 mRNA, partial cds	NM_015156	Hs.78398	NP_055971
miob6597	NM_015161	ADP-ribosylation factor-like 6 interacting protein (ARL6IP), mRNA /cds=(70,681) /gb=NM_015161 /gi=24308006 /ug=Hs.75249 /len=2280	NM_015161	Hs.75249	NP_055976
1111000007	11-101_010101	1/1011 2200	11414 0 10 10 1	1110.10270	111 _000970

I iguic o	c Cont'd.				
		Novel mRNA from			
		chromosome 1,			
		which has			
		similarities to BAT2			
		genes			
		_			
		/cds=(58,8163)			
		/gb=AL096857	İ		
	ŀ	/gi=5541862			
1		/ug=Hs.69559	Ī		
hfcr1760	AL096857	/len=10174	NM_015172	Hs.69559	NP_055987
		DKFZp564D177			
		protein			
		(DKFZp564D177),			1
		mRNA			
		/cds=(106,849)			
		/gb=NM_015469			
1		/gi=22267435	İ	[.]
		1 -			
	NINA 045400	/ug=Hs.24608	NINA 045400	112 04000	ND osess
ncrc3927	NM_015469	/len=1664	NM_015469	Hs.24608	NP_056284
		Similar to nectin 3;			
		DKFZP566B0846			
		protein, clone			
		IMAGE:3461033,	1		
ncrb2449	BC001336	mRNA, partial cds	NM_015480	Hs.21201	NP_056295
	Î		_		
		autism susceptibility			
		candidate 2			
		(AUTS2), mRNA			
		1,			
		/cds=(322,4101)			
		/gb=NM_015570			
		/gi=17864089		1	
		/ug=Hs.32168			
fcr5026	NM_015570	/len=5972	NM_015570	Hs.32168	NP_056385
		SUMO-1-specific			
		protease (SUSP1),		1	
		mRNA		1	
		/cds=(1,3339)			
		/gb=NM_015571]		
		/gi=7662311			
		/ug=Hs.27197			
seoa7647	NM 015571	/len=4210	NIM 015571	He 27107	ND 056396
3504/04/	1 / CC O _ IVIP		NM_015571	Hs.27197	NP_056386
		retinoic acid			
	ì	induced 14 (RAI14),		}	
1		mRNA	1		
		/cds=(112,3054)	[
		/gb=NM_015577	1	1	
		/gi=13470085	Ì	1	
		/ug=Hs.15165		1	
miod1265	NM_015577	/len=4925	NM_015577	Hs.15165	NP_056392
miod1265	INM_015577	/len=4925	INM_015577	Hs.15165	NP_056392

- I iguie ot	Contid.				
fcrb3330	NM_015640	PAI-1 mRNA- binding protein (PAI- RBP1), mRNA /cds=(86,1249) /gb=NM_015640 /gi=7661625 /ug=Hs.165998 /len=2201	NM_015640	Hs.165998	NP_056455
miod5195	BC032345	DKFZP586D0824 protein, clone MGC:40527 IMAGE:5208411, mRNA, complete cds /cds=(65,1078) /gb=BC032345 /gi=21595443 /ug=Hs.128797 /len=1499	NM_015660	Hs.128797	NP_056475
ncrc2404	NM_015683	hypothetical protein CLONE24945 (CLONE24945), mRNA /cds=(144,1367) /gb=NM_015683 /gi=18373304 /ug=Hs.30882 /len=2518	NM_015683	Hs.30882	NP_056498
fcr5259	NM_015866	PR domain containing 2, with ZNF domain (PRDM2), transcript variant 2, mRNA	NM_012231;	Hs.26719	NP_056950
ncr5168	NM_015902	progestin induced protein (DD5), mRNA /cds=(34,8433) /gb=NM_015902 /gi=15147336 /ug=Hs.278428 /len=8838	NM_015902	Hs.278428	NP_056986
mioc2188	NM_015952	PTD013 protein (PTD013), mRNA /cds=(87,812) /gb=NM_015952 /gi=7706269 /ug=Hs.22679 /len=982	NM_015952	Hs.22679	NP_057036

r	J Conta.	Ta		r	· · · · · · · · · · · · · · · · · · ·
		Similar to			
1		lymphocyte			
		activation-			
		associated protein,			
		clone	1		
		IMAGE:3892557,			
		mRNA	İ		İ
fcrc6655	BC010867	(=AK001698.1)		Hs.272239	NP 057074
10100000	BC010007	(-AR001030.1)		115.272239	NF_057074
	1				
		CUO domoin CDDO			
		SH3-domain GRB2-			
		like endophilin B1			
		(SH3GLB1), mRNA			
		/cds=(82,1179)			
		/gb=NM_016009			
		/gi=21359904			
		/ug=Hs.136309			
miod5612	NM_016009	/len=1561	NM_016009	Hs.136309	NP_057093
		CGI-94 protein			
		(CGI-94), mRNA			
		/cds=(70,831)			
	1	/gb=NM_016037			
		/gi=7705808			
		/ug=Hs.111449			
seob4079	NM 016037	/len=1025	NM_016037	Hs.111449	NP 057121
		CGI-115 protein			
1		(CGI-115), mRNA			
		/cds=(35,814)			
		/gb=NM_016052			
		/gi=7705619			
		/ug=Hs.56043			
mich7750	NIM O16050	1 -	NIM 016050	Un E6042	ND 057436
miob7750	NM_016052	/len=1308	NM_016052	Hs.56043	NP_057136
1		mitochondrial			
1		ribosomal protein			
		S16 (MRPS16),			
		nuclear gene			
		encoding	ŀ		
		mitochondrial			
	1	protein, mRNA			
		/cds=(170,583)	i		
		/gb=NM_016065			
		/gi=16554612			
	ļ	/ug=Hs.180312	ļ		
miob2714	NM_016065	/len=704	NM 016065	Hs.180312	NP 057149
		PTD009 protein			
miob1746	NM 016146	(PTD009), mRNA	NM 016146	Hs.279901	NP_057230
	10 .0 170	10. 12000), mixid	10.0170	15.27 555 1	1.11 _007200

Figure 0	c Cont'd.				
	1	NDRG family			
		member 2			
		(NDRG2), mRNA			
		/cds=(97,1170)			
		/gb=NM 016250			
		/gi=10280619			
		/ug=Hs.243960			
fcrb6431	NIM 016350	/len=2024	NIM 046050	Un 242060	ND 057224
10100431	NM_016250_		NM_016250	Hs.243960	NP_057334
		WW domain			
		binding protein 11			
		(WBP11), mRNA			
		/cds=(162,2087)			
		/gb=NM_016312			
1		/gi=18375679			
		/ug=Hs.334811			
seoa2181	NM 016312	/len=2690	NM 016312	Hs.334811	NP 057396
	† - -	clone HQ0477			
		PRO0477p			
		(LOC51204),			
	}	mRNA			
		/cds=(201,1094)			1
		/gb=NM_016360			
	1	/gi=27545314			
		/ug=Hs.174134			
ncr8112	NM_016360	/len=1491	NM_016360	Hs.174134	NP_057444
	}	hypothetical protein			
		LOC51255			
		(LOC51255),			
	1	mRNA			
		/cds=(31,492)			
	1	/gb=NM_016494			
		/gi=24475978			
		/ug=Hs.11156			
ncrc0194	NM_016494	/len=601	NM 016494	Hs.11156	NP 057578
110100104	11111_010404	ubiquitin associated		1113.11100	141 _007070
		protein 1 (UBAP1),		:	
		mRNA			
	1				
	1	/cds=(236,1744)			
		/gb=NM_016525			
	1	/gi=22212941			
		/ug=Hs.75425	<u> </u>	l	
ncrc0095	NM_016525	/len=2757	NM_016525	Hs.75425	NP_057609
		hepatitis B virus x	}	}	
		associated protein			
		(HBXAP), mRNA			
		/cds=(1062,4631)			
		/gb=NM_016578			
		/gi=10835261			
1		/ug=Hs.20509	1		
seob6486	NM_016578	/len=5323	NM_016578	Hs.20509	NP_057662
		1	1	1	1

1 194100	c Conta.				
		chloride intracellular channel 5 (CLIC5), mRNA /cds=(298,1053) /gb=NM_016929 /gi=8393146 /ug=Hs.283021			
ncrc5232	NM_016929	/len=2380	NM_016929	Hs.283021	NP_058625
		hypothetical protein LOC55580 (LOC55580), mRNA /cds=(759,2987) /gb=NM_017571 /gi=8923837 /ug=Hs.254122			
mioc8531	NM_017571	/len=3109	NM_017571	Hs.254122	NP_060041
		transmembrane protein vezatin (VEZATIN), mRNA /cds=(177,1886) /gb=NM_017599 /gi=19923537 /ug=Hs.24135			
mioc5182	NM_017599	/len=3949	NM_017599	Hs.24135	NP_060069
		likely ortholog of mouse embryonic epithelial gene 1 (EEG1), mRNA /cds=(319,1794) /gb=NM_017611 /gi=18252046 /ug=Hs.274453	 NM_014096;		
fcrb8622	NM_017611	/len=2630	NM_017611	Hs.274453	NP_060081
mioc8117	AJ420591	mRNA full length insert cDNA clone EUROIMAGE 701679	_	Hs.10784	NP_060103
miod4437	NM 017661	hypothetical protein FLJ20086 (FLJ20086), mRNA /cds=(48,1313) /gb=NM_017661 /gi=8923096 /ug=Hs.46821 /len=3572	NM 017661	Hs.46821	NP 060131
	1:0 // 00 /	1		1oooz .	<u>,000,0, </u>

	J Conta.	chromosome 20	<u> </u>		1
miod0228	NM_017798	open reading frame 21 (C20orf21), mRNA /cds=(10,603) /gb=NM_017798 /gi=8923363 /ug=Hs.11747 /len=2429	NM_017798	Hs.11747	NP_060268
		7.01. 2.120	14.0017700	113.117-47	141_000200
		O-sialoglycoprotein endopeptidase (OSGEP), mRNA /cds=(130,1137) /gb=NM_017807 /gi=8923379 /ug=Hs.108894			
seoc0068	NM_017807	/len=1394	NM_017807	Hs.108894	NP_060277
seoa3758	NM_017822	hypothetical protein FLJ20436 (FLJ20436), mRNA /cds=(505,963) /gb=NM_017822 /gi=8923410 /ug=Hs.268189 /len=1901	NM_017822	Hs.268189	NP_060292
seob6883	NM_017837	hypothetical protein FLJ20477 (FLJ20477), mRNA /cds=(332,1813) /gb=NM_017837 /gi=21361770 /ug=Hs.26994 /len=2380	NM_017837	Hs.26994	NP_060307
hfcr5228	NM_017991	hypothetical protein FLJ10081 (FLJ10081), mRNA /cds=(437,2812) /gb=NM_017991 /gi=21361733 /ug=Hs.7871 /len=5249	NM_017991	Hs.7871	NP_060461

7 19410 00	Conta.	RNA-binding region (RNP1, RRM) containing 4 (RNPC4), mRNA /cds=(187,1461) /gb=NM_018107 /gi=21361701			
ncrc3908	NM_018107	/ug=Hs.4997 /len=2442	NM_018107	Hs.4997	NP_060577
		hypothetical protein FLJ10618 (FLJ10618), mRNA /cds=(210,1142) /gb=NM_018155 /gi=8922550 /ug=Hs.42484			
ncr1646	NM_018155	/len=2001	NM_018155	Hs.42484	NP_060625
fcrb4760	NIM 049304	cytoskeleton associated protein 2 (CKAP2), mRNA /cds=(97,2145) /gb=NM_018204 /gi=19923520 /ug=Hs.24641	NIM 049204	Hs.24641	ND 000074
ICID4760	NM_018204	/len=3626 hypothetical protein FLJ11301 (FLJ11301), mRNA /cds=(21,1997) /gb=NM_018385 /gi=14149719 /ug=Hs.301724	NM_018204	INS.24041	NP_060674
fcrb8625	NM_018385	/len=3290 hypothetical protein, clone 2746033	NM_018385	Hs.301724	NP_060855
		(HSA272196), mRNA /cds=(39,593) /gb=NM_018405 /gi=24475639 /ug=Hs.8179			
miob8012	NM_018405	/len=861	NM_018405	Hs.8179	NP_060875

1 19410 01	Conta.	<u></u>	· · · · · · · · · · · · · · · · · · ·		
		TPA regulated			
		locus (TPARL),			
		mRNA			
		/cds=(195,1169)			
		/gb=NM_018475			
	İ	/gi=8923860			
		/ug=Hs.236510			
b0463	NINA 040475	1 •	NINA 040475	11- 000540	ND 000045
ncrb0163	NM_018475	/len=1913	NM_018475	Hs.236510	NP_060945
		hypothetical protein			
		ASH1 (ASH1),			
		mRNA			
		/cds=(310,9219)		ĺ	
		/gb=NM_018489			
		/gi=8922080	i		
		/ug=Hs.102652			
seob6675	NM_018489	/len=9926	NM_018489	Hs.102652	NP 060959
		mitochondrial	0.0.00		000000
		solute carrier			
		protein (MSCP),	NM_016612;		
forb1000	NIM 040570	l, , , , , , , , , , , , , , , , , , ,		LIA 000740	ND 004040
fcrb1922	NM_018579	mRNA	NM_018579	Hs.283716	NP_061049
		ahaamaaama 11			
		chromosome 14			
		open reading frame	ļ		
		116 (C14orf116),			
		mRNA			
		/cds=(270,458)			
		/gb=NM_018589			
		/gi=20127573			
		/ug=Hs.60548			
miob7134	NM 018589	/len=1654	NM_018589	Hs.60548	NP_061059
		H2A histone family,			
		member Y2			
		(H2AFY2), mRNA	1		
		1.			
		/cds=(214,1332)			
		/gb=NM_018649			
		/gi=8923919			
		/ug=Hs.92023			
fcrb9565	NM_018649	/len=1932	NM_018649	Hs.92023	NP_061119
		ER-resident protein			
		ERdj5 (ERdj5),			
		mRNA			
		/cds=(416,2797)			
		/gb=NM_018981			
		/gi=24308126			
		/ug=Hs.1098			
miob4822	NM_018981	/len=4193	NM 018981	Hs.1098	NP 061854
111004022	1 9801 0 10801	Men-4 193	10801 NINI	1113.1030	[NF_U0 1004

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		hypothetical protein FLJ20152 (FLJ20152), mRNA /cds=(217,1287) /gb=NM_019000 /gi=21361616 /ug=Hs.82273			
seob8261	NM_019000	/len=2989	NM_019000	Hs.82273	NP_061873
		HIF-1 responsive RTP801 (RTP801), mRNA /cds=(198,896) /gb=NM_019058 /gi=9506686 /ug=Hs.111244			
ncrb3417	NM_019058	/len=1760	NM 019058	Hs.111244	NP 061931
		clone MGC:13446 IMAGE:4275731, mRNA, complete			
ncr8171	BC009777	cds SLC2A4 regulator	NM_019071	Hs.143198	NP_061944
mioc8220	NM_020062	(SLC2A4RG), mRNA /cds=(1,1164) /gb=NM_020062 /gi=13236503 /ug=Hs.170088 /len=1727	NM_020062	Hs.170088	NP_064446
fcrb9292	NM_020187	DC12 protein (DC12), mRNA	NM 020187	Hs.166096	NP 064572
		DC13 protein (DC13), mRNA /cds=(176,415) /gb=NM_020188 /gi=9910183 /ug=Hs.6879	_		
mioc7440	NM_020188	/len=716	NM_020188	Hs.6879	NP_064573
	NIA 000007	cyclin L ania-6a (LOC57018), mRNA /cds=(55,1635) /gb=NM_020307 /gi=9945319 /ug=Hs.4859	ANA 000007	4050	ND 004700
ncr3686	NM_020307	/len=2076	NM_020307	Hs.4859	NP_064703

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0000F267	NIM 020422	hypothetical protein DKFZp564F013 (DKFZP564F013), mRNA /cds=(107,2194) /gb=NM_020432 /gi=24308192 /ug=Hs.128653 /len=4572	NIM 020422	No. 420052	ND 005405
seoc5267	NM_020432		NM_020432	Hs.128653	NP_065165
forth 4000	NM 020470	Yip1p-interacting factor (YIF1P), mRNA /cds=(116,997) /gb=NM_020470 /gi=9994168 /ug=Hs.406422	NIM 000470	II. 400 400	ND coroon
fcrb4226	NM_020470	/len=1078	NM_020470	Hs.406422	NP_065203
mioc3413	NM_020648	twisted gastrulation 1 (Drosophila) (TWSG1), mRNA /cds=(106,777) /gb=NM_020648 /gi=21314788 /ug=Hs.247302 /len=3693	NM_020648	Hs.247302	NP_065699
miob8396	AK022459	cDNA FLJ12397 fis, clone MAMMA1002769, weakly similar to cell cycle progression restoration 8 protein (CPR8) mRNA	NM_004748	Hs.82506	NP_065790
hfcr3404	NM_020873	KIAA1497 protein (KIAA1497), mRNA /cds=(10,1305) /gb=NM_020873 /gi=23308734 /ug=Hs.126085 /len=2728	NM_020873	Hs.126085	NP_065924

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Figure 60	Conta.				
		Similar to RIKEN			
		cDNA 2310026P19			
		gene, clone			
		MGC:49935			
		IMAGE:6175382,			ļ .
		mRNA, complete			
		cds			
		/cds=(288,3329)			
		/gb=BC043352			
		/gi=27694113			
		/ug=Hs.35096			
mioa1383	BC043352	/len=5900		Hs.35096	NP 065950
		amylase, alpha 2B;	,		
		pancreatic			
		(AMY2B), mRNA			
		/cds=(365,1900)			
		/gb=NM_020978			
		/gi=20070311			!
		/ug=Hs.335493			ļ
miob9734	NM 020978	/len=1963	NM 020978	Hs.335493	NP 066188
		adenylate cyclase 6			
		(ADCY6), transcript			
		variant 1, mRNA			
		/cds=(695,4201)			
		/gb=NM_015270			
		/gi=10947059			
		/ug=Hs.12373	NM 015270;		
fcrb7533	NM_015270	/len=6594	NM 020983	Hs.12373	NP 066193
10.5.000	0 10210	7.6.1 666 1	020000		
		polypyrimidine tract			
		binding protein 2			
		(PTBP2), mRNA			
		/cds=(53,1648)			
		/gb=NM_021190		ŀ	
		/gi=10863996			
		/ug=Hs.34956			
seoc6689	NM_021190	/len=3054	NM 021190	Hs.34956	NP 067013
-	021100	kelch-like protein	021100	1.0.0 1000	
		C3IP1 (C3IP1),			
		mRNA			
		/cds=(201,1907)			
		/gb=NM_021633			
		/gi=21361889	Ì		
		/ug=Hs.3826			
mioa8747	NM_021633	/len=3338	NM_021633	Hs.3826	NP_067646
	1	1		1	1

- I Iguic o	Conta.	· · · · · · · · · · · · · · · · · · ·			
		supervillin (SVIL),			
		transcript variant 2,			
		mRNA			
		/cds=(754,7398)			
		/gb=NM_021738			
l		/gi=11496981			
		/ug=Hs.154567	NM_003174;		
fcrb1503	NM_021738	/len=8300	NM_021738	Hs.154567	NP_068506
10121000	1111_021100	MDS024 protein	11111_021700	110.104007	141 _000000
		(MDS024), mRNA			
		/cds=(65,838)			
		/gb=NM_021820			
		/gi=11141892			
		/ug=Hs.425659			
ncrb6640	NM_021820	/len=2103	NM_021820	Hs.425659	NP_068592
	ļ	hypothetical protein			
		FLJ13149			
	ĺ	(FLJ13149), mRNA			
		/cds=(291,2585)			
	 	/gb=NM_021826			
		/gi=11141902			
		/ug=Hs.112188			
hfcr2229	NM 021826	/len=2836	NM_021826	Hs.112188	NP 068598
		hypothetical protein			
		FLJ13188			
		(FLJ13188), mRNA			
		/cds=(247,948)			
				1	
		/gb=NM_022063			
		/gi=11545770			
		/ug=Hs.11859			
mioc2662	NM_022063	/len=2746	NM_022063	Hs.11859	NP_071346
		cDNA: FLJ23144			
		fis, clone			
mioa8273	AK026797	LNG09262	NM_022068	Hs.293907	NP_071351
		transcription factor			
		B2, mitochondrial			
		(TFB2M), mRNA			
		/cds=(125,1315)			
		/gb=NM_022366			
		/gi=11641288			
		/ug=Hs.7395			
fcrc6461	NM_022366	/len=1803	NM 022366	Hs.7395	NP_071761
		FAD104 (FAD104),			
	l	mRNA			
		/cds=(58,3672)			
		/gb=NM_022763			
		* -			
		/gi=27477058			
mioc9494	NIM COOZCO	/ug=Hs.299883	NINA COOZOO	112 200000	ND 070000
mioc8481	NM_022763	/len=6894	NM_022763	Hs.299883	NP_073600

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	EPS8-related	I	1	1
NM_022772	protein 2 (EPS8R2), mRNA /cds=(273,2420) /gb=NM_022772 /gi=21264615 /ug=Hs.55016 /len=3181	NM_022772	Hs.55016	NP_073609
NM_022780	hypothetical protein FLJ13910 (FLJ13910), mRNA /cds=(99,1274) /gb=NM_022780 /gi=19923839 /ug=Hs.75277 /len=3239	NM_022780	Hs.75277	NP_073617
NM_022802	C-terminal binding protein 2 (CTBP2), transcript variant 2, mRNA /cds=(137,3094) /gb=NM_022802 /gi=12746589 /ug=Hs.171391 /len=3780	NM_001329; NM_022802	Hs.171391	NP_073713
NM_023018	NAD kinase (FLJ13052), mRNA /cds=(206,1978) /gb=NM_023018 /gi=20070325 /ug=Hs.220324 /len=3676	NM_023018	Hs.220324	NP_075394
AK025702	cDNA: FLJ22049 fis, clone HEP09444. /gb=AK025702 /gi=10438304 /ug=Hs.423737 /len=2435		Hs.423737	NP_075447
NIM 023020	family A (RFXANK- like), 2 (ANKRA2), mRNA /cds=(648,1589) /gb=NM_023039 /gi=21362082 /ug=Hs.239154	NIM 022020	□ c 220454	NP 075526
	NM_022780 NM_022802	/gb=NM_022772 /gi=21264615 /ug=Hs.55016 NM_022772 /len=3181 hypothetical protein FLJ13910 (FLJ13910), mRNA /cds=(99,1274) /gb=NM_022780 /gi=19923839 /ug=Hs.75277 NM_022780 /len=3239 C-terminal binding protein 2 (CTBP2), transcript variant 2, mRNA /cds=(137,3094) /gb=NM_022802 /gi=12746589 /ug=Hs.171391 NM_022802 /len=3780 NAD kinase (FLJ13052), mRNA /cds=(206,1978) /gb=NM_023018 /gi=20070325 /ug=Hs.220324 NM_023018 /len=3676 cDNA: FLJ22049 fis, clone HEP09444. /gb=AK025702 /gi=10438304 /ug=Hs.423737 /len=2435 ankyrin repeat, family A (RFXANK-like), 2 (ANKRA2), mRNA /cds=(648,1589) /gb=NM_023039 /gi=21362082 /ug=Hs.239154	/gb=NM_022772 /gi=21264615 /ug=Hs.55016 NM_022772 /len=3181 hypothetical protein FLJ13910 (FLJ13910), mRNA /cds=(99,1274) /gb=NM_022780 /gi=19923839 /ug=Hs.75277 NM_022780 /len=3239 C-terminal binding protein 2 (CTBP2), transcript variant 2, mRNA /cds=(137,3094) /gb=NM_022802 /gi=12746589 /ug=Hs.171391 NM_022802 /len=3780 NM_022802 /len=3780 NM_022802 NAD kinase (FLJ13052), mRNA /cds=(206,1978) /gb=NM_023018 /gi=20070325 /ug=Hs.220324 NM_023018 /len=3676 CDNA: FLJ22049 fis, clone HEP09444. /gb=AK025702 /gi=10438304 /ug=Hs.423737 AK025702 /len=2435 ankyrin repeat, family A (RFXANK- like), 2 (ANKRA2), mRNA /cds=(648,1589) /gb=NM_023039 /gi=21362082 /ug=Hs.239154	/gb=NM_022772 /gi=21264615 /ug=Hs.55016 NM_022772 /len=3181 hypothetical protein FLJ13910 (FLJ13910), mRNA /cds=(99,1274) /gb=NM_022780 /gi=19923839 /ug=Hs.75277 NM_022780 /len=3239 C-terminal binding protein 2 (CTBP2), transcript variant 2, mRNA /cds=(137,3094) /gb=NM_022802 /gi=12746589 /ug=Hs.171391 NM_022802 /len=3780 NM_022802 NM_022802 NM_023018 /gi=20070325 /ug=Hs.220324 NM_023018 /len=3676 cDNA: FLJ22049 fis, clone HEP09444 /gb=AK025702 /gi=10438304 /ug=Hs.423737 AK025702 /len=2435 ankyrin repeat, family A (RFXANK- like), 2 (ANKRA2), mRNA /cds=(648,1589) /gb=NM_023039 /gi=21362082 /ug=Hs.239154

1 iguie o	c Cont'd.	,		,	
		hypothetical protein MGC3077 (MGC3077), mRNA /cds=(137,703) /gb=NM_024051 /gi=13129017 /ug=Hs.433404			
ncrb4248	NM 024051	/len=1195	NM 024051	Hs.433404	NP 076956
	_	AHNAK			
		nucleoprotein			
mioc1019	M80902	mRNA, 5' end		Hs.165215	NP_076965
		likely ortholog of mouse phosducin- like 2 (PDCL2), mRNA /cds=(101,820) /gb=NM_024065 /gi=13129043 /ug=Hs.94576			
ncr8827	NM_024065	/len=1044	NM_024065	Hs.94576	NP_076970
miod6210	BE966653	601661342R1 NIH_MGC_72 cDNA clone IMAGE:3915994 3', mRNA sequence /clone=IMAGE:391 5994 /clone_end=3' /gb=BE966653 /gi=11772295 /ug=Hs.330958 /len=703 MEP50 protein (MEP50), mRNA /cds=(40,1068) /gb=NM_024102		Hs.330958	NP_076974
		/gb=NM_024102 /gi=20127622			
		/ug=Hs.11039			
fcrb6635	NM_024102	/len=2428	NM_024102	Hs.11039	NP_077007
ncr1168	NM_024120	chromosome 20 open reading frame 7 (C20orf7), mRNA /cds=(31,507) /gb=NM_024120 /gi=13129143 /ug=Hs.44296 /len=1715	NM_024120	Hs.44296	NP_077025

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1 iguic o	Conta.				
mioc7764	NM_024571	hypothetical protein FLJ22940 (FLJ22940), mRNA /cds=(984,1382) /gb=NM_024571 /gi=13443017 /ug=Hs.15277 /len=1704	NM_024571	Hs.15277	NP_078847
seob8853	NM_024941	hypothetical protein FLJ13611 (FLJ13611), mRNA /cds=(207,1271) /gb=NM_024941 /gi=13376418 /ug=Hs.282958 /len=2726	NM_024941	Hs.282958	NP_079217
mioc5536	NM_025057	hypothetical protein FLJ23189 (FLJ23189), mRNA /cds=(60,746) /gb=NM_025057 /gi=13376590 /ug=Hs.287733 /len=2157	NM_025057	Hs.287733	NP_079333
fcrc1803	NM_030571	Nedd4 family interacting protein 1 (NDFIP1), mRNA /cds=(105,770) /gb=NM_030571 /gi=13386479 /ug=Hs.9788 /len=1837	NM_030571	Hs.9788	NP_085048
miod0110	BQ228526	AGENCOURT_759 1767 NIH_MGC_92 cDNA clone IMAGE:6067123 5', mRNA sequence /clone=IMAGE:606 7123 /clone_end=5' /gb=BQ228526 /gi=20409926 /ug=Hs.282204 /len=1263		Hs.282204	NP_110390

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Tigure oc	Cont'd.		,		
		intermediate			
		filament protein			1
		syncoilin			
		(SYNCOILIN),			
		ImRNA			
				·	
		/cds=(169,624)			
		/gb=NM_030786		1	
		/gi=13540560		1	
		/ug=Hs.348415		İ	
seob4775	NM_030786	/len=2114	NM 030786	Hs.348415	NP_110413
	_	sorting nexin 27		1	
seoc7016	NM 030918	(SNX27), mRNA	NM_030918	Hs.67619	NP 112180
36067010	14141_000010	hypothetical protein	14141_000010	113.07013	112100
		MGC12904			
		(MGC12904),		1	
		mRNA			
ļ		/cds=(196,951)			
		/gb=NM_031219			
1		/gi=13654293			
		/ug=Hs.7739			
forboons	NINA COACAC	/len=1143	NIM 024240	Ho 7720	ND 440406
fcrb8333	NM_031219	J	NM_031219	Hs.7739	NP_112496
		hypothetical protein		İ	1
		MGC13033			
		(MGC13033),			
		mRNA	1		
		/cds=(201,305)		1	
		/gb=NM_031447			
ļ		/gi=13899280			
		_			
	l	/ug=Hs.423808			
seoc2336	NM_031447	/len=1339	NM_031447	Hs.423808	NP_113635
		frizzled 8			
l		(Drosophila)			
		(FZD8), mRNA			
		/cds=(6,2090)			
		/gb=NM_031866			
		/gi=13994189	1		
1		1 -	· ·		
		/ug=Hs.302634			
miod5338	NM_031866	/len=3195	NM_031866	Hs.302634	NP_114072
		RAB34, member			
		RAS oncogene			
		family (RAB34),			
	1	mRNA "			
		/cds=(206,985)			
1		1 ' '	}		
		/gb=NM_031934			
1		/gi=21361998			
1		/ug=Hs.301853			
fcrb9169	NM_031934	/len=1340	NM_031934	Hs.301853	NP_114140

Figure 6	Conta.				
		poly(rC) binding			
		protein 2 (PCBP2),			
		transcript variant 1,			
		mRNA			
		/cds=(89,1189)			
		/gb=NM_005016			
		/gi=14141167			
		/ug=Hs.63525	NM_005016;		
seoc4416	NM 005016	/len=1362	NM_031989	Hs.63525	NP 114366
00001110	11111_000010	CDA02 protein	14141_00 1000	113.00020	1117300
		(CDA02), mRNA			
		/cds=(3,1832)			
		/gb=NM_032025			
		/gi=14042940			
		/ug=Hs.332404			1
seob0817	NIM 022025	/len=2179	NIM 022025	110 222404	ND 44444
26000017	NM_032025	1/16/1-21/9	NM_032025	Hs.332404	NP_114414
		hunothotical aretain			
ŀ		hypothetical protein			
		DKFZp434K1421			
		(DKFZP434K1421),			
		mRNA			
		/cds=(29,1705)			
		/gb=NM_032141			
		/gi=14149806			
		/ug=Hs.374609			
seoc6099	NM_032141	/len=2547	NM_032141	Hs.374609	NP_115517
		hypothetical protein			
		MGC4549			
		(MGC4549), mRNA			
		/cds=(29,280)			
		/gb=NM_032377			
		/gi=14150202			
		/ug=Hs.326422			
fcrb8430	NM_032377	/len=991	NM_032377	Hs.326422	NP 115753
			_		
1		eukaryotic			
		translation			
		elongation factor 1			
		delta (guanine			
		nucleotide			
		exchange protein)			
		(EEF1D), transcript			
Ì	Ì	variant 1, mRNA	Ì	Ì	
		/cds=(198,2141)			
		/gb=NM_032378			
		/gi=25453473			
		/ug=Hs.334798	NM_001960;		
fcrc6234	NM_032378	/len=2216	NM_032378	Hs.334798	NP_115754
110100204		MGH-22 10		13.554 <i> </i> 3 0	INF 110/04

	bromodomain adjacent to zinc			
	(BAZ1B), transcript			
	1			
	/gb=NM_023005			
	/gi=14670389 /ug=Hs.194688	NM_023005;		
NM_023005	/len=6079	NM_032408	Hs.194688	NP_115784
AB058707	partial cds	NM_032435	Hs.50883	NP_115811
	S6 (MRPS6),			
	mitochondrial			
	/gb=NM_032476			
	T			
NM_032476	/len=959	NM_032476	Hs.424751	NP_115865
	1			
	mRNA			
	1 ' '			
	/gi=27545312			
NM 032557	•	NM 032557	Hs 332841	NP 115946
1411_002007		1414_002007	113.002041	110040
	1			
	(MGC5370), mRNA			
	/gi=14249363			
NM 032739	1 •	NM 032739	Hs 332938	NP 116128
	hypothetical protein FLJ14600			
	(FLJ14600), mRNA			
	1			
	/gi=14249497			
NM_032810	/ug=Hs.100861 /len=2334	NM_032810	Hs.100861	NP 116199
	NM_032476 NM_032557	adjacent to zinc finger domain, 1B (BAZ1B), transcript variant 1, mRNA /cds=(353,4804) /gb=NM_023005 /gi=14670389 /ug=Hs.194688 NM_023005 /len=6079 mRNA for KIAA1804 protein, partial cds mitochondrial ribosomal protein S6 (MRPS6), nuclear gene encoding mitochondrial protein, mRNA /cds=(124,501) /gb=NM_032476 /gi=16554615 /ug=Hs.424751 NM_032476 /len=959 HP43.8KD protein (HP43.8KD), mRNA /cds=(507,3635) /gb=NM_032557 /gi=27545312 /ug=Hs.332841 NM_032557 /len=4684 hypothetical protein MGC5370 (MGC5370), mRNA /cds=(189,269) /gb=NM_032739 /gi=14249363 /ug=Hs.332938 NM_032739 /len=974 hypothetical protein FLJ14600 (FLJ14600), mRNA /cds=(309,764) /gb=NM_032810 /gi=14249497 /ug=Hs.100861	adjacent to zinc finger domain, 1B (BAZ1B), transcript variant 1, mRNA /cds=(353,4804) /gb=NM_023005 /gi=14670389 /ug=Hs.194688 NM_023005 /len=6079 MRNA for KIAA1804 protein, partial cds mitochondrial ribosomal protein S6 (MRPS6), nuclear gene encoding mitochondrial protein, mRNA /cds=(124,501) /gb=NM_032476 /gi=16554615 /ug=Hs.424751 NM_032476 /Hen=959 MM_032476 /Hen=959 MM_032476 /gi=27545312 /ug=Hs.332841 NM_032557 /hgi=27545312 /ug=Hs.332841 NM_032557 /hypothetical protein MGC5370 (MGC5370), mRNA /cds=(189,269) /gb=NM_032739 /gi=14249363 /ug=Hs.332938 NM_032739 /len=974 NM_032810 /gb=NM_032810 /gi=14249497 /ug=Hs.100861	adjacent to zinc finger domain, 1B (BAZ1B), transcript variant 1, mRNA /cds=(353,4804) /gb=NM_023005 /gi=14670389 /ug=Hs.194688 NM_032408 NM_032408 MRNA for KIAA1804 protein, partial cds mitochondrial ribosomal protein S6 (MRPS6), nuclear gene encoding mitochondrial protein, mRNA /cds=(124,501) /gb=NM_032476 /gi=16554615 /ug=Hs.424751 NM_032476 /len=959 HP43.8KD), mRNA /cds=(507,3635) /gb=NM_032557 /gi=27545312 /ug=Hs.332841 NM_032557 NM_032557 NM_032739 /len=4684 NM_032739 /len=974 NM_032739 NM_032739 NM_032739 /len=974 NM_032739 NM_032739 NM_032739 /len=974 NM_032810 /gj=14249497 /ug=Hs.100861

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I Iguie o	c Cont'd.				
		hypothetical protein FLJ14735 (FLJ14735), mRNA /cds=(7,1509) /gb=NM_032832 /gi=14249539 /ug=Hs.334762			
miob9054	NM_032832	/len=3260	NM_032832	Hs.334762	NP_116221
		SR rich protein (DKFZp564B0769), mRNA /cds=(33,2450) /gb=NM_032870 /gi=18699723 /ug=Hs.18368			
seoa8750	NM 032870	/len=2663	NM 032870	Hs.18368	NP 116259
		ZW10 interactor (ZWINT), transcript variant 2, mRNA /cds=(25,858) /gb=NM_032997 /gi=14602426 /ug=Hs.42650	NM_007057;		_
fcrb9354	NM_032997	/len=1851	NM_032997	Hs.42650	NP_127490
ncr7090	BC009336	clone MGC:16714 IMAGE:4128220, mRNA, complete cds	NM_033116	Hs.7200	NP_149107
miob3594	NM_033535	F-box and leucine- rich repeat protein 5 (FBXL5), transcript variant 2, mRNA /cds=(586,2283) /gb=NM_033535 /gi=21536439 /ug=Hs.5548 /len=3475	NM_012161; NM_033535	Hs.5548	NP 277077
		ribosomal protein L36 (RPL36), transcript variant 2, mRNA /cds=(153,470) /gb=NM_015414 /gi=16117793 /ug=Hs.433411	NM_015414;		
ncr0097	NM_015414	/len=545	NM_033643	Hs.433411	NP_378669

r igure oc	Cont'd.	, , , , , , , , , , , , , , , , , , , 			
		acidic repeat			
		containing (ACRC),			
		mRNA	ļ		
		/cds=(3,2078)			
		/gb=NM_052957			
		1 -			
		/gi=16445032			
		/ug=Hs.135167			
miob9875	NM_052957	/len=2692	NM_052957	Hs.135167	NP_443189
		hypothetical protein			
		MGC14327			
		(MGC14327),			
	ļ	mRNA			
		/cds=(225,635)			
		1 '			
		/gb=NM_053045			
		/gi=16596685			
ŀ		/ug=Hs.231029			
fcrb4340	NM_053045	/len=1576	NM_053045	Hs.231029	NP_444273
1		endothelial			
1		differentiation,			
		lysophosphatidic			
		acid G-protein-			
		1			
		coupled receptor, 2			
		(EDG2), transcript			
		variant 2, mRNA			
		/cds=(394,1488)			
		/gb=NM_057159			•
		/gi=16950637		}	
		/ug=Hs.75794	NM_001401;		
seoc1791	NM 057159	/len=2732	NM_057159	Hs.75794	NP 476500
36001731	14101_037 138	<u> </u>	14141_037 139	П5.737 34	NF_470000
		protein tyrosine			
		phosphatase type	!		
		IVA, member 2			
		(PTP4A2),			
		transcript variant 1,			
		mRNA			
		/cds=(1011,1514)			
		/gb=NM_003479			
		/gi=18104974	NM_003479;		
		_			
	NINA 600 :==	/ug=Hs.82911	NM_080391;		
ncr8413	NM_003479	/len=3925	NM_080392	Hs.82911	NP_536317
		synaptotagmin-like			
	ļ	4 (granuphilin-a)			
		(SYTL4), mRNA			
		/cds=(333,2348)			
		/gb=NM_080737			
		/gi=18152766			
		1 -		į	
	NINA 000707	/ug=Hs.247525			
mioc1784	NM_080737	/len=3914	NM_080737	Hs.247525	NP_542775

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Figure 6	c Cont'd.				
		oxysterol binding			
		protein-like 1A			
		(OSBPL1A),			
		transcript variant			
		OSBPL1B, mRNA			
		/cds=(175,3027)			1
		/gb=NM_080597			Ì
		/gi=19718740	NM_018030;		
		•	NM 080597;		
		/ug=Hs.252716		050740	
seoa5382	NM_080597	/len=4165	NM_133268	Hs.252716	NP_579802
		chromosome 6			
		open reading frame			
		33 (C6orf33),			
		mRNA			
		/cds=(165,1229)			
		/gb=NM_133367			1
		/gi=19115959			
		/ug=Hs.239388			
fcrb3518	NM_133367	/len=4650	NM 133367	Hs.239388	NP 588608
1.5.255.6	1	SOCS box-		1	
		containing WD			
		•			
		protein SWiP-1			
		(WSB1), transcript			
		variant 3, mRNA		ļ	
		/cds=(317,1051)			
		/gb=NM_134264			
		1 * -	NINA 045000:		1
		/gi=20143909	NM_015626;		,
		/ug=Hs.187991	NM_134264;		
fcr4477	NM_134264	/len=4243	NM_134265	Hs.187991	NP_599027
		hypothetical protein			
		BC018147	İ		
		(LOC123169),			
		1.			
		mRNA			
		/cds=(29,2029)			
		/gb=NM_138792			
		/gi=20270336			
	1	/ug=Hs.296420			
C0000E27	NIM 120702	/len=2174	NM 138792	Hs.296420	NP 620147
seoa9537	NM_138792		14W_130/32	113.430440	INF_020141
		CD151 antigen	1		
		(CD151), transcript	1		
		variant 1, mRNA	1		
		/cds=(130,891)			
		/gb=NM_004357	1		
}	1	1 * =	}	}	}
		/gi=21237747			
	1	/ug=Hs.75564	NM_004357;		
fcrb8994	NM_004357	/len=1552	NM_139030	Hs.75564	NP_620599
Ì		cDNA: FLJ22554	1		
fcrb5629	AK026207	fis, clone HSI01092	[Hs.93842	NP_631903
10100023	MINUZUZUI	Tilo, Giorie Froit 1032	L	1113.00072	111 _001300

Cont'd.		_		
	cDNA FLJ37791			
	fis, clone			
	BRHIP3000131.			
	/gb=AK095110		1	
	•			
	•			
AK095110	. •	NM 144628	Hs 350534	NP_653229
7 11 10 00 1 10		1111020	110.000001	141 _000220
	i e			
	1'			
	1 ' '			
	_			
	1 *			
NINA 144701	•	NINA 144701	Un 142602	ND 652222
144721	1	NIVI_144721	HS. 143092	NP_653322
	. •			
	1'			
	1			
	, ,			
	· ' '			
	_			
	•			
	_			
NM_003188	/len=2912	NM_145333	Hs.7510	NP_663306
	_Strait15106_FL30			
AJ295983	4		Hs.292653	NP_689526
	FLJ33282			
	(FLJ33282), mRNA			
	/cds=(225,1523)			
	/gb=NM_152388			
	/gi=22748830			
	/ug=Hs.346509			
NM_152388	/len=2078	NM_152388	Hs.346509	NP_689601
	hypothetical protein]
	FLJ35779			
	(FLJ35779), mRNA			
	1,			
	1 -			
	_			
	1 T			
NM_152408	/len=1698	NM_152408	Hs.432726	NP_689621
	NM_144721 NM_003188 AJ295983 NM_152388	CDNA FLJ37791 fis, clone BRHIP3000131. /gb=AK095110 /gi=21754304 /ug=Hs.350534 /len=3820 hypothetical protein MGC30052 (MGC30052), mRNA /cds=(35,703) /gb=NM_144721 /gi=21389506 /ug=Hs.143692 /len=2260 mitogen-activated protein kinase kinase r / (MAP3K7), transcript variant A, mRNA /cds=(306,2045) /gb=NM_003188 /gi=21735560 /ug=Hs.7510 /len=2912 mRNA for hypothetical protein (ORF1), clone Telethon(Italy_B41)	CDNA FLJ37791 fis, clone BRHIP3000131. /gb=AK095110 /gi=21754304 /ug=Hs.350534 AK095110 /len=3820 NM_144628 hypothetical protein MGC30052 (MGC30052), mRNA /cds=(35,703) /gb=NM_144721 /gi=21389506 /ug=Hs.143692 NM_144721 /gi=2160 mitogen-activated protein kinase kinase kinase kinase kinase r (MAP3K7), transcript variant A, mRNA /cds=(306,2045) /gb=NM_003188 yi=21735560 yig=Hs.7510 yig=H	CDNA FLJ37791 fis, clone BRHIP3000131. /gb=AK095110 /gi=21754304 /ug=Hs.350534 AK095110 I/en=3820 I/en=3820 I/en=3820 I/en=3820 I/en=3820 I/en=3820 I/en=3820 I/en=3820 I/en=3820 I/en=3820 I/en=3820 I/en=263 I/gb=NM_144721 /gi=21389506 /ug=Hs.143692 I/en=2260 I/en=2260 I/en=2260 I/en=2260 I/en=2260 I/en=2260 I/en=2260 I/en=210 I/en=260 I/en=210 I/en=260 I/en=210 I/en=260 I/en=2

1 igure oc	Conta.				
seob1646	NM_152520	hypothetical protein FLJ25270 (FLJ25270), mRNA /cds=(244,1353) /gb=NM_152520 /gi=22749086 /ug=Hs.6295 /len=2493	NM_152520	Hs.6295	NP 689733
fcrb2722	NM 012425	Ras suppressor protein 1 (RSU1), mRNA /cds=(70,903) /gb=NM_012425 /gi=10800408 /ug=Hs.75551 /len=1436	NM 012425	Hs.75551	NP 689937
fcrb9649	NM_153649	tropomyosin 3 (TPM3), mRNA /cds=(52,798) /gb=NM_153649 /gi=24119202 /ug=Hs.85844 /len=2089	NM_152263; NM_153649	Hs.85844	NP_705935
seoc6266	 NM_138962	musashi 2 (Drosophila) (MSI2), transcript variant 1, mRNA	NM_138962; NM_170721	Hs.103512	NP_733839
miod7470	NM_172070	similar to F10G7.10.p (KIAA2024), mRNA /cds=(343,1374) /gb=NM_172070 /gi=25453393 /ug=Hs.46826 /len=3703	NM_172070	Hs.46826	NP_742067
fcrb9184	NM_172239	exonuclease GOR (GOR), mRNA /cds=(628,1584) /gb=NM_172239 /gi=26665874 /ug=Hs.373854 /len=6609	 NM_172239	Hs.373854	NP_758439

		sperm associated			
mioc3936	NM 003971	antigen 9 (SPAG9), transcript variant 1, mRNA /cds=(79,4002) /gb=NM_003971 /gi=27436919 /ug=Hs.129872 /len=4663	NM_003971; NM_172345	Hs.129872	NP 758853
1111003330	14141_003371	Bardet-Biedl	14141_172040	115.129012	INF_/30033
miod0441	NM_176824	syndrome 7 (BBS7), transcript variant 1, mRNA	NM_018190; NM_176824		NP_789794
		clone MGC:16435 IMAGE:3946253, mRNA, complete cds /cds=(137,1471) /gb=BC013374 /gi=15426525 /ug=Hs.179661			
fcr0485	BC013374	/len=2519	NM_178014	Hs.179661	NP 821133
seob7765	AK023762	cDNA FLJ13700 fis, clone PLACE2000216, highly similar to SPECTRIN BETA CHAIN, BRAIN	NM_003128; NM_178313	Hs.107164	NP_842565
forth 422.4	NIM 004052	eukaryotic translation initiation factor 4 gamma, 1 (EIF4G1), mRNA /cds=(369,4559) /gb=NM_004953 /gi=4826709 /ug=Hs.433750	NIM 004052	No. 422750	ND 999555
fcrb4334	NM_004953	/len=5018	NM_004953	Hs.433750	NP_886553
ncrc5310	NM 018682	myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax Drosophila) (MLL5), mRNA /cds=(202,5778) /gb=NM_018682 /gi=23503326 /ug=Hs.333300 /len=6543		Hs.333300	NP 891847

1 iguie o	c Cont'd.				
		mRNA; cDNA DKFZp686J19116 (from clone DKFZp686J19116) /gb=AL833458 /gi=21734100			
miod3546	AL833458	/ug=Hs.428760 /len=3297		Hs.428760	NP_037387
ncrb4962	U55184	G protein Golf alpha gene, exon 12 and complete cds	NM_002071		NP_002062
fcrb5966	U18270	thymopoietin (TMPO) gene, exons 4 and 5, and complete cds for thymopoietin alpha	NM_003276		NP_003267
seob6525	NM_131105	Danio rerio alpha- tropomyosin (tpma), mRNA	NM_131105	Dr.20815	NP_571180
mioa3679	NM_138713	nuclear factor of activated T-cells 5, tonicity-responsive (NFAT5), transcript variant 2, mRNA	NM_006599; NM_138713; NM_138714; NM_173214; NM_173215		NP_006590; NP_619727; NP_619728; NP_775321; NP_775322
seoa0491	J00123	preproenkephalin precursor (PEN) gene, exon 3 and complete cds	NM_006211		NP_006202
seob4068	AB030001	gene for SGRF, complete cds	NM_016584		NP_057668
seoc0951	NM_033071	spectrin repeat containing, nuclear envelope 1 (SYNE1), transcript variant longest, mRNA	NM_015293; NM_033071; NM_133650		NP_056108; NP_149062; NP_598411
seob9302	NM_025199	hypothetical protein FLJ20886 (FLJ20886), mRNA mRNA; cDNA	NM_025199	Hs.241558	NP_079475
seoc6222	AL832582	DKFZp451G0416 (from clone DKFZp451G0416)	NM_015878; NM_148174		NP_056962; NP_680479
seoc7548	AY207372	cyclin I (CCNI) gene, complete cds			AAO13492

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		Danio rerio troponin	 	
		mRNA, complete		
seob1128	AF539738	cds		AAN31755

	FIGURE 6d: O	A stage specific			
	markers for se				
Clone	Genbank	Description	RefSeq	UniCono	D. 84
name	Genbank	Description collagen, type I,	KeiSeq	UniGene	Rep_prot
		alpha 1 (COL1A1),			
		mRNA	:		
		/cds=(120,4514)			
		/gb=NM_000088			
		/gi=14719826			
		/ug=Hs.172928			
ncrb8285	NM_000088	/len=5921	NM_000088	Hs.172928	NP_000079
		ferritin, light			
		polypeptide (FTL),			
		mRNA			
		/cds=(189,716) /gb=NM 000146			
		/gi=20149497			
		/ug=Hs.430150			
ncrc2319	NM 000146	/len=878	NM_000146	Hs.430150	NP 000137
				1	
		GTP cyclohydrolase			
		1 (dopa-responsive			
		dystonia) (GCH1),			
		mRNA			
		/cds=(149,901)			:
		/gb=NM_000161 /gi=4503948			
		/ug=Hs.86724			
mioc4119	NM 000161	/len=2921	NM 000161	Hs.86724	NP 000152
		glucose phosphate			
		isomerase (GPI),			
		mRNA			
		/cds=(104,1780)			
		/gb=NM_000175			
		/gi=18201904			
fcrc1965	NM 000175	/ug=Hs.406458	NIM 000475	115 406450	ND 000466
10101900	INIVI_000175	/len=2075 lipoprotein lipase	NM_000175	Hs.406458	NP_000166
		(LPL), mRNA			
		/cds=(175,1602)			
		/gb=NM_000237			
		/gi=4557726			
	1	/ug=Hs.180878			
mioa9147	NM_000237	/len=3549	NM_000237	Hs.180878	NP_000228

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Figure 6	d Cont'd.				
		phosphoglycerate			
		kinase 1 (PGK1),			
		mRNA			
		/cds=(70,1323)			
		/gb=NM_000291	İ		
		/gi=22095338			
				ĺ	
10750		/ug=Hs.78771		l	l <u>-</u>
seob2750	NM_000291	/len=2338	NM_000291	Hs.78771	NP_000282
		thrombomodulin			
		(THBD), mRNA			
		/cds=(542,2269)			
		/gb=NM_000361			
		/gi=4507482			
		/ug=Hs.2030			
mioa0218	NM_000361	/len=4050	NM 000361	Hs.2030	NP 000352
		xeroderma			
		pigmentosum,			
		complementation			
		group A (XPA),			
		ImRNA			
		/cds=(27,848)			
		/gb=NM_000380			
		/gi=4507936			
		/ug=Hs.192803			
ncrb7675	NM_000380	/len=1377	NM_000380	Hs.192803	NP_000371
		bleomycin			
	İ	hydrolase (BLMH),			
		mRNA			
		/cds=(79,1446)			
		/gb=NM_000386			
]		/gi=4557366			
}		/ug=Hs.78943			
fcr7059	NM_000386	/len=1932	NM_000386	Hs.78943	NP 000377
1017000	14141_000000	gonadotropin-	14141_000300	115.70343	NF_000377
		releasing hormone			
		receptor (GNRHR),			
		mRNA			
		/cds=(1749,2735)			
		/gb=NM_000406			
		/gi=4504058			
		/ug=Hs.73064			
seoc0394	NM_000406	/len=2735	NM_000406	Hs.73064	NP_000397
		hemoglobin, alpha 2			
		(HBA2), mRNA			
		/cds=(38,466)			
		/gb=NM_000517			
		/gi=14043068			
		/ug=Hs.347939			
fcrb2704	NM_000517	/len=575	NM 000517	Hs.347939	NP_000508
.3.02.0	<u></u>	1	. 1.11_000017	1.10.077.000	[11]

Figure o	d Cont'd.				
		insulin-like growth			
		factor binding			
		protein 3 (IGFBP3),			
		mRNA			
		/cds=(88,963)			
		/gb=NM_000598			
		/gi=19923110			
		/ug=Hs.77326			
fcr2546	NM_000598	/len=2506	NM 000598	Hs.77326	NP 000589
1012010	11111_000000	B-cell		110.77 020	111 _000000
		CLL/lymphoma 2			
1					
		(BCL2), nuclear			
		gene encoding			
		mitochondrial			
		protein, transcript			
		variant alpha,			
		mRNA			
		/cds=(32,751)		:	
		/gb=NM_000633			
		/gi=4557354			
		/ug=Hs.79241	NM_000633;		
fcrb3205	NM_000633	/len=6030	NM_000657	Hs.79241	NP_000648
		ATPase, Na /K			
1		transporting, alpha			
		1 polypeptide			
		(ATP1A1), mRNA			
		/cds=(262,3333)			
		/gb=NM_000701			
		/gi=21361180			
		/ug=Hs.76549			
fcrb9371	NM 000701	/len=3680	NM 000701	Hs.76549	NP 000692
	Break .	cytochrome P450,			
		family 51 (CYP51),			
		mRNA			
		/cds=(332,1861)]
		/gb=NM_000786			1
		/gi=13929427			
		/ug=Hs.226213			
fcrc3704	NM 000786	/len=3381	NM_000786	Hs.226213	NP_000777
	<u> </u>				
		monoamine oxidase			
		B (MAOB), nuclear			
İ		gene encoding			
Ì	ì	10	}	}	}
		mitochondrial			
1	1	protein, mRNA			
		/cds=(78,1640)			
	1	/gb=NM_000898			
		/gi=4505092			
		/ug=Hs.82163		ŀ	
nor5710	NIM OOOOO	/len=2491	NIM ODDODO	Uc 92162	ND 00000
ncr5719	NM_000898	/ICII-2491	NM_000898	Hs.82163	NP_000889

i iguie o	d Cont'd.				
		ribosomal protein			
		L6 (RPL6), mRNA			
		/cds=(32,898)			
		/gb=NM_000970			
		/gi=16753226			
		/ug=Hs.409045			
ncrc3544	NM_000970	/len=950	NM_000970	Hs.409045	NP 000961
	<u> </u>	ribosomal protein		†	
		L6 (RPL6), mRNA			
		/cds=(32,898)			
		/gb=NM_000970			
		/gi=16753226			
		/ug=Hs.409045			
seob7309	NM 000970	/len=950	NM_000970	Hs.409045	NP 000961
		ribosomal protein			
		L7 (RPL7), mRNA			
		/cds=(22,768)			
		/gb=NM_000971			
		/gi=15431300			
		/ug=Hs.153		1	
mioa0607	NM 000971	/len=838	NM_000971	Hs.153	NP 000962
1111000007	14101_00007 1	ribosomal protein	14141_000071	113.100	141 _000302
		L12 (RPL12),			
		mRNA			
		/cds=(89,586)		•	
		/gb=NM_000976			
		/gi=15431291			
	ł	/ug=Hs.405042			
ncrc5230	NM_000976	/len=632	NM 000976	Hs.405042	NP 000967
110100200	14141_000970	ribosomal protein	14141_000970	113.403042	145_000901
		L19 (RPL19),			
		mRNA			
		/cds=(29,619)			
		/gb=NM_000981			
		/gi=17158042			
		/ug=Hs.426977			
seoa7605	NM 000981	/len=698	NM 000981	Hs.426977	NP 000972
36047003	14141_000301	ribosomal protein	14141 000901	113.420311	147_000972
]	L17 (RPL17),			
		mRNA			
		/cds=(287,841)			
		1 ' '			1
		/gb=NM_000985			
}	1	/gi=14591906			Ì
mindagas	NIM OCCOSE	/ug=Hs.82202	NIM OCCOSE	110 00000	ND 000070
miod2225	NM_000985	/len=898	NM_000985	Hs.82202	NP_000976

Figure c	id Cont'd.				
		ribosomal protein			
		L37a (RPL37A),			
		mRNÀ			
		/cds=(36,314)			
ļ		/gb=NM_000998			
		I * —			
		/gi=16306561			
		/ug=Hs.296290	l		
fcrb6000	NM_000998	/len=392	NM_000998	Hs.296290	NP_000989
		ribosomal protein			
		L39 (RPL39),			
		mRNA			
		/cds=(68,223)			
		/gb=NM_001000			
		/gi=16306563	İ		
		/ug=Hs.300141	•		
mioa0909	NM 001000	/len=401	NM 001000	Hs.300141	ND 000004
1111020303	14141_001000		111111_001000	HS.300141	NP_000991
		ribosomal protein			
		S4, X-linked			
		(RPS4X), mRNA			
		/cds=(36,827)			
ļ		/gb=NM_001007			
		/gi=17981705			
		/ug=Hs.389933			
fcrb5503	NM_001007	/len=916	NM 001007	Hs.389933	NP 000998
		ribosomal protein			
		S8 (RPS8), mRNA			
		/cds=(24,650)	Ì		
		/gb=NM_001012			
		_			
		/gi=4506742			
		/ug=Hs.399720			
mioa8984	NM_001012	/len=705	NM_001012	Hs.399720	NP_001003
		ribosomal protein			
		S17 (RPS17),			
		mRNA			
		/cds=(26,433)			
		/gb=NM_001021			
		/gi=14591913			
ł		/ug=Hs.5174			
mioa3987	NM_001021	/len=515	NM 001021	Hs.5174	ND 001012
111003307	14141_001021		14141_001021	1115.0174	NP_001012
	1	actinin, alpha 1			
		(ACTN1), mRNA			
		/cds=(184,2862)			
	}	/gb=NM_001102	1	}	}
		/gi=12025669			
		/ug=Hs.119000			
fcrb5756	NM_001102	/len=3398	NM_001102	Hs.119000	NP_001093
10100700	[NIVI_001102	nen=3398	[NN]_001102	[HS.119000	INP_001093

Application of: Liew, et. al. Our Docket #: 4231/2042 Figure 6d Cont'd.

Figure 6	d Cont'd.				
		basic transcription			
		factor 3 (BTF3),		ľ	
		mRNA			
		/cds=(240,728)			
			1		
		/gb=NM_001207			
		/gi=20070129			
		/ug=Hs.101025		[1
fcrb1809	NM_001207	/len=952	NM_001207	Hs.101025	NP_001198
1		basic transcription			
		factor 3 (BTF3),			
		mRNA			
		/cds=(240,728)			
		/gb=NM_001207			
1		/gi=20070129			
}		/ug=Hs.101025			
2222255	NINA 001207	1 -	NINA 004007	112 404005	ND 004400
seoa3555	NM_001207	/len=952	NM_001207	Hs.101025	NP_001198
		cyclin H (CCNH),			
		mRNA			
		/cds=(233,1204)			İ
		/gb=NM_001239			
		/gi=17738313			
		/ug=Hs.514			
seob5942	NM 001239	/len=1398	NM 001239	Hs.514	NP 001230
		enolase 1, (alpha)			001200
	Ì	(ENO1), mRNA			
		/cds=(152,1456)			
		/gb=NM_001428			
				ļ	
1		/gi=16507965			
	l	/ug=Hs.254105	l		
fcr7060	NM_001428	/len=1812	NM_001428	Hs.254105	NP_001419
]	enolase 1, (alpha)			
		(ENO1), mRNA			
		/cds=(152,1456)			
		/gb=NM_001428			
		/gi=16507965			
		/ug=Hs.254105			
hfcr2664	NM 001428	/len=1812	NM 001428	Hs.254105	NP 001419
		FYN binding protein	001720	1.0.204100	14, 001410
		mRNA, complete			
ncrc1531	AF001862	cds	NM 001465	He 59425	ND 001456
110101031	/\\ 00100Z	GDP dissociation	14101_001400	Hs.58435	NP_001456
		1			
		inhibitor 2 (GDI2),			
1		mRNA		}	
		/cds=(153,1490)			
		/gb=NM_001494			
		/gi=6598322			
		/ug=Hs.56845			
seob6156	NM_001494	/len=2274	NM_001494	Hs.56845	NP 001485
		·	L	l	

i igaic o	d Cont'd.	15		γ	,
1	1	Similar to general	1		
		transcription factor			
		IIH, polypeptide 3,		Ì	
Ì		34kDa, clone			
		IMAGE:5582960,			
miob2257	BC039726	mRNA		Hs.30724	NP 001507
1111002237	DC039720		1	П5.30724	NF_001307
		eukaryotic			1
1		translation initiation			
1		factor 3, subunit 6			
		48kDa (EIF3S6),			
		mRNA			
		/cds=(23,1360)			
		/gb=NM_001568			
		/gi=4503520			
		/ug=Hs.106673			
fcrb6574	NM 001568	/len=1510	NM_001568	Hs.106673	NP 001559
13120014	100.1000	actin, alpha 2,	11111_001000	113.100073	141 _001009
		smooth muscle,			
1					
		aorta (ACTA2),			
		mRNA	; ;		
		/cds=(48,1181)			
		/gb=NM_001613	•		
		/gi=4501882			
		/ug=Hs.195851			
fcrb2745	NM 001613	/len=1330	NM_001613	Hs.195851	NP 001604
		ATPase, H		.,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	
		transporting,			
		lysosomal 70kDa,			
		V1 subunit A,]
İ		isoform 1			
		1			
		(ATP6V1A1),			
		mRNA			
		/cds=(67,1920)			
		/gb=NM_001690			
		/gi=19913423			
		/ug=Hs.281866			
mioa8034	NM_001690	/len=4567	NM_001690	Hs.281866	NP 001681
	 	ATPase, H			
		transporting,			
		lysosomal			
		56/58kDa, V1			
		subunit B, isoform 2			
		(ATP6V1B2),	}		
		mRNA			
		/cds=(208,1743)			
		/gb=NM_001693			
		/gi=19913427			
		/ug=Hs.1697			
ncr1428	NM_001693	/len=3054	NM_001693	Hs.1697	NP_001684

- I iguie o	a Conta.		·		
		runt-related			
		transcription factor			:
		1 (acute myeloid			
		leukemia 1; aml1			
		oncogene)			
		(RUNX1), mRNA			
		/cds=(445,1887)			
		/gb=NM_001754			
		/gi=19923197			
1	l	/ug=Hs.129914			
seob1860	NM_001754	/len=6212	NM_001754	Hs.129914	NP_001745
		cyclin D2 (CCND2),			
		mRNA			
		/cds=(270,1139)			
		/gb=NM_001759			
		/gi=16950656			
		/ug=Hs.75586			
ncr3642	NM_001759	/len=6480	NM 001759	Hs.75586	NP 001750
10.0042	1.1.11_00 11 00	CD1D antigen, d	1.111_001700	1.0.70000	141_001/00
		polypeptide (CD1D),			
		ImRNA			
		/cds=(165,1172)			
		/gb=NM_001766			
		/gi=4502648			
		/ug=Hs.1799			
fcrb3966	NM_001766	/len=1903	NM_001766	Hs.1799	NP_001757
		CD9 antigen (p24)			
		(CD9), mRNA			
		/cds=(112,798)			
		/gb=NM 001769			
		/gi=21237762			
		/ug=Hs.1244			
seoa0913	NM 004760	/len=1246	NM 004760	LL 1244	ND 004760
196090913	NM_001769		NM_001769	Hs.1244	NP_001760
		CDC28 protein			
		kinase regulatory			
		subunit 2 (CKS2),			
		mRNA			
		/cds=(96,335)			
		/gb=NM_001827			
		/gi=4502858			
		/ug=Hs.83758			
seob0752	NM 001827	/len=627	NM 001827	Hs.83758	NP 001818
		calponin 3, acidic,			
Ì	Ì	clone MGC:1775		•	
		IMAGE:3505668,			
	D0005070	mRNA, complete	NINA 004000	11- 40 4000	ND 004000
seoa0526	BC025372	cds	NM_001839	Hs.194662	NP_001830

Figure 6	id Cont'd.				
		cytochrome c oxidase subunit IV isoform 1 (COX4I1),			
		nuclear gene			
		encoding			
		mitochondrial			-
		protein, mRNA			
		/cds=(165,674)			
		/gb=NM_001861		į	
		/gi=17017985			
fcrb2993	NM_001861	/ug=Hs.433419 /len=802	NM 001861	Hs.433419	ND 004950
10102993	14141_00 180 1	/ieii-002	14101_00 166 1	П5.433419	NP_001852
		cellular retinoic acid			
		binding protein 2			
		(CRABP2), mRNA			
		/cds=(138,554)			
		/gb=NM_001878			
		/gi=6382069 /ug=Hs.183650			
fcr4308	NM 001878	/len=969	NM_001878	Hs.183650	NP_001869
		casein kinase 2,			
		alpha prime			
		polypeptide			
		(CSNK2A2), mRNA /cds=(164,1216)			
		/gb=NM_001896			
		/gi=4503096			
		/ug=Hs.82201			
fcr7656	NM_001896	/len=1677	NM_001896	Hs.82201	NP_001887
		a. deam atia			
		eukaryotic translation initiation			
		factor 4A, isoform 2			
		(EIF4A2), mRNA			
		/cds=(16,1239)	:		
		/gb=NM_001967			
i		/gi=9945313			
ncrc2495	NM 001067	/ug=Hs.173912 /len=1864	NINA 004007	LI- 470040	ND 004050
ncrc2495	NM_001967	glycyl-tRNA	NM_001967	Hs.173912	NP_001958
		synthetase (GARS),			
		mRNA			
		/cds=(519,2576)			
		/gb=NM_002047			
		/gi=6996009			
fcrc6452	NM 002047	/ug=Hs.293885	NIM 002047	Ha 202005	ND 000000
10100452	NM_002047	/len=2742	NM_002047	Hs.293885	NP_002038

1 iguie o	oa Conta.	122:2:			
		major			
		histocompatibility			
		complex, class I, C			
		(HLA-C), mRNA			
		1 1			
		/cds=(16,1116)			
		/gb=NM_002117			
		/gi=19557676			
		/ug=Hs.277477			
ncr5066	NM_002117	/len=1549	NM 002117	Hs.277477	NP 002108
1101000	11002.11	mRNA; cDNA	14141_002111	110.277777	141 _002 100
		•			
		DKFZp566M063			
		(from clone			
seoc5963	AL110194	DKFZp566M063)		Hs.6727	NP_002119
		integrin, alpha V			
		(vitronectin		1	
		receptor, alpha	ŀ		
		polypeptide, antigen	Ì		
		CD51) (ITGAV),			
		mRNA			
		/cds=(42,3188)			
		/gb=NM_002210			
		/gi=4504762			
		1 -			
		/ug=Hs.295726			
seob5976	NM_002210	/len=5717	NM_002210	Hs.295726	NP_002201
	ĺ	laminin receptor 1			
		(ribosomal protein			
		SA, 67kDa)			
		(LAMR1), mRNA			
		1.			
		/cds=(86,973)			
		/gb=NM_002295			
		/gi=9845501			
		/ug=Hs.181357			
ncrc9228	NM 002295	/len=1039	NM 002295	Hs.181357	NP 002286
		lectin, galactoside-			111 _002200
		binding, soluble, 1			
		•			
1		(galectin 1)			
	1	(LGALS1), mRNA			
		/cds=(69,476)			
		/gb=NM_002305			
	1	/gi=6006015			,
		/ug=Hs.382367			,
00050040	NIM COORDS		NINA COCCO	00000	ND 00000
seob0810	NM_002305	/len=526	NM_002305	Hs.382367	NP_002296
1	Ì	malic enzyme 1,			
		NADP()-			
1		dependent,			
		cytosolic (ME1),			
		mRNA			
	[1			
		/cds=(108,1826)			
		/gb=NM_002395			
		/gi=13435400			
1		/ug=Hs.14732			
ncr8780	NM 002395	/len=2212	NM_002395	Hs.14732	NP_002386
		1			002000

Figure 6	Sd Cont'd.				
		antigen identified by			
		monoclonal			
		antibody Ki-67			
		(MKI67), mRNA			
		/cds=(197,9967)			
		/gb=NM_002417			
		/gi=19923216			Ī
1		/ug=Hs.80976			
hfcr2696	NM_002417	/len=12515	NM_002417	Hs.80976	NP_002408
		myosin, light			
		polypeptide 5,	ļ		
		regulatory (MYL5),			
		mRNA			
		/cds=(106,627)		Ì	
		/gb=NM_002477			ļ
		/gi=4505304			
		/ug=Hs.170482			İ
fcr2218	NM_002477	/len=661	NIM 002477	La 170492	ND 000400
10122 10	14141_002411	Similar to nidogen	NM_002477	Hs.170482	NP_002468
		_		1	1
		(enactin), clone			
		MGC:33141			
		IMAGE:5271590,			
		mRNA, complete			
seoa4400	BC045606	cds		Hs.356624	NP_002499
		5'-nucleotidase,			
		ecto (CD73)			
seoa2726	NM_002526	(NT5E), mRNA	NM_002526	Hs.153952	NP 002517
				W	
		serine (or cysteine)			
		proteinase inhibitor,			
		clade F (alpha-2			
		antiplasmin,			
İ		pigment epithelium			İ
		derived factor),			
		, ,			
		member 1			
		(SERPINF1),			
		mRNA			
ļ		/cds=(39,1082)			
		/gb=NM_002615			
1		/gi=4505708			
		/ug=Hs.173594			
hfcr1724	NM 002615	/len=1199	NM 002615	Hs.173594	NP 002606
		period 1			
		(Drosophila)			
		(PER1), mRNA			
		/cds=(188,4060)			
1					
		/gb=NM_002616			
		/gi=4505712			
b0101	NINA 000040	/ug=Hs.68398		l .	
ncrb8191	NM_002616	/len=4656	NM_002616	Hs.68398	NP_002607

		phosphomannomut			
hfcr1689	NM_002676	ase 1 (PMM1), mRNA /cds=(5,793) /gb=NM_002676 /gi=4505904 /ug=Hs.75835 /len=1210	NM_002676	Hs.75835	NP_002667
ncrb4402	NM 002696	polymerase (RNA) II (DNA directed) polypeptide G (POLR2G), mRNA /cds=(107,625) /gb=NM_002696 /gi=4505946 /ug=Hs.14839 /len=828	NM 002696	Hs.14839	NP 002687
		protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1) (PRKAR1A), mRNA /cds=(88,1233) /gb=NM_002734 /gi=4506062 /ug=Hs.183037 /len=3036			
	NM_002734	prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy) (PSAP), mRNA /cds=(39,1613) /gb=NM_002778 /gi=11386146 /ug=Hs.406455	NM_002734	Hs.183037	NP_002725
		/len=2767 proteasome (prosome, macropain) subunit, alpha type, 5 (PSMA5), mRNA /cds=(86,811) /gb=NM_002790 /gi=23110941 /ug=Hs.76913 /len=1023	NM_002778	Hs.406455	NP_002769

rigure c	d Cont'd.		r		
1		parathyroid-like		1	
		protein (associated			
		with humoral			
		hypercalcemia of		1	
forb9027	103590	malignancy) mRNA,	NM 00000	Un 00000	ND 000044
fcrb8937	J03580	complete cds protein tyrosine	NM_002820	Hs.89626	NP_002811
		1.			
	İ	phosphatase, non-			ļ
		receptor type 12 (PTPN12), mRNA			
		1.			
		/cds=(30,2372)			
ł		/gb=NM_002835		1	
		/gi=18375651		1	
pere1247	NIM 002925	/ug=Hs.62 /len=3161	NIM OCCOSE	LL 62	ND 000000
ncrc1247	NM_002835	protein tyrosine	NM_002835	Hs.62	NP_002826
		phosphatase,	l		
}	1	receptor type, G			
		(PTPRG), mRNA			
	1	/cds=(718,5055)			
		/gb=NM_002841			
	1	/gi=18860897			
		/ug=Hs.89627			
seob6395	NM 002841	/len=5787	NM 002841	Hs.89627	ND 003933
36000333	14141_002041	RAB5B, member	14141_002041	113.03027	NP_002832
		RAS oncogene			
		family, clone			
		IMAGE:6191566,			
ncrb3989	BC050558	mRNA, partial cds			NP 002859
	2000000	ribophorin II			141 _002039
		(RPN2), mRNA			
		/cds=(289,2184)			
1		/gb=NM_002951			
1		/gi=4506676			
		/ug=Hs.406532		i	
fcr4984	NM 002951	/len=2509	NM 002951	Hs.406532	NP 002942
		syndecan 1 (SDC1),		1.0. 100002	
		mRNA			
[/cds=(253,1185)			
		/gb=NM_002997			
		/gi=21359855			
!		/ug=Hs.82109			ļ
fcr2427	NM 002997	/len=2484	NM_002997	Hs.82109	NP 002988
		nuclear antigen			
		Sp100 (SP100),			
		mRNA			
		/cds=(32,2671)			
		/gb=NM_003113			
		/gi=19923235			
		/ug=Hs.77617			
seob6153	NM_003113	/len=3579	NM_003113	Hs.77617	NP 003104
		•			

Application of: Liew, et. al. Our Docket #: 4231/2042 Figure 6d Cont'd.

	a Conta.				
miob3252	NM_003613	cartilage intermediate layer protein, nucleotide pyrophosphohydrola se (CILP), mRNA /cds=(130,3684) /gb=NM_003613 /gi=4502844 /ug=Hs.151407 /len=4175 peroxisomal biogenesis factor 3 (PEX3), mRNA	NM_003613	Hs.151407	NP_003604
miob5675	NM_003630	/cds=(64,1185) /gb=NM_003630 /gi=4505726 /ug=Hs.7277 /len=1979	NM_003630	Hs.7277	NP_003621
ncr0179	NM_003729	RTC domain containing 1 (RTCD1), mRNA /cds=(171,1271) /gb=NM_003729 /gi=4506588 /ug=Hs.27076 /len=1539	NM_003729	Hs.27076	NP_003720
fcrb7588	NM_003746	dynein, cytoplasmic, light polypeptide 1 (DNCL1), mRNA /cds=(94,363) /gb=NM_003746 /gi=4505812 /ug=Hs.5120 /len=643	NM_003746	Hs.5120	NP_003737
ncr3948	NM 003851	cellular repressor of E1A-stimulated genes (CREG), mRNA /cds=(34,696) /gb=NM_003851 /gi=4503036 /ug=Hs.5710 /len=1989	NM 003851	Hs.5710	NP_003842

Application of: Liew, et. al. Our Docket #: 4231/2042 Figure 6d Cont'd.

T iguic c	od Conta.			, 	
		WNT1 inducible			
		signaling pathway			
	Ī	protein 2 (WISP2),			
		mRNA			
		/cds=(148,900)			
		/gb=NM_003881			
				1	İ
		/gi=18491001			
		/ug=Hs.194679			
seob1078	NM_003881	/len=1433	NM_003881	Hs.194679	NP_003872
		мсм3			
		minichromosome			
		maintenance			
		deficient 3 (S.			
		cerevisiae)			
		associated protein			
		(MCM3AP), mRNA			
		/cds=(38,5980)	1		
	Ì				
		/gb=NM_003906			
		/gi=19923190		ļ	:
		/ug=Hs.168481			
ncrc6678	NM_003906	/len=6114	NM_003906	Hs.168481	NP_003897
		sarcoglycan, epsilon			
		(SGCE), mRNA			
		/cds=(69,1382)			
		/gb=NM_003919			
		/gi=10835046			
	1	/ug=Hs.110708			:
seob3869	NM_003919	/len=1658	NM 003919	Un 110700	ND 002040
36003009	14141_003919	CDC-like kinase 3	MM_003919	Hs.110708	NP_003910
		(CLK3), transcript			
		variant phclk3,			
		mRNA			
		/cds=(57,1529)			
		/gb=NM_003992			
		/gi=4502884			
		/ug=Hs.73987	NM_001292;		
hfcr3444	NM 003992	/len=1762	NM 003992	Hs.73987	NP_003983
		ornithine			
		decarboxylase			
		antizyme 1 (OAZ1),			
		mRNA			
		/gb=NM_004152		ł	j l
		/gi=9845504			
<u></u>		/ug=Hs.281960			
fcrb6181	NM_004152	/len=986	NM_004152	Hs.281960	NP_004143

rigule o	a Conta.		·		
		ubiquitin carboxyl-			
		terminal esterase]	
		L1 (ubiquitin			
		thiolesterase)			
		1			
		(UCHL1), mRNA			
		/cds=(75,746)			
		/gb=NM_004181			
		/gi=21361090			
		/ug=Hs.76118			
fcr1182	NM_004181	/len=1119	NM 004181	Hs.76118	NP 004172
1011102	11111_001101	acetylserotonin O-	11111_00 7 10 1	110.70110	111 _00+172
		methyltransferase-			
		like (ASMTL),			
		mRNA			
		/cds=(1,1890)			
		/gb=NM_004192			
	ļ	/gi=4757793			
		/ug=Hs.70327			
fcr6915	NM 004192	/len=1890	NM 004192	Hs.70327	NP 004183
1010010	14111_00+102	fatty acid	14141_00-102	113.70027	141 _004100
		desaturase 2			
		(FADS2), mRNA			
		/cds=(151,1485)			
		/gb=NM_004265			
		/gi=14141180			
		/ug=Hs.184641			
hfcr1639	NM_004265	/len=3149	NM 004265	Hs.184641	NP 004256
	ļ	cofactor required for			
	7	Sp1 transcriptional			
		activation, subunit		ł	
		8, 34kDa (CRSP8),			
		mRNA /cds=(1,822)			
		/gb=NM_004269			
		/gi=4758065			
		/ug=Hs.374262			
fcrb5455	NM 004269	/len=822	NM 004269	Hs 374262	NP 004260
12.22.100		pituitary tumor-		1.10.01 4202	55-7255
		transforming 1			
		. •			
		interacting protein			
		(PTTG1IP), mRNA			
	}	/cds=(211,753)		}	
}		/gb=NM_004339			
		/gi=11038670			
		/ug=Hs.111126			
ncrb5254	NM_004339	/len=2737	NM 004339	Hs.111126	NP_004330
		1			

Figure 6	d Cont'd.				
		centrin, EF-hand			
		protein, 2 (CETN2),			
		mRNA			
		/cds=(48,566)			İ
		/gb=NM 004344			
		/gi=4757901			
		/ug=Hs.82794			
ncr3825	NM_004344	/len=1087	NM 004344	Hs.82794	NP 004335
1.0.0020	11111_00 10 11	NADH	1414_004044	113.02734	141 _004000
]		dehydrogenase			
		(ubiquinone) Fe-S			
İ		protein 5, 15kDa	į		
		(NADH-coenzyme			
		1.			
		Q reductase)			
		(NDUFS5), mRNA			
		/cds=(72,392)			
		/gb=NM_004552			
		/gi=4758789			
		/ug=Hs.409829			l <u>.</u>
ncrc5464	NM_004552	/len=540	NM_004552	Hs.409829	NP_004543
		CDK2-associated			
		protein 1			
		(CDK2AP1), mRNA			
		/cds=(523,870)			
		/gb=NM_004642			
		/gi=17978492	:		
		/ug=Hs.433201			
seob7928	NM_004642	/len=1627	NM_004642	Hs.433201	NP_004633
		splicing factor,			
		arginine/serine-rich			
	ļ	2, interacting protein			
		(SFRS2IP), mRNA			
		/cds=(1211,4657)			
		/gb=NM_004719			
		/gi=4759171			
		/ug=Hs.51957			
miob0496	NM_004719	/len=5307	NM_004719	Hs.51957	NP_004710
		transcription		.	
		elongation factor A			
		(SII)-like 1			
		(TCEAL1), mRNA			
		/cds=(165,638)			
		/gb=NM 004780			
		/gi=4759215			
		/ug=Hs.95243			
seoa4102	NM_004780	/len=1174	NM_004780	Hs.95243	NP 004771
		kinesin family	55-47-55		1.400-7/11
		member 3B	[
seoa6930	NM_004798	(KIF3B), mRNA	NM_004798	Hs.301206	NP_004789
2000000	100-77.00	IVAN OD), INIXIAA	1111 007/30	113.001200	141UU-+1 08

1 19410 0	u Contu.				
		geranylgeranyl diphosphate synthase 1 (GGPS1), mRNA /cds=(233,1135) /gb=NM_004837 /gi=21359876 /ug=Hs.55498			
ncrc0174	NM 004837	/len=1489	NM 004837	Hs.55498	NP 004828
		anti-oxidant protein 2 (non-selenium glutathione peroxidase, acidic calcium- independent phospholipase A2) (AOP2), mRNA /cds=(44,718) /gb=NM_004905 /gi=4758637			
10404		/ug=Hs.120			
seob2161	NM_004905	/len=1653 NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase) (NDUFS1), mRNA /cds=(85,2268) /gb=NM_005006 /gi=28269700 /ug=Hs.8248	NM_004905	Hs.120	NP_004896
seoa0066	NM_005006	/len=2382 U2 small nuclear ribonucleoprotein auxiliary factor, small subunit 1 (U2AF1RS1), mRNA /cds=(112,1551) /gb=NM_005083 /gi=13186299 /ug=Hs.103962	NM_005006	Hs.8248	NP_004997
ncr7915	NM_005083	/len=1566	NM_005083	Hs.103962	NP_005074

1 19410 0	d Conta.				
		B-cell			
		CLL/lymphoma 3		1	
		(BCL3), mRNA			
		/cds=(42,1382)			
		/gb=NM_005178			
		/gi=20336471			
		/ug=Hs.31210			
ncr3380	NM_005178	/len=1813	NM_005178	Hs.31210	NP_005169
		dolichyl-			
		diphosphooligosacc			
		haride-protein			
		glycosyltransferase			
		(DDOST), mRNA			
1	ļ	/cds=(60,1430)			
		/gb=NM_005216			
		/gi=20070196			
		/ug=Hs.34789		<u> </u>	
fcrb3288	NM_005216	/len=2045	NM_005216	Hs.34789	NP_005207
		high density			
		lipoprotein binding			
		protein (vigilin)		1	
seoa4548	NM_005336	(HDLBP), mRNA	NM_005336	Hs.177516	NP_005327
		Similar to Rho-			
		associated, coiled-		i	
		coil containing			
1		protein kinase 1,			
		clone			
		IMAGE:5269982,			
seoc3552	BC041849	mRNA		Hs.17820	NP_005397
		chemokine (C-C			
1		motif) ligand 13			
		(CCL13), mRNA			
		/cds=(76,372)			
		/gb=NM_005408			
		/gi=22538799			
		/ug=Hs.11383			
seoa5473	NM_005408	/len=861	NM_005408	Hs.11383	NP_005399
		eps8 binding protein			
		e3B1 mRNA,			
seoc4060	AF006516	complete cds	NM_005470	Hs.24752	NP_005461

rigure d	od Conta.	T-1-4005 - 4	· = · · · · · · · · · · · · · · · · · ·		
		ah42f05.s1			
		Soares_testis_NHT			
		cDNA clone			
		1292193 3' similar			
		to P54687			
		BRANCHED-			
		CHAIN AMINO			
		ACID			
	}	AMINOTRANSFER			
		ASE, CYTOSOLIC			
		;, mRNA sequence			
		/clone=1292193			
		/clone_end=3'		İ	
1		/gb=AA705851			
		/gi=2715769			
		/ug=Hs.443872			
miob7231	AA705851	/len=412		Hs.443872	NP 005495
		high-mobility group			
1	[nucleosomal			
1		binding domain 2			
		(HMGN2), mRNA			
		1.			
		/cds=(108,380)			
		/gb=NM_005517			
		/gi=5031748			:
		/ug=Hs.181163			
fcrb0623	NM_005517	/len=1198	NM_005517	Hs.181163	NP_005508
		interferon, gamma-			
		inducible protein 16			
		(IFI16), mRNA]	
		/cds=(265,2454)			
1		/gb=NM_005531			
		/gi=5031778			
		/ug=Hs.155530		İ	
seoc0514	NM 005531	/len=2709	NM 005531	Hs.155530	NP 005522
55555514	11111_000001	inhibitor of growth	14141_000001	113.100000	141 _000022
		family, member 1			
		(ING1), mRNA			
		/cds=(433,1701)			
		/gb=NM_005537			
		/gi=19923770			
		/ug=Hs.46700			
seoa6393	NM_005537	/len=2886	NM_005537	Hs.46700	NP_005528
1	-	inositol		}	
1		polyphosphate-5-			
		phosphatase,			
ł		40kDa (INPP5A),			
Ì		mRNA `			
		/cds=(102,1193)			
		/gb=NM_005539			
		/gi=5031796			
		/ug=Hs.124029			
fcr0535	NM_005539	/len=2640	NM_005539	Hs.124029	ND ODESO
11010000	114141 000000	men-2040	[14]AI_00999	113.124029	NP_005530

r iguie o	a Conta.		,		
	1	immunoglobulin			
		superfamily			
		containing leucine-			ļ
		rich repeat (ISLR),			İ
		mRNA			
		/cds=(99,1385)	İ		
		/gb=NM_005545			
		/gi=5031808			
		, -			
	NIM 005545	/ug=Hs.102171		11: 400474	ND 005500
seoa2639	NM_005545	/len=2110	NM_005545	Hs.102171	NP_005536
		LIM damain			
		LIM domain			
		containing preferred			
İ		translocation			
		partner in lipoma			
		(LPP), mRNA			-
	1	/cds=(247,2085)			1
		/gb=NM_005578			
		/gi=5031886			
		/ug=Hs.180398		1	
mioc1440	NM_005578	/len=5656	NM_005578	Hs.180398	NP 005569
		MRE11 meiotic			
		recombination 11 A			
		(S. cerevisiae)			
		(MRE11A),			
		transcript variant 1,			
		mRNA			
İ		/cds=(160,2286)			
		/gb=NM_005591			
		/gi=24234691			
	l	/ug=Hs.20555	NM_005590;		
seoa0737	NM_005591	/len=4852	NM_005591	Hs.20555	NP_005582
		synaptobrevin-like 1			
1		(SYBL1), mRNA			
		/cds=(115,777)			
ł		/gb=NM_005638			
		/gi=27545446			
		/ug=Hs.24167			
seoa8669	NM_005638	/len=2588	NM_005638	Hs.24167	NP_005629
		telomeric repeat			
		binding factor 2			
		(TERF2), mRNA			
	ļ	/cds=(126,1628)		1	
		/gb=NM_005652			
		/gi=21536372			<u> </u>
		/ug=Hs.100030		Ì	!
seob1744	NM 005652	/len=2909	NM 005652	Hs.100030	NP 005643
33331144	000002	cDNA FLJ31097 fis,	. 4111_000002	113.100030	141 _000040
		clone			
seoa7910	AK055659	IMR321000210	NM 005723	Uc 9027	ND 005744
13COa7 3 10	IVI/000009	IIVIN32 10002 10	[NIVI_UU0/23	Hs.8037	NP_005714

Figure 6d Cont'd.

Ä

	a Conta.		<u> </u>		
		tetraspan 2 (TSPAN	1		
		2), mRNA			
		/cds=(33,698)			
		/gb=NM_005725			
		/gi=21264579	ļ		
		/ug=Hs.234863			
miod5622	NM_005725	/len=3179	NM_005725	Hs.234863	NP_005716
		serologically defined			
		colon cancer			
		antigen 33			
		(SDCCAG33),			
		mRNA			
		/cds=(295,2358)			
		/gb=NM_005786			
		/gi=15451922			
		/ug=Hs.284217			
mioc5226	NM_005786	/len=2858	NM_005786	Hs.284217	NP_005777
		calcitonin receptor-			
		like (CALCRL),			
		mRNA			
		/cds=(555,1940)			
		/gb=NM_005795			
		/gi=5031620			
		/ug=Hs.152175			
mioc8793	NM_005795	/len=3018	NM_005795	Hs.152175	NP 005786
		highly charged			
		protein			
1		(D13S106E), mRNA			
		/cds=(178,3456)			
		/gb=NM_005800	:		
		/gi=5031648		;	
		/ug=Hs.151236			
mioa6807	NM_005800	/len=3650	NM_005800	Hs.151236	NP_005791
		immunoglobulin			
		superfamily,			,
		member 6 (IGSF6),			
		mRNA			
		/cds=(45,770)			
		/gb=NM_005849			
		/gi=5031672			
		/ug=Hs.135194			
miob5010	NM 005849	/len=1019	NM_005849	Hs.135194	NP 005840

		zinc metalloproteinase (STE24 yeast) (ZMPSTE24), mRNA /cds=(166,1593) /gb=NM_005857 /gi=18379365 /ug=Hs.25846			
mioa9510	NM 005857	/len=3103	NM 005857	Hs.25846	NP 005848
		MAD, mothers against decapentaplegic 5 (Drosophila) (MADH5), mRNA /cds=(193,1590) /gb=NM_005903 /gi=20070216 /ug=Hs.37501			
mioa3080	NM 005903	/len=2049	NM_005903	Hs.37501	NP 005894
		mannosidase, alpha, class 1A, member 1 (MAN1A1), mRNA /cds=(443,2404) /gb=NM_005907 /gi=24497518 /ug=Hs.25253		10.07001	_000004
ncrc2289	NM_005907	/len=4139	NM 005907	Hs.25253	NP 005898
		ubiquinol- cytochrome c reductase, Rieske iron-sulfur polypeptide 1 (UQCRFS1), nuclear gene encoding mitochondrial protein, mRNA /cds=(91,915) /gb=NM_006003 /gi=5174742 /ug=Hs.3712			
seob1161	NM_006003	/len=1203	NM_006003	Hs.3712	NP 005994
fcrb9454	 NM_006067	neighbor of COX4 (NOC4), mRNA /cds=(209,841) /gb=NM_006067 /gi=19923775 /ug=Hs.173162 /len=1950	 NM_006067		NP_006058

i iguie c	oa Conta.	n=			
		tubulin, beta, 4			
		(TUBB4), mRNA			
		/cds=(1,1353)			
1		/gb=NM_006086	1	1	1
1					
1		/gi=5174736			
1	1	/ug=Hs.159154	1		
hfcr4114	NM_006086	/len=1648	NM_006086	Hs.159154	NP 006077
		nucleobindin 1			
		(NUCB1), mRNA			
		/cds=(27,1412)		1	
		/gb=NM_006184			
	1	/gi=20070227	1		
		/ug=Hs.172609	1		
fcrb5181	NM_006184	/len=2311	NM_006184	Hs.172609	NP_006175
1		serine (or cysteine)			
		proteinase inhibitor,			
		clade E (nexin,			
		plasminogen			
		activator inhibitor			
		type 1), member 2			
		(SERPINE2),			
		mRNA		i	
	<u> </u>	1			
		/cds=(210,1406)			
		/gb=NM_006216			
		/gi=24307906			
l		/ug=Hs.21858			
seob3148	NM 006216	/len=2129	NM 006216	Hs.21858	NP_006207
		polymerase (DNA		1.10.2.1000	141 _000207
		directed), delta 2,			
		regulatory subunit			
		50kDa (POLD2),		Ì	
		mRNA			
		/cds=(79,1488)			
		/gb=NM_006230			
		/gi=5453923		ļ	
		I =			
		/ug=Hs.74598		l <u>-</u>	
fcr2611	NM_006230	/len=1584	NM_006230	Hs.74598	NP_006221
]		polymerase (RNA)			
		II (DNA directed)			
		polypeptide I,			
1		14.5kDa (POLR2I),			
		mRNA			
Ì				ì	
		/cds=(36,413)			
		/gb=NM_006233			
		/gi=14589954			
1		/ug=Hs.47062			
hfcr6600	NM_006233	/len=458	NM_006233	Hs.47062	NP_006224
	1.1.11_000200	7.00	14141_000200	113.77002	INI ⁻ _000224

rigule 0	id Cont'd.				
		SMC1 structural			
		maintenance of			
		chromosomes 1-like			
1		1 (yeast) (SMC1L1),			
seoa1582	NM 006306	mRNA	NM 006306	Hs.211602	NP 006297
		 			
		tubulin, gamma	Í		
		complex associated			
ļ		protein 3			
	ļ	(TUBGCP3), mRNA			
		/cds=(85,2808)	ļ		
		/gb=NM_006322			
		/gi=5453659			
6-1-0400	NIA 000000	/ug=Hs.9884		l	
fcrb8162	NM_006322	/len=3795	NM_006322	Hs.9884	NP_006313
		DAN Sis			
		RAN, member RAS			
		oncogene family			
		(RAN), mRNA			
		/cds=(115,765)			
		/gb=NM_006325			
		/gi=6042206			
		/ug=Hs.10842			
fcr3367	NM_006325	/len=1656	NM_006325	Hs.10842	NP_006316
		fibulin 5 (FBLN5),			
		mRNA			
		/cds=(463,1809)			
		/gb=NM_006329			
		/gi=19743802			
		/ug=Hs.11494			
ncr5509	NM 006329	/len=2646	NM_006329	Hs.11494	NP 006320
		high mobility group			000020
		nucleosomal			
		binding domain 4			
1		(HMGN4), mRNA			
		/cds=(239,511)			
1		/gb=NM_006353			
		/gi=23238232			
		/ug=Hs.236774			
hfcr4446	NM 006353	/len=1980	NM 006353	Hs.236774	ND OOGS44
111017770	14141_000000	NS1-associated	[NIVI_000303	115.230//4	NP_006344
		protein 1 (NSAP1),			
		mRNA			
		/cds=(526,2397)			
		/gb=NM_006372			
		/gi=23397426			
h60=0504	NINA 000070	/ug=Hs.373499	NINA 000000		
hfcr2524	NM_006372	/len=2932	NM_006372	Hs.373499	NP_006363

90.00	a Conta.	·			
mioa0072	NM 006409	actin related protein 2/3 complex, subunit 1A, 41kDa (ARPC1A), mRNA /cds=(148,1260) /gb=NM_006409 /gi=22907051 /ug=Hs.90370 /len=1619	NM_006409	Hs.90370	ND 006400
11110a0072	14141_006409	<u> </u>	14141_006409	HS.90370	NP_006400
		chaperonin containing TCP1, subunit 2 (beta) (CCT2), mRNA /cds=(58,1665) /gb=NM_006431 /gi=5453602 /ug=Hs.432970			
seob5792	NM 006431	/len=1935	NM 006431	Hs.432970	NP 006422
seoc1058	NM 006474	lung type-I cell membrane- associated glycoprotein (T1A- 2), mRNA /cds=(234,722) /gb=NM_006474 /gi=18767663 /ug=Hs.135150 /len=1081	NM 006474	Hs.135150	NP 006465
1	NIN_000474	glioma-amplified sequence-41 (GAS41), mRNA /cds=(222,905) /gb=NM_006530 /gi=5729837 /ug=Hs.4029	1411_000474	113.133130	NF_000403
ncrb7586	NM_006530	/len=1404	NM_006530	Hs.4029	NP 006521
		CUG triplet repeat, RNA binding protein 2 (CUGBP2), mRNA /cds=(35,1564) /gb=NM_006561 /gi=5729815 /ug=Hs.211610			
hfcr3007	NM_006561	/len=5516	NM_006561	Hs.211610	NP_006552

Figure 6	6d Cont'd.				
ncr9502	NM_006682	fibrinogen-like 2 (FGL2), mRNA /cds=(34,1353) /gb=NM_006682 /gi=5730074 /ug=Hs.351808 /len=1496 similar to S. pombe	NM_006682	Hs.351808	NP_006673
fcrc1738	NM_006701	dim1 (DIM1), mRNA /cds=(141,569) /gb=NM_006701 /gi=20070233 /ug=Hs.433683 /len=1415	NM_006701	Hs.433683	NP_006692
fcrc5160	NM_002313	actin binding LIM protein 1 (ABLIM1), transcript variant ABLIM-I, mRNA /cds=(100,2436) /gb=NM_002313 /gi=21284382 /ug=Hs.158203 /len=7581	NM_002313; NM_006719; NM_006720	Hs.158203	NP_006711
ncrb3541	NM_006766	runt-related transcription factor binding protein 2 (RUNXBP2), mRNA /cds=(394,6408) /gb=NM_006766 /gi=5803097 /ug=Hs.82210 /len=7869	NM_006766	Hs.82210	NP_006757
ncrc3690	BG166990	602344930F1 NIH_MGC_89 cDNA clone IMAGE:4454934 5', mRNA sequence /clone=IMAGE:4454 934 /clone_end=5' /gb=BG166990 /gi=12673693 /ug=Hs.440568 /len=1137		Hs.440568	NP_006764

- I iguic c	d Cont'd.				
		EH-domain			
		containing 1			
		(EHD1), mRNA			
		/cds=(247,1851)			
		/gb=NM_006795			
		/gi=5803008]		
		/ug=Hs.155119			
mioc5751	NM 006795	/len=3508	NM 006795	Hs.155119	NP 006786
1111003731	14141_000733	RAB31, member	14101_000793	1118.133119	NF_000780
		1			
		RAS oncogene			
		family (RAB31),			
1		mRNA			
		/cds=(61,645)			
		/gb=NM_006868			
		/gi=5803130		·	
		/ug=Hs.223025			
hfcr1918	NM_006868	/len=921	NM_006868	Hs.223025	NP_006859
		homeodomain			
1		protein (OG12)			
		mRNA, complete	NM_003030;		İ
fcrc6409	AF022654	cds	NM_006884	Hs.55967	NP_006875
		ATP synthase, H			
1		transporting,			
		mitochondrial F1			
		complex, epsilon			
		subunit (ATP5E),	Ì		
		nuclear gene			
		encoding			
		mitochondrial			
		protein, mRNA		1	
		I'			
		/cds=(95,250)		•	
		/gb=NM_006886			
		/gi=21327678			
1		/ug=Hs.177530			
fcr0955	NM_006886	/len=417	NM_006886	Hs.177530	NP_008817
		splicing factor,			
		arginine/serine-rich			
		5 (SFRS5), mRNA			
		/cds=(219,542)			
		/gb=NM_006925			
}		/gi=5902077			
İ		/ug=Hs.166975	ĺ		
miob5752	NM_006925	/len=1865	NM_006925	Hs.166975	NP 008856

rigule 0	d Cont'd.				
		solute carrier family			
		19 (thiamine			
		transporter),			
1		member 2		1	
		(SLC19A2), mRNA		İ	
		1			
		/cds=(238,1731)			1
		/gb=NM_006996	ļ		
		/gi=27734718	į]	
}		/ug=Hs.30246			
ncrb0462	NM_006996	/len=3668	NM 006996	Hs.30246	NP_008927
		transforming, acidic		7.10.002.10	111 _000027
		coiled-coil			
		1			
		containing protein 2			
		(TACC2), mRNA			
		/cds=(87,3167)			İ
	1	/gb=NM_006997			
		/gi=11119413			
		/ug=Hs.272023			
mioc3107	NM 006997	/len=3686	NM 006997	Hs.272023	NP 008928
1111000101		cleavage and	14141_000007	113.272020	141 _000320
		polyadenylation			
		specific factor 6,			
		68kDa (CPSF6),			
		mRNA			
		/cds=(35,1690)			
		/gb=NM_007007			'
	ļ	/gi=5901927			
1		/ug=Hs.64542			
fcrb1406	NM_007007	/len=3426	NM_007007	Hs.64542	ND 000000
10101400	14141_007007		141VI_007007	IDS.04042	NP_008938
		ATP synthase, H			
		transporting,			
		mitochondrial F0			
		complex, subunit e			
	•	(ATP5I), mRNA			
1		/cds=(64,273)			
		/gb=NM_007100			
		/gi=6005716		ĺ	
		/ug=Hs.85539	:		
forb6974	NINA 007400	_	NIM 007400	LI- 05500	ND 000004
fcrb6874	NM_007100	/len=336	NM_007100	Hs.85539	NP_009031
		ribosomal protein			
		L10a (RPL10A),			
		mRNA			ĺ
	}	/cds=(16,669)			ļ
		/gb=NM_007104			
		/gi=15431287			
		/ug=Hs.425293			
fcrb2334	NM 007104	/len=700	NM 007404	Un 425202	ND OOOOS
10102334	NM_007104	/ieii-/00	NM_007104	Hs.425293	NP_009035

Figure 6	d Cont'd.				
		zinc finger protein			
		184 (Kruppel-like)			
Î		(ZNF184), mRNA			
		/cds=(268,2523)			
		/gb=NM_007149			
		/gi=24307934		-	
		/ug=Hs.158174			
miob7223	NM_007149	/len=3095	NM 007149	Hs.158174	NP 009080
		patched related			
		protein translocated			
		in renal cancer			
		(TRC8), mRNA			
		/cds=(215,2209)			
		/gb=NM_007218			
		/gi=21314653			
		/ug=Hs.28285			
seoc1561	NM_007218	/len=2481	NM_007218	Hs.28285	ND 000140
36001301	TVIVI_007210	DEAD/H (Asp-Glu-	14101_00/210	118.20200	NP_009149
	,	Ala-Asp/His) box			
		polypeptide 19			
		(DBP5 yeast)			
		(DDX19), mRNA			
		` ' ' ' ' ' ' ' ' ' ' ' ' ' ' ' ' ' '		İ	
1		/cds=(105,1544)			
		/gb=NM_007242			
		/gi=13787207			
f 1- 0000	N. 4 007040	/ug=Hs.289097			
fcrb0993	NM_007242	/len=1806	NM_007242	Hs.289097	NP_009173
1		xylosylprotein beta			
		1,4-			
ļ		galactosyltransferas			
		e, polypeptide 7			
		(galactosyltransfera			
		se I) (B4GALT7),			
		mRNA			
		/cds=(41,1024)			
		/gb=NM_007255			
		/gi=6005951			
		/ug=Hs.54702			
fcrb4860	NM_007255	/len=1669	NM_007255	Hs.54702	NP_009186
		coatomer protein			
		complex, subunit			
}		epsilon (COPE),		}	
		mRNA			
		/cds=(43,969)			
		/gb=NM_007263			
		/gi=6005734			
		/ug=Hs.10326			
hfcr6394	NM_007263	/len=1130	NM_007263	Hs.10326	NP_009194

rigure d	d Cont'd.				
		putative DNA			
		binding protein			
		(M96), mRNA			
		/cds=(244,2025)			
		/gb=NM_007358			
		/gi=6678763			
		/ug=Hs.31016			
fcrb7051	NM 007358	/len=2648	NM_007358	Hs.31016	NP_031384
		chaperonin		1.0.0.0	
		containing TCP1,			
		subunit 5 (epsilon)			
		(CCT5), mRNA			
		/cds=(92,1717)			
		/gb=NM_012073			
		/gi=24307938			
		/ug=Hs.1600			
fcrb7852	NM 012073	/len=1961	NM 012073	Hs.1600	NP 036205
10107002	14141_012073	general	14141_0120/3	1 13. 1000	147_030203
		transcription factor			
		IIIC, polypeptide 3,			
1		102kDa (GTF3C3),			
		mRNA			
		/cds=(94,2754)			
		/gb=NM_012086			
		/gi=6912397			
		/ug=Hs.90847		l	
miod5114	NM_012086	/len=2961	NM_012086	Hs.90847	NP_036218
		golgi apparatus			
		protein 1 (GLG1),			
		mRNA			
		/cds=(27,3560)			
		/gb=NM_012201			
		/gi=6912389		1	
		/ug=Hs.78979			
hfcr2201	NM_012201	/len=3909	NM_012201	Hs.78979	NP_036333
	1	U6 snRNA-			
		associated Sm-like			
		protein (LSM4),			
		mRNA			
		/cds=(49,468)			
		/gb=NM_012321			
		/gi=6912485			
}		/ug=Hs.76719			
fcr6866	NM_012321	/len=1033	NM_012321	Hs.76719	NP 036453
		cDNA FLJ12859 fis,			
	1	clone			
		NT2RP2003522,			
		highly similar to zinc			
		finger DNA binding			
		protein 99 (ZNF281)			
fcrb9448	AK022921	mRNA		Hs.59757	NP_036614
		1		1. 10.00101	1.11 _000017

- riguic o	a Conta.					
		zinc finger protein 215 (ZNF215), mRNA /cds=(589,2142) /gb=NM_013250				
		/gi=7019582				
ļ	ĺ	/ug=Hs.161427				ļ
seoc3229	NM 013250	/len=3480	NM C	013250	Hs.161427	NP_037382
				710200	110.101121	NI _007002
seoc6295	NM_013252	C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 5 (CLECSF5), mRNA /cds=(198,764) /gb=NM_013252 /gi=10281668 /ug=Hs.126355 /len=3510	NM_0	013252	Hs.126355	NP_037384
		Rac GTPase activating protein 1 (RACGAP1), mRNA /cds=(225,2123) /gb=NM_013277 /gi=21361396 /ug=Hs.23900				
hfcr6376	NM_013277	/len=3237	NM_0)13277	Hs.23900	NP_037409
		hypoxia-inducible protein 2 (HIG2), mRNA /cds=(206,397) /gb=NM_013332 /gi=7019408 /ug=Hs.61762				
ncr0531	NM_013332	/len=1372	NM_0	13332	Hs.61762	NP_037464
minoF442	NIM 012042	chloride intracellular channel 4 (CLIC4), mRNA /cds=(198,959) /gb=NM_013943 /gi=7330334 /ug=Hs.25035		M20.40	05005	ND 00000
mioc5113	NM_013943	/len=4318	INIVI_U	13943	Hs.25035	NP_039234

rigure c	oa Conta.	TOKE 7 DECOMAGE OF	1		
		DKFZP586A0522			
		protein			
		(DKFZP586A0522),			
1		mRNA	1		
i		/cds=(21,755)			
		/gb=NM_014033			
		/gi=13378140			
		/ug=Hs.288771			
miob7970	NM 014033	/len=1705	NM_014033	Hs.288771	NP 054752
1111007070	11111_014000	mitochondrial	14141_014033	113.200771	NF_004702
		ribosomal protein			
		•		1	
		S18B (MRPS18B),			
		nuclear gene			
		encoding			
		mitochondrial			
		protein, mRNA			
		/cds=(38,814)			
		/gb=NM_014046			
		/gi=16554601			
İ		/ug=Hs.274417	}		
ncrc5335	NM_014046	/len=1439	NM 014046	Hs.274417	NP 054765
11010000	11111_014040	DKFZP586O0120	14141_014040	113.274417	141 _00+700
		protein		ļ	
		(DKFZP586O0120),			
		1'		İ	
		mRNA			
		/cds=(21,359)		ļ	
		/gb=NM_014077			
		/gi=7661695			
		/ug=Hs.4766			
fcrb1890	NM_014077	/len=1465	NM_014077	Hs.4766	NP_054796
		cDNA FLJ39357 fis,			
		clone			
		PEBLM2003914.			
		/gb=AK096676	•		
		/gi=21756220			
		/ug=Hs.22635			
seob5629	AK096676	/len=2315		Hs.22635	NP 054874
		HSPC070 protein		1.0.22000	141 _00-101-1
		(HSPC070), mRNA			
		/cds=(332,1582)			
	}				
		/gb=NM_014160			
		/gi=8850222			
1		/ug=Hs.279474		l -	
seoa6395	NM_014160	/len=3050	NM_014160	Hs.279474	NP_054879
1		ecotropic viral			
		integration site 2A			
		(EVI2A), mRNA			
		/cds=(220,918)			
		/gb=NM_014210			
		/gi=7657074			
		/ug=Hs.70499			
miob3411	NM_014210	/len=1563	NM_014210	Hs.70499	NP 055025
		<u> </u>			

	a Conta.		 		
		DnaJ (Hsp40)			
		subfamily C,			
		member 8			
		(DNAJC8), mRNA			
		/cds=(8,802)			
		/gb=NM_014280			
		/gi=7657610			
		/ug=Hs.433540			
mioa1944	NM 014280	/len=1525	NM_014280	Hs.433540	NP 055095
	1 -	pM5 protein (PM5),	=		
		mRNA			
1		/cds=(1,3669)			
1		/gb=NM_014287			
		/gi=10947030			
		/ug=Hs.439182			
seob4197	NM_014287	/len=4182	NM 014287	Hs.439182	NP 055102
		chromobox 6			
		(CBX6), mRNA			
		/cds=(30,1268)			
		/gb=NM 014292			
		/gi=10140848			
		/ug=Hs.107374			
fcrb7760	NM 014292	/len=6014	NM 014292	Hs.107374	NP 055107
10/10/100	14141_014202	integral inner	14141_014232	113.107374	NF_033107
		nuclear membrane			
		protein (MAN1),			
		mRNA			
		I .			
		/cds=(7,2742)			
		/gb=NM_014319			
		/gi=7706606			
	NIM O44240	/ug=Hs.7256	NINA 044040	U. 7050	ND 055404
ncrc2227	NM_014319	/len=4703	NM_014319	Hs.7256	NP_055134
		immunoglobulin			
		superfamily,			
		member 4 (IGSF4), mRNA			
		/cds=(4,1332)			
		/gb=NM_014333			
		/gi=22095346			
10055		/ug=Hs.70337			
miod2255	NM_014333	/len=3512	NM_014333	Hs.70337	NP_055148
		mitochondrial			
	1	carrier 1 (MTCH1),			}
		nuclear gene			
		encoding			
		mitochondrial			
		protein, mRNA			
		/cds=(1,1119)			
		/gb=NM_014341			
		/gi=7657344			
	l	/ug=Hs.279939			
seoa0388	NM_014341	/len=1890	NM_014341	Hs.279939	NP_055156

Figure 6	3d Cont'd.		·	·	
		growth hormone			
		inducible			1
		transmembrane			
		protein (GHITM),			
		mRNA			
ļ		/cds=(130,1089)			
		/gb=NM 014394			
		/gi=7657479			
		/ug=Hs.433957			
000b0574	NM 014394	/len=2374	NM 014394	Uc 422057	ND 055200
seob9574	14101_014394	TAF5-like RNA	14101_014394	Hs.433957	NP_055209
	,	polymerase II,			
	·	p300/CBP-			
		associated factor			
		(PCAF)-associated			
		factor, 65kDa			
		(TAF5L), mRNA			
	•	/cds=(98,1867)			
	:	/gb=NM_014409			
		/gi=21269865			
		/ug=Hs.26782			
mioa4770	NM 014409	/len=3065	NM 014409	Hs.26782	NP 055224
111104-7770	1410 014400	schwannomin	14141_014400	113.20702	141 _000224
		interacting protein 1			
			İ		
		(SCHIP1), mRNA			
		/cds=(70,1533)			ŀ
		/gb=NM_014575			
		/gi=7657539			
Ì		/ug=Hs.61490			
miob0487	NM_014575	/len=2112	NM_014575	Hs.61490	NP_055390
		gene predicted from			
		cDNA with a			
İ		complete coding			
		sequence (CMT2),			
		mRNA /cds=(4,828)			
					1
foregod	NIM 044600	•	NINA 04 4000	L 404	ND 055440
1010001	14028	//e/i-1233	14028	ITIS. 124	INP_U00443
		1.			1
		1.			1
		/cds=(921,1382)			
		/gb=NM_014656		[
		/gi=7657258			
					1
		/ug=Hs.158282			
fcr6801	NM_014628	/gb=NM_014656	NM_014628	Hs.124	NP_055443

T iguic o	a Conta.	- 			
		KIAA0152 gene product (KIAA0152), mRNA /cds=(129,1007) /gb=NM_014730 /gi=7661947 /ug=Hs.181418			
seob3105	NM_014730	/len=6322	NM_014730	Hs.181418	NP_055545
fcr4376	D14657	hypothetical protein (KIAA0101) RB1-inducible	NM_014736	Hs.81892	NP_055551
		coiled-coil 1 (RB1CC1), mRNA /cds=(516,5291) /gb=NM_014781 /gi=7661991 /ug=Hs.50421			
miod4140	NM_014781	/len=6614	NM_014781	Hs.50421	NP_055596
55000		chromosome 14 open reading frame 92 (C14orf92), mRNA /cds=(33,1898) /gb=NM_014828 /gi=7662273 /ug=Hs.194035			
fcr5029	NM_014828	/len=4174 chromosome 14 open reading frame 92 (C14orf92), mRNA /cds=(33,1898) /gb=NM_014828 /gi=7662273 /ug=Hs.194035	NM_014828	Hs.194035	NP_055643
miob0986	NM_014828	/len=4174 KIAA1116 protein (KIAA1116), mRNA /cds=(186,4001) /gb=NM_014892 /gi=7662491 /ug=Hs.227602	NM_014828	Hs.194035	NP_055643
ncrb3942	NM_014892	/len=4664	NM_014892	Hs.227602	NP_055707

Figure 6	d Cont'd.				
		zinc finger and BTB domain containing 1 (ZBTB1), mRNA /cds=(263,2197) /gb=NM_014950 /gi=7662437 /ug=Hs.372699			
miob3314	NM_014950	/len=3990	NM_014950	Hs.372699	NP_055765
		mitotic control protein dis3 (DIS3), mRNA /cds=(37,2913) /gb=NM_014953 /gi=19923415 /ug=Hs.323346			
miod1316	NM 014953	/len=7320	NM 014953	Hs.323346	NP 055768
		RAB21, member RAS oncogene family (RAB21), mRNA /cds=(256,933) /gb=NM_014999 /gi=7661921 /ug=Hs.184627			
mioa9062	NM_014999	/len=2630	NM_014999	Hs.184627	NP_055814
mioc1697	BC014378	clone IMAGE:4044107, mRNA		Hs.64691	NP_055991
mioc2082	NM_015247	cylindromatosis (turban tumor syndrome) (CYLD), mRNA /cds=(392,3262) /gb=NM_015247 /gi=14165257 /ug=Hs.18827 /len=5371	NM_015247	Hs.18827	NP_056062
mioa6404	NM 015252	KIAA0903 protein (KIAA0903), mRNA /cds=(349,4044) /gb=NM_015252 /gi=24308022 /ug=Hs.16218 /len=5048	NM 015252	Hs.16218	NP 056067
	1	T	<u> </u>	1	000001

Figure 6	d Contd.				
		additional sex			
1		combs like 1		İ	
		(Drosophila)	Į		
		(ASXL1), mRNA			
		/cds=(259,4884)			
		/gb=NM_015338			
		/gi=27734730			
		1 —			
		/ug=Hs.3686	l	1	
seoa4422	NM_015338	/len=6864	NM_015338_	Hs.3686	NP_056153
		cervical cancer 1			
1		protooncogene			
		(DKFZP586A011),			
		mRNA			
		/cds=(9,1091)			
		/gb=NM_015416			
		/gi=21166356			
		/ug=Hs.75884			
fcrc5789	NM 015416	/len=2118	NM 015416	Hs.75884	NP 056231
10100709	14141_013410	71611-2110	14141_013410	113.73004	INF_030231
		ring finger protein			
		19 (RNF19), mRNA			
		/cds=(318,2834)			
		/gb=NM_015435			
		/gi=19923421			
		/ug=Hs.48320			
mioa4196	NM_015435	/len=4357	NM_015435	Hs.48320	NP_056250
		DKFZP586G1517			
		protein			
		(DKFZP586G1517),			
		mRNA		<u> </u>	
		/cds=(127,2328)			
		/gb=NM 015440			
	1				
	ļ	/gi=24308062			
	N. 045440	/ug=Hs.44155			
mioa8607	NM_015440	/len=2749	NM_015440	Hs.44155	NP_056255
		mRNA; cDNA			
		DKFZp761G0111			
		(from clone			
mioc7209	AL833852	DKFZp761G0111)	NM_015472	Hs.24341	NP_056287
		synovial sarcoma			
		translocation gene			
	1	on chromosome 18-			
		like 1 (SS18L1),			
}	1	mRNA	}	l	
		/cds=(61,1251)			
		/gb=NM_015558			
		/gi=27754185			
		/ug=Hs.154429			
seoa7373	NM 015558	/len=3723	NM_015558	Hs.154429	NP 056373

IP_056390
IP 056517
IP 056983
15_020802
ID 050000
IP_056986
IP_057049
!
į
IP_057143
<u> </u>

GTP-binding protein Sara (LOC51128), mRNA /cds=(151,747) /gb=NM 016103 /gi=7705826 /ug=Hs.279582 mioa5729 NM 016103 /len=1280 Hs.279582 | NP_057187 NM_016103 zinc finger RNA binding protein (ZFR), mRNA /cds=(44,1300) /gb=NM_016107 /gi=7706372 /ug=Hs.173518 ncrc6888 NM_016107 /len=2734 NM_016107 Hs.173518 NP_057191 COP9 constitutive photomorphogenic subunit 4 (Arabidopsis) (COPS4), mRNA /cds=(7,1224) /gb=NM_016129 /gi=7705844 /ug=Hs.6671 seob7369 NM 016129 /len=1613 NM 016129 Hs.6671 NP_057213 retinoic acid receptor, beta (RARB), transcript variant 1, mRNA /cds=(469,1815) /gb=NM_000965 /gi=14916493 /ug=Hs.171495 NM 000965; seoa4464 NM 000965 /len=3119 NM 016152 Hs.171495 NP 057236 dynactin 4 (p62) (DCTN4), mRNA /cds=(22,1404) /gb=NM_016221 /gi=19923450 /ug=Hs.328865 fcrb5166 NM 016221 /len=3837 NM_016221 Hs.328865 NP_057305 high-glucoseregulated protein 8 (HGRG8), mRNA /cds=(151,1863) /gb=NM_016258 /gi=7705410 /ug=Hs.20993 miob4793 NM 016258 /len=2730 NM 016258 Hs.20993 NP 057342

- riguic o	a Conta.		,	,	
seoa3578	NM_016302	protein x 0001 (LOC51185), mRNA /cds=(34,1044) /gb=NM_016302 /gi=10047097 /ug=Hs.18925 /len=1668	NM_016302	Hs.18925	NP_057386
miob6721	NM_016315	CED-6 protein (CED-6), mRNA /cds=(429,1343) /gb=NM_016315 /gi=7705317 /ug=Hs.107056 /len=3277	NM_016315	Hs.107056	NP_057399
mioa5902	NM_016331	zinc finger protein ANC_2H01 (LOC51193), mRNA /cds=(446,1903) /gb=NM_016331 /gi=7705934 /ug=Hs.22879 /len=3013	NM_016331	Hs.22879	NP_057415
fcrb4280	NM_016404	hypothetical protein HSPC152 (HSPC152), mRNA /cds=(36,413) /gb=NM_016404 /gi=7705476 /ug=Hs.79259 /len=612	NM_016404	Hs.79259	NP_057488
seoa7583	NM_016570	CDA14 (LOC51290), mRNA /cds=(89,1225) /gb=NM_016570 /gi=7706104 /ug=Hs.26813 /len=1378	NM_016570	Hs.26813	NP_057654
ncrc6015	NM_016617	hypothetical protein BM-002 (BM-002), mRNA /cds=(40,297) /gb=NM_016617 /gi=7705299 /ug=Hs.367646 /len=2529	NM_016617	Hs.367646	NP_057701

T iguic c	a Conta.			, ———	
seob7614	NM_016648	HDCMA18P protein (HDCMA18P), mRNA /cds=(532,1176) /gb=NM_016648 /gi=7705400 /ug=Hs.278635 /len=1438	NM_016648	Hs.278635	NP_057732
	NIM 040047	chromosome 6 open reading frame 48 (C6orf48), mRNA /cds=(42,422) /gb=NM_016947 /gi=8393383 /ug=Hs.109798	NN 040047	U- 400 7 00	
seob5556	NM_016947	/len=711 nucleoporin 54kDa (NUP54), mRNA /cds=(129,1652) /gb=NM_017426 /gi=26051236 /ug=Hs.9082	NM_016947		NP_058643
miod5060	NM_017426	/len=2358 gp25L2 protein (HSGP25L2G), mRNA /cds=(76,720) /gb=NM_017510 /gi=24475637 /ug=Hs.279929 /len=1420	NM_017426	Hs.9082 Hs.279929	NP_059122
fcr5836	NM_017510	gp25L2 protein (HSGP25L2G), mRNA /cds=(76,720) /gb=NM_017510 /gi=24475637 /ug=Hs.279929 /len=1420	NM_017510 NM_017510	Hs.279929	NP_059980 NP_059980
fcrb5536	NM_017607	protein phosphatase 1, regulatory (inhibitor) subunit 12C (PPP1R12C), mRNA /cds=(19,2367) /gb=NM_017607 /gi=14149715 /ug=Hs.235975 /len=2944	NM_017607	Hs.235975	NP_060077

Figure 6	d Cont'd.				
		hypothetical protein			
		FLJ20073			
		(FLJ20073), mRNA			
		/cds=(17,1909)			
		/gb=NM 017654			
		/gi=8923080			
1		/ug=Hs.65641			
mioc0222	NM 017654	/len=3401	NM 017654	Hs.65641	NP 060124
IIIOCOZZZ	14101_017004	hypothetical protein	14101_017004	113.00041	141_000124
ì		FLJ20509			
İ		(FLJ20509), mRNA			
		/cds=(418,1041)			
		/gb=NM_017851			
		/gi=8923470			
		/ug=Hs.30634			
miod3739	NM_017851	/len=2369	NM_017851	Hs.30634	NP_060321
		hypothetical protein			
		FLJ20552			
		(FLJ20552), mRNA			
		/cds=(130,1065)			
		/gb=NM_017876			
}		/gi=21361772			
		/ug=Hs.69554			
ncr2842	NM 017876	/len=1681	NM 017876	Hs.69554	NP 060346
		RUN and FYVE			
		domain containing 2			
		(RUFY2), mRNA			
		/cds=(12,1832)			
		/gb=NM_017987			
		/gi=24850106			
		/ug=Hs.154091			
ncr1941	NM_017987	/len=2080	NM_017987	Hs.154091	NP_060457
11011941	14141_017907	hypothetical protein	14141_017967	ПS. 15409 I	NP_060457
		FLJ10154			
		(FLJ10154), mRNA			
		/cds=(246,1067)			
		/gb=NM_018011			
Ì		/gi=8922258			
1_		/ug=Hs.179972			
fcrc0039	NM_018011	/len=1734	NM_018011	Hs.179972	NP_060481
1		hypothetical protein			
		FLJ10159			
		(FLJ10159), mRNA			
}		/cds=(1,807)			
		/gb=NM_018013			
		/gi=8922262			
		/ug=Hs.22505			
ncr8156	NM_018013	/len=2070	NM 018013	Hs.22505	NP 060483
		<u> </u>			

rigule	oa Conta.				
		hypothetical protein FLJ10193			
	,	(FLJ10193), mRNA			
	ļ	/cds=(57,497)			
		/gb=NM_018019			
		/gi=22907057			}
ŀ		/ug=Hs.235195			
seoc5911	NM_018019	/len=2222	NM 018019	Hs.235195	NP 060489
36000311	114141_010019	hypothetical protein	14141_010019	118.233193	INF_000409
		FLJ10350			'
		(FLJ10350), mRNA		ŀ	
		/cds=(676,2340)	İ	ľ	
		/gb=NM_018067	İ		
		/gi=21361780			
		/ug=Hs.177596		İ	
fcrc5850	NM 018067	/len=2811	NM 019067	Uc 177506	NP 060537
10103030	114141_0 10007	solute carrier family	NM_018067	Hs.177596	INP_U0U03/
İ		4 (anion			
		,			
		exchanger),	,		
		member 1, adaptor			
•		protein			
1		(SLC4A1AP),	l		
	1	mRNA			
		/cds=(283,2673)			
		/gb=NM_018158			
		/gi=8922556			
		/ug=Hs.306000			
mioa3939	NM_018158	/len=2954	NM_018158	Hs.306000	NP_060628
		hypothetical protein		1	l . I
		FLJ10687		Ī	
		(FLJ10687), mRNA			
		/cds=(46,903)			
		/gb=NM_018178			
		/gi=21361715	į		
		/ug=Hs.29379		1	
miod6646	NM_018178	/len=2992	NM_018178	Hs.29379	NP_060648
		hypothetical protein			
		FLJ10700			
		(FLJ10700), mRNA			ľ
	ĺ	/cds=(184,1872)		ļ	
		/gb=NM_018182			
}		/gi=8922595			
		/ug=Hs.295909			
fcrb6202	NM_018182	/len=3434	NM_018182	Hs.295909	NP_060652
		polybromo-1 (PB1)			
		mRNA, complete			
		cds, alternatively	NM_018165;		
seoc1163	AF225871	spliced	NM_018313	Hs.44143	NP 060783
		<u> </u>			

Figure 6	d Conta.		····		
		hypothetical protein			
•		FLJ11184			
		(FLJ11184), mRNA			
		/cds=(113,724)			
i		/gb=NM_018352			
		/gi=8922922			
		/ug=Hs.267446			
seob6139	NM_018352	/len=1748	NM_018352	Hs.267446	NP_060822
		TBC1 domain			
		family, member 2			
]		(TBC1D2), mRNA			
		/cds=(1622,3028)			
		/gb=NM_018421			
		/gi=8922166			
		/ug=Hs.135917			
seob6084	NM_018421	/len=3431	NM_018421	Hs.135917	NP 060891
	-	uncharacterized		· · · · · · · · · · · · · · · · · · ·	
		hematopoietic			
		stem/progenitor			
					,
		cells protein			
		MDS030 (MDS030),			
		mRNA			
1		/cds=(206,649)			
		/gb=NM_018465			
		/gi=8923931			
	NII 040405	/ug=Hs.181385		11 404005	
mioc6970	NM_018465	/len=927	NM_018465	Hs.181385	NP_060935
		hypothetical protein			
		PRO1843			
1		(PRO1843), mRNA			
		/cds=(965,1255)			
1		/gb=NM 018507			
1		_			
1		/gi=8924082			
	l	/ug=Hs.283330			
ncrc0151	NM_018507	/len=1268	NM_018507	Hs.283330	NP_060977
		clone MGC:32681			
1		IMAGE:4809776,			
1		mRNA, complete			
ncrb0757	BC029427	icds		Hs.410294	NP 061008
110120101	20020-121	zinc finger protein	-	1.13.7 10204	111 _00 1000
		302 (ZNF302),			
		mRNA			
		/cds=(337,1773)			
}	}	/gb=NM_018675	İ		
		/gi=11034834			
		/ug=Hs.125287	NM_018443;		
mioc6360	NM 019675	/len=2978		Uc 125207	ND 061145
111111111111111111111111111111111111111	NM 018675	/I C II-29/0	NM_018675	Hs.125287	NP_061145

1 19410 0	od Conta.				
ncr0004	NM_018847	KIAA1354 protein (KIAA1354), mRNA /cds=(514,2367) /gb=NM_018847 /gi=24308180 /ug=Hs.106283 /len=4373	NM_018847	Hs.106283	NP_061335
ncroud4	INIVI_U 10047	mRNA; cDNA	NIVI_U18847	Ins. 100203	NP_061335
		DKFZp434P0721 (from clone DKFZp434P0721); partial cds /cds=(1,3481) /gb=AL133623 /gi=6599261			
		/ug=Hs.82501			
seoa5586	AL133623	/len=8281 chromosome 20		Hs.82501	NP_061874
		open reading frame 155 (C20orf155),			
fcrb6613	NM_019095	mRNA	NM_019095	Hs.3569	NP_061968
seoc2614	NM_019095	hypothetical protein (LOC54675), mRNA /cds=(1,906) /gb=NM_019095 /gi=10092646 /ug=Hs.3569 /len=906	NM_019095	Hs.3569	NP_061968
mioc5039	NM_020038	ATP-binding cassette, sub-family C (CFTR/MRP), member 3 (ABCC3), transcript variant MRP3B, mRNA /cds=(71,1603) /gb=NM_020038 /gi=9955973 /ug=Hs.90786 /len=5380	NM_003786; NM_020037; NM_020038	Hs.90786	NP 064422
111000000	1444_020000	SAR1 protein	14141_020000	113.30700	141 _007422
fcrb2317	NM _020150	(SAR1), mRNA /cds=(125,721) /gb=NM_020150 /gi=21361614 /ug=Hs.110796 /len=3003	NIM 020150	He 110706	ND 064525
10102317		/len-3003	NM_020150	Hs.110796	NP_064535

_ i iguie c	a Conta.		·		
		methylcrotonoyl-			
		Coenzyme A			
		carboxylase 1			
		(alpha) (MCCC1),			
		mRNA			
		/cds=(133,2310)			
		/gb=NM_020166			
		/gi=13518227	ł		
		/ug=Hs.47649			
mioa5059	NM 020166	/len=2528	NM 020166	Hs.47649	NP 064551
	525755	disrupter of		710:11010	111 _004001
		silencing 10			
	Î	(SAS10), mRNA			
		/cds=(162,1601)			
		/gb=NM_020368			
		/gi=9966798			
		/ug=Hs.322901			
seoc3854	NM 020368	/len=2035	NIM ODOGEO	LL 222004	ND 005404
56003034	111111_020300	neuron navigator 1	NM_020368	Hs.322901	NP_065101
1		. •			
1		(NAV1), mRNA			
i		/cds=(348,5972)			
		/gb=NM_020443			
		/gi=27262621			
1		/ug=Hs.6298		l	
miob2601	NM_020443	/len=11365	NM_020443	Hs.6298	NP_065176
		mRNA; cDNA			
		DKFZp564D0462			
		(from clone		l <u>.</u>	
miod0935	AL080079	DKFZp564D0462)	NM_020455	Hs.44197	NP_065188
		54TMp (54tm)			
	l	(=S83365 RAB5-			
fcr4056	AF004876	interaction protein)	NM_020470	Hs.406422	NP_065203
		nuclear factor of			
		kappa light		:	
		polypeptide gene			
		enhancer in B-cells			
1		inhibitor, alpha	1		
		(NFKBIA), mRNA			
		/cds=(95,1048)			
1		/gb=NM_020529			
1		/gi=10092618			
1		/ug=Hs.81328			
ncrc9528	NM_020529	/len=1550	NM_020529	Hs.81328	NP_065390
		retinol			
1		dehydrogenase 14			
		(all-trans and 9-cis)			
		(RDH14), mRNA			
		/cds=(64,1074)			
		/gb=NM_020905			
		/gi=10190745			
1		/ug=Hs.288880			
mioa7955	NM_020905	/len=1538	NM_020905	Hs.288880	NP_065956
		*			

- I iguie o	d Cont'd.				
		latent transforming			
		growth factor beta			
}		binding protein 3			
		(LTBP3), mRNA]		
		/cds=(1,3771)			
		/gb=NM_021070			
	İ	/gi=18497287			
		1 ~			
	NIA 004070	/ug=Hs.289019	NINA 004070		
fcrb8134	NM_021070	/len=4064	NM_021070	Hs.289019	NP_066548
		zinc finger protein 2			
		(A1-5) (ZNF2),			
		mRNA			
		/cds=(855,1733)			
		/gb=NM_021088			
		/gi=20304090			
		/ug=Hs.192285			
seoa0302	NM_021088	/len=2630	NM_021088	Hs.192285	NP_066574
		thymosin, beta 4, X			
		chromosome			
]	(TMSB4X), mRNA			
]	/cds=(78,212)			
		/gb=NM_021109			
	į	/gi=11056060			
		/ug=Hs.75968			
seoa0040	NM 021109	/len=556	NINA 024400	Un 75000	ND 000000
Se0a0040	14101_021109	/len-556	NM_021109	Hs.75968	NP_066932
		reversion-inducing-			
		cysteine-rich protein			İ
	ĺ	with kazal motifs			
		(RECK), mRNA			
į		/cds=(93,3008)			
		/gb=NM_021111			
l .		/gi=11863155			
		/ug=Hs.29640			
miob0931	NM_021111	/len=4414	NM_021111	Hs.29640	NP 066934
					=
		hypothetical protein			
		similar to small G			
		proteins, especially			
		RAP-2A			
		(LOC57826), mRNA			
ļ		/cds=(17,568)			
		1			
		/gb=NM_021183			
		/gi=10880976			
7010	NA 004465	/ug=Hs.225979			
seoc7910	NM_021183	/len=3165	NM_021183	Hs.225979	NP_067006

i iguie o	a Conta.				
i		DC2 protein (DC2),		İ	
		mRNA			
		/cds=(60,509)			
		/gb=NM_021227			
		/gi=24308270			
		•			
1		/ug=Hs.103180			
fcrb5961	NM_021227	/len=1090	NM_021227	Hs.103180	NP_067050
		adaptor-related			-
		protein complex 2,			
		sigma 1 subunit			
		(AP2S1), transcript			
		variant AP17,			
		•			
		mRNA			
		/cds=(71,499)			
		/gb=NM_004069			
		/gi=11038644			
		/ug=Hs.119591	NM_004069;		
fcrb6279	NM 004069	/len=781	NM 021575	Hs.119591	NP 067586
		zinc-finger protein			
		ZBRK1 (ZBRK1),			
		mRNA			
		l .			
		/cds=(184,1782)		1	
		/gb=NM_021632		1	
		/gi=11056003			
		/ug=Hs.130965			
seob3404	NM_021632	/len=2260	NM_021632	Hs.130965	NP_067645
		hypothetical protein	_		
		MDS025 (MDS025),			
		mRNA			
		/cds=(363,1127)			
	ļ	1 ' '			
		/gb=NM_021825			
		/gi=21361605			į
1		/ug=Hs.154938			
fcrb5051	NM_021825	/len=1585	NM_021825	Hs.154938	NP_068597
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		DKFZp586A0722			
		(from clone			
seoc1216	AL049447	DKFZp586A0722)		Hs.433334	NP 068603
		FXYD domain		1.0.10004	
		containing ion			
ļ		Ţ			
ŀ		transport regulator 6			
		(FXYD6), mRNA			
		/cds=(67,354)		ļ	
	Ì	/gb=NM_022003			
		/gi=11612654			
		/ug=Hs.3807			
fcrb1547	NM_022003	/len=1677	NM 022003	Hs.3807	NP_071286
		1	<u> </u>		1.11 _07 1200

<u> </u>	a Conta.				_
		leucine zipper			
		protein FKSG14			1
		(FKSG14), mRNA			ļ
		/cds=(265,1074)			
		/gb=NM 022145			
	•	/gi=16905072			
		/ug=Hs.192843			
seoa9665	NM_022145	/len=1794	NIM 022145	Hs.192843	ND 074400
Secasoco	14101_022 143		NM_022145	ITS. 192043	NP_071428
		hypothetical protein FLJ21657			
		(FLJ21657), mRNA			
		/cds=(342,989)			
		/gb=NM_022483			
		/gi=19923589			
		/ug=Hs.26498			
miod7052	NM_022483	/len=2995	NM_022483	Hs.26498	NP_071928
		similar to rat nuclear			
		ubiquitous casein			
		kinase 2 (NUCKS),			
		mRNA			
		/cds=(67,558)			
		/gb=NM 022731			
		/gi=12232386			
		/ug=Hs.118064			
mioa2851	NM 022731	/len=1811	NM 022731	Hs.118064	NP 073568
1111042031	IVIVI_022731	similar to rat nuclear	INIVI_022731	П5. 1 10004	INP_073300
		ubiquitous casein			
		kinase 2 (NUCKS),			
		mRNA			
		/cds=(67,558)			
		/gb=NM_022731			
		/gi=12232386			
		/ug=Hs.118064			
mioc0121	NM_022731	/len=1811	NM_022731	Hs.118064	NP_073568
		hypothetical protein			
		FLJ11730			
		(FLJ11730), mRNA			
		/cds=(33,608)		1	
		/gb=NM_022756			
		/gi=20149668			
		/ug=Hs.17118			
ncrc9642	NM 022756	/len=1558	NM 022756	Hs.17118	NP 073593
	022700	FAD104 (FAD104),	022700	1.13.17.110	141_070000
mioa8074	NM 022763	mRNA	NM_022763	Hs.299883	NP_073600
111000074	14141_022700	FAD104 (FAD104),	14141_022103	1 13.233003	1147_073000
		,			
1		mRNA			
1		/cds=(58,3672)			
1		/gb=NM_022763		1	
1		/gi=27477058		1	
		/ug=Hs.299883		l	
seob3747	NM_022763	/len=6894	NM_022763	Hs.299883	NP_073600

rigure o	d Cont'd.				
		core-binding factor,			
		beta subunit			
		(CBFB), transcript	NM_001755;		
miod6988	NM 022845	variant 1, mRNA	NM_022845	Hs.179881	NP 074036
		mRNA; cDNA		110.170001	111 _07 1000
		DKFZp761C169			
		1	}		
		(from clone			
		DKFZp761C169);			:
		partial cds		}	
		/cds=(997,2475)			
		/gb=AL161991		:	
		/gi=7328122			
		/ug=Hs.71252			
seoc0422	AL161991	/len=3324	NM 022913	Hs.71252	NP_075064
00000 122	7.2101001	mRNA; cDNA	022010	113.7 1202	141 _070004
		DKFZp761C169			
1		1 '			
		(from clone			
		DKFZp761C169);			
1		partial cds]		
		/cds=(997,2475)			
		/gb=AL161991			
		/gi=7328122			
		/ug=Hs.71252	1		
seob4011	AL161991	/len=3324	NM_022913	Hs.71252	NP 075064
00021011	7.2.10.1001	hypothetical protein	11111_022010	110.7 1202	141 _07 0004
		FLJ12895	·		
					:
		(FLJ12895), mRNA			
		/cds=(410,1942)			
1		/gb=NM_023926			
İ		/gi=21314715			
		/ug=Hs.235390			
ncrc3116	NM_023926	/len=2804	NM_023926	Hs.235390	NP_076415
			_		
		hypothetical protein	ľ		
		MGC2941			
		(MGC2941), mRNA			
		/cds=(172,969)	l		
		/gb=NM_024297			
		/gi=13236519			
		/ug=Hs.288217			
fcrc1849	NM_024297	/len=2005	NM_024297	Hs.288217	NP_077273
Ì		hypothetical protein			
		FLJ22555			
}	}	(FLJ22555), mRNA			
		/cds=(323,1198)			
		/gb=NM_024520			
		/gi=13375659			
		1 -			
minh2044	NINA 004500	/ug=Hs.3592	N. 00 4500	11- 2522	ND 070700
miob2944	NM_024520	/len=1530	NM_024520	Hs.3592	NP_078796

Figure 6	id Cont'd.				
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		(FLJ21432), mRNA			
		/cds=(110,886)			
		/gb=NM_024551			
		/gi=13375714			
		/ug=Hs.334854			
ncrc7038	NM_024551	/len=3500	NM_024551	Hs.334854	NP_078827
		chromodomain			
		helicase DNA	ŀ		
		binding protein 1-		}	
		like (CHD1L),			
		lmRNA /			
	1	/cds=(332,1897)			
		/gb=NM_024568			
		/gi=24308292			
		/ug=Hs.14570			
	NIM 00.4500	1 •	1114 004500	44570	ND 070044
seob8986	NM_024568	/len=2936	NM_024568	Hs.14570	NP_078844
		Similar to			
		hypothetical protein			
		FLJ21212, clone			
		MGC:24384		1	
		IMAGE:4064736,			
		mRNA, complete			
seoa6389	BC013945	cds	NM 024642	Hs.47099	NP 078918
		hypothetical protein			
		FLJ11565			
		(FLJ11565), mRNA			
		/cds=(19,2301)			
		1			
		/gb=NM_024657			
		/gi=21362027	ļ		İ
	l	/ug=Hs.61763			
ncr2899	NM_024657	/len=3037	NM_024657	Hs.61763	NP_078933
		hypothetical protein		ĺ	
		FLJ11753		ĺ	
		(FLJ11753), mRNA			
		/cds=(14,832)			
		/gb=NM_024659			
1		/gi=13375910			
1		/ug=Hs.62348			
miod4023	NM 024659	/len=1868	NM_024659	Hs.62348	NP 078935
		hypothetical protein	02 1000		0,0000
		FLJ14007			
		(FLJ14007), mRNA	}		
		1.			
		/cds=(15,821)			
		/gb=NM_024699			
1		/gi=13375984			
		/ug=Hs.99519			
mioc4929	NM_024699	/len=1793	NM_024699	Hs.99519	NP_078975

I igule 0	a Conta.				
		hypothetical protein			
		FLJ13213			
		(FLJ13213), mRNA			
		/cds=(234,1670)			
		/gb=NM_024755			
ł		/gi=13376087			
		/ug=Hs.331328			
mioa7617	NM_024755	/len=2617	NM_024755	Hs.331328	NP_079031
		hypothetical protein			
		FLJ12888			
		(FLJ12888), mRNA			
		/cds=(333,2210)			
	•	/gb=NM_024945			
		/gi=13376426			
		/ug=Hs.284137			
ncr7532	NM_024945	/len=3413	NM_024945	Hs.284137	NP_079221
		mRNA; cDNA			
		DKFZp666L233			
		(from clone			
seoc3801	AL832993	DKFZp666L233)	NM_030571	Hs.9788	NP_085048
		matrilin 2 (MATN2),	1		
		transcript variant 1,			
		mRNA			
		/cds=(126,2996)			
		/gb=NM_002380			
		/gi=13518036			
	N. 1. 000000	/ug=Hs.19368	NM_002380;	40000	LUD 005070
mioa4183	NM_002380	/len=3496	NM_030583	Hs.19368	NP_085072
		transcription factor			
		8 (represses			
		interleukin 2			
		expression) (TCF8), mRNA			
		/cds=(25,3399)]
		/gb=NM_030751 /gi=28077090]
		/ug=Hs.232068			
mioa2970	NM 030751	/len=3952	NM 030751	Hs.232068	NP 110378
1111002570	[141VI_U3U/31	thioredoxin domain	14M_030731	1 15.232000	ווער ווטטוס
		containing, clone			
		IMAGE:5764221,			
miob9233	BC050366	mRNA			NP 110382
111003233	10000000	11111/17/21			INF_I 1030Z
		hypothetical protein			
		AF311304			
		(AF311304), mRNA			
		/cds=(21,185)			
		/gb=NM_031214			
		/gi=13654285			
		/ug=Hs.300624			
seoa3274	NM_031214	/len=1138	NM_031214	Hs.300624	NP_112491
	1	1,1011 1100	1.4141_001213	110.000024	1.1 1.2701

Figure 6	d Cont'd.				
b 7027	AIN 024240	sec13-like protein (SEC13L), mRNA /cds=(107,1189) /gb=NM_031216 /gi=14591917 /ug=Hs.301048	NNA 004040		NP 440400
seob7637	NM_031216	/len=3492	NM_031216	Hs.301048	NP_112493
		SH3 domain binding glutamic acid-rich protein like 3 (SH3BGRL3), mRNA /cds=(72,353) /gb=NM_031286 /gi=13775197 /ug=Hs.109051			
fcrb2933	NM_031286	/len=764	NM_031286	Hs.109051	NP_112576
seoa4324	NM_031287	SF3b10 (SF3b10), mRNA	NM_031287	Hs.110695	NP_112577
mioc1808	NM_031452	hypothetical protein MGC2560 (MGC2560), mRNA /cds=(195,551) /gb=NM_031452 /gi=13899288 /ug=Hs.80624 /len=1229	NM_031452	Hs.80624	NP_113640
fcrb7247	NM_031453	hypothetical protein MGC11034 (MGC11034), mRNA /cds=(246,641) /gb=NM_031453 /gi=13899290 /ug=Hs.103378 /len=3301	NM_031453	Hs.103378	NP_113641
ncrc2705	NM_031461	CocoaCrisp (LOC83690), mRNA /cds=(376,1878) /gb=NM_031461 /gi=21314740 /ug=Hs.182364 /len=2962	NM_031461	Hs.182364	NP_113649

poly(rC) binding protein 2 (PCBP2), transcript variant 1, mRNA /cds=(89,1189) /gb=NM_005016 /gi=1414167 /ug=Hs.63525 NM_005016; /len=1362 NM_031989 Hs.63525 NP_11436 (NCALD), mRNA /cds=(121,702) /gb=NM_032041 /gi=14042973 /ug=Hs.90063 NM_032041 Hs.90063 NP_11443 hypothetical protein DKFZp564K142 similar to implantation—associated protein (DKFZp564K142), mRNA /cds=(30,1037)	- I iguie c	a Conta.				,
Mm_031469 Nm_031469 Nm_031469 Nm_031469 Nm_031469 Nm_031469 Nm_031469 Nm_031469 Nm_031469 Nm_031469 Nm_031469 Nm_031469 Nm_031469 Nm_031469 Nm_031469 Nm_031469 Nm_031469 Nm_031469 Nm_031469 Nm_031483 Nm_0			glutamic acid-rich protein like 2 (SH3BGRL2), mRNA /cds=(180,503) /gb=NM_031469 /gi=13899316			
itchy E3 ubiquitin protein ligase (mouse) (ITCH), mRNA /cds=(171,2759) /gb=NM_031483 /gi=27477108 /ug=Hs.98074 /len=6357 NM_031483 Hs.98074 NP_11367 poly(rC) binding protein 2 (PCBP2), transcript variant 1, mRNA /cds=(89,1189) /gb=NM_005016 /gi=14141167 /ug=Hs.63525 NM_005016; /len=1362 NM_031989 Hs.63525 NP_11436 (NCALD), mRNA /cds=(121,702) /gb=NM_032041 /gi=14042973 /ug=Hs.90063 NM_032041 Hs.90063 NP_11443 hypothetical protein DKFZp564K142 similar to implantation-associated protein (DKFZp564K142), mRNA /cds=(30,1037)	miod6896	NM 031469		NM 031469	He 9167	ND 113657
poly(rC) binding protein 2 (PCBP2), transcript variant 1, mRNA /cds=(89,1189) /gb=NM_005016 /gi=14141167 /ug=Hs.63525 NM_005016; /len=1362 NM_031989 Hs.63525 NP_11436 neurocalcin delta (NCALD), mRNA /cds=(121,702) /gb=NM_032041 /gi=14042973 /ug=Hs.90063 NM_032041 Hs.90063 NP_11443 hypothetical protein DKFZp564K142 similar to implantation-associated protein (DKFZp564K142), mRNA /cds=(30,1037)			itchy E3 ubiquitin protein ligase (mouse) (ITCH), mRNA /cds=(171,2759) /gb=NM_031483 /gi=27477108			
poly(rC) binding protein 2 (PCBP2), transcript variant 1, mRNA /cds=(89,1189) /gb=NM_005016 /gi=14141167 /ug=Hs.63525 NM_005016; /len=1362 NM_031989 Hs.63525 NP_11436 NP_	mioc3370	NM 031483	/len=6357	NM 031483	Hs.98074	NP 113671
neurocalcin delta (NCALD), mRNA /cds=(121,702) /gb=NM_032041 //gi=14042973 /ug=Hs.90063 seoc0861 NM_032041 //len=3300 NM_032041 Hs.90063 NP_11443 hypothetical protein DKFZp564K142 similar to implantation- associated protein (DKFZp564K142), mRNA /cds=(30,1037)	mioa2173	NM 005016	protein 2 (PCBP2), transcript variant 1, mRNA /cds=(89,1189) /gb=NM_005016 /gi=14141167 /ug=Hs.63525	. –	Hs 63525	NP 114366
hypothetical protein DKFZp564K142 similar to implantation- associated protein (DKFZp564K142), mRNA /cds=(30,1037)			neurocalcin delta (NCALD), mRNA /cds=(121,702) /gb=NM_032041 /gi=14042973 /ug=Hs.90063	_		NP_114430
/gi=14149774 /ug=Hs.323562			hypothetical protein DKFZp564K142 similar to implantation- associated protein (DKFZp564K142), mRNA /cds=(30,1037) /gb=NM_032121 /gi=14149774 /ug=Hs.323562			NP_115497

1 iguic c	oa Conta.				
mioc8079	NM_032148	hypothetical protein DKFZp434K0427 (DKFZP434K0427), mRNA /cds=(342,1814) /gb=NM_032148 /gi=14149818 /ug=Hs.238996 /len=2375 lysyl oxidase-like 4 (LOXL4), mRNA /cds=(152,2422) /gb=NM_032211	NM_032148	Hs.238996	NP_115524
		/gi=19923658			
fana0424	NINA 022244	/ug=Hs.306814	NINA 000044	11. 200044	ND 445507
fcrc0134	NM_032211	/len=3665	NM_032211	Hs.306814	NP_115587
seob2953	NM_032273	hypothetical protein DKFZp586C1924 (DKFZp586C1924), mRNA /cds=(106,693) /gb=NM_032273 /gi=14150016 /ug=Hs.108338 /len=782	NM_032273	Hs.108338	NP_115649
ncrc9055	NM_032313	hypothetical protein MGC3232 (MGC3232), mRNA /cds=(85,2181) /gb=NM_032313 /gi=14150077 /ug=Hs.8715 /len=2316	NM_032313	Hs.8715	NP_115689
fcrb8110	NM_032347	zinc finger protein 397 (ZNF397), mRNA /cds=(136,963) /gb=NM_032347 /gi=14150142 /ug=Hs.269914 /len=1439	NM 032347		NP 115723
	1002071	1,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	1.111_002071	11.10.2000 14	110120

rigure o	id Cont'd.	-			
		hypothetical protein MGC5139 (MGC5139), mRNA /cds=(14,115) /gb=NM_032661 /gi=14249217 /ug=Hs.127610			
mioa9258	NM 032661	/len=457	NM_032661	Hs.127610	NP 116050
1111043230	14141_002001	forkhead box P1	14141_002001	113.127010	111_110000
		(FOXP1), mRNA			
	j	/cds=(432,2465)			
		/gb=NM_032682			
		/gi=19923670			
		/ug=Hs.274344			
ncr2304	NM_032682	/len=4954	NM_032682	Hs.274344	NP_116071
		hypothetical protein FLJ14668 (FLJ14668), mRNA /cds=(59,475) /gb=NM_032822 /gi=14249519 /ug=Hs.334644			
seoc3443	NM 032822	/len=1786	NM 032822	Hs.334644	NP 116211
miod2082	NIM 022950	hypothetical protein FLJ14906 (FLJ14906), mRNA /cds=(131,736) /gb=NM_032859 /gi=14249591 /ug=Hs.183528 /len=2492	NINA 022050		
1111002002	NM_032859	SR rich protein	NM_032859	Hs.183528	NP_116248
		(DKFZp564B0769), mRNA /cds=(33,2450) /gb=NM_032870 /gi=18699723 /ug=Hs.18368			
ncrc3773	NM_032870	/len=2663	NM_032870	Hs.18368	NP_116259
		hypothetical protein MGC14421 (MGC14421), mRNA /cds=(474,1616) /gb=NM_032907 /gi=14249681 /ug=Hs.334713			
fcrb7573	NM_032907	/len=1772	NM_032907	Hs.334713	NP_116296

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fcr3287	NM_002607	platelet-derived growth factor alpha polypeptide (PDGFA), transcript variant 1, mRNA /cds=(839,1474) /gb=NM_002607 /gi=15208657 /ug=Hs.37040 /len=2797	NM_002607; NM_033023	Hs.37040	NP 148983
ncr7768	NM_033055	likely ortholog of mouse hippocampus abundant gene transcript 1 (HIAT1), mRNA /cds=(6,1124) /gb=NM_033055 /gi=24308343 /ug=Hs.21015 /len=2230	NM 033055	Hs.21015	NP 149044
fcr1150	NM_033209	Thy-1 co- transcribed (LOC94105), mRNA /cds=(1289,1717) /gb=NM_033209 /gi=24475732 /ug=Hs.345643 /len=1818	_		NP_149986
fcr6395	NM_003672	CDC14 cell division cycle 14 A (S. cerevisiae) (CDC14A), transcript variant 1, mRNA /cds=(466,2250) /gb=NM_003672 /gi=15451928 /ug=Hs.65993 /len=4262	NM_003672; NM_033312; NM_033313	Hs.65993	NP_201570
miod2665	NM_033318	hypothetical gene supported by AL449243 (LOC91689), mRNA /cds=(80,403) /gb=NM_033318 /gi=21314768 /ug=Hs.306083 /len=1586	NM_033318	Hs.306083	NP_201575

	d Cont'd.			г	T
mioc2720	NM_033495	KIAA1309 protein (KIAA1309), mRNA /cds=(211,2025) /gb=NM_033495 /gi=15741229 /ug=Hs.348262 /len=3119	NM_033495	Hs.348262	NP 277030
1111002720	74111_000400	ribosomal protein	1411_000400	113.040202	277000
		L36 (RPL36),			
		transcript variant 2, mRNA			
		/cds=(153,470)			
		/gb=NM_015414			
		/gi=16117793 /ug=Hs.433411	NM_015414;		
fcrb1296	NM_015414	/len=545	NM_033643	Hs.433411	NP_378669
		cell recognition molecule CASPR3 (CASPR3), transcript variant 1,			
		mRNA /cds=(408,3872) /gb=NM_033655 /gi=16306508			
min n 45 40	NIM 022055	/ug=Hs.212839	NM_024879;	11- 040000	ND 207504
mioa4542	NM_033655	/len=5017	NM_033655	Hs.212839	NP_387504
ncrc9916	BQ109159	imageqc_6_2001/sn k86bdrr81.y1 NIH_MGC_12 cDNA clone IMAGE:5110111 5', mRNA sequence /clone=IMAGE:5110 111 /clone_end=5' /gb=BQ109159 /gi=20158813 /ug=Hs.433575		Llc 422575	ND 297506
ncrc9916	BQ109159	/len=604 NADH		Hs.433575	NP_387506
		dehydrogenase (ubiquinone) flavoprotein 1, 51kDa (NDUFV1), mRNA /cds=(70,1464) /gb=NM_007103 /gi=20149567 /ug=Hs.7744			
fcrb6870	NM_007103	/len=1566	NM_007103	Hs.7744	NP_438172

I iguic o	d Cont d.				
		chromosome 1			
		open reading frame			
		24 (C1orf24),			
		mRNA			
		/cds=(195,2981)			
		/gb=NM_052966			
		/gi=16757969			
		/ug=Hs.48778	NM_022083;		
ncrc9758	NM_052966	/len=6919	NM_052966	Hs.48778	NP_443198
		myosin, light	NM_005965;		
		polypeptide kinase	NM_053025;		
1		(MYLK), transcript	NM_053026;		
		variant 1, mRNA	NM_053027;		
		/cds=(120,5864)	NM_053028;		
			_		
1		/gb=NM_053025	NM_053029;		
1		/gi=16950610	NM_053030;]
		/ug=Hs.211582	NM_053031;		
ncr1912	NM_053025	/len=5925	NM_053032	Hs.211582	NP_444260
1		endothelial			
		differentiation,			
		lysophosphatidic			
1		acid G-protein-			
		coupled receptor, 2,			
		, .			
		clone MGC:33157			
		IMAGE:5272431,			
		mRNA, complete	NM_001401;		
ncr5909	BC036034	cds	NM_057159	Hs.75794	NP_476500
		chromosome 20			
		open reading frame			
		108 (C20orf108),			
		mRNA			
		/cds=(41,619)			
		/gb=NM_080821			
		/gi=18201877			
		/ug=Hs.352413	l	l <u></u> .	
seoa2795	NM_080821	/len=3026	NM_080821	Hs.352413	NP_543011
		collectin sub-family			
		member 12			
		(COLEC12),			
		transcript variant II,			
		mRNA			
		/cds=(172,2040)			
		/gb=NM 030781	}		
		_			
		/gi=18641357			
1	l	/ug=Hs.29423	NM_030781;		
miod7066	NM_030781	/len=4685	NM_130386	Hs.29423	NP_569057

, rigare o	d Conta.				·
		leucine-rich PPR-			
		motif containing			
		(LRPPRC), mRNA			
		/cds=(46,3867)			
	ļ	/gb=NM_133259			
		/gi=18959201			
		/ug=Hs.182490			
mioc8640	NM_133259	/len=4782	NM_133259	Hs.182490	NP_573566
		CD109 (CD109),			
		mRNA	ļ		
		/cds=(113,4450)			
		/gb=NM_133493			
		/gi=19424129			
}		/ug=Hs.55964			
seoa1661	NM_133493	/len=5883	NM_133493	Hs.55964	NP_598000
		zinc finger protein			
		274 (ZNF274),			
		transcript variant	ļ		
1		ZNF274c, mRNA			
		/cds=(460,2421)			
		/gb=NM_133502			
		/gi=19743800	NM_016324;		
		/ug=Hs.83761	NM_016325;		
mioc2340	NM_133502	/len=2839	NM_133502	Hs.83761	NP_598009
		decorin (DCN),			
		transcript variant			
		A1, mRNA	NM_001920;		
		/cds=(200,1279)	NM_133503;		
		/gb=NM_001920	NM_133504;		
İ		/gi=19743844	NM_133505;		
		/ug=Hs.433989	NM_133506;		
seob3112	NM_001920	/len=1751	NM_133507	Hs.433989	NP_598014
		synaptic nuclei			
		expressed gene 1			
		(SYNE-1), transcript			
		variant beta, mRNA			
		/cds=(121,10086)			
		/gb=NM_015293			
		/gi=19526752	NM_015293;		
		/ug=Hs.192102	NM_033071;		
seob6379	NM_015293	/len=10742	NM_133650	Hs.192102	NP_598411
		smoothelin (SMTN),			
}	Ì	transcript variant 2,			
		mRNA			
		/cds=(219,2966)]
		/gb=NM_134269			
		/gi=19913395	NM_006932;		
		/ug=Hs.149098	NM_134269;		
fcr4784	NM_134269	/len=3294	NM_134270	Hs.149098	NP_599032

Figure o	a Conta.				
		helicase II			
		(RAD54L) mRNA,	!		
		complete cds.			
		/cds=(54,4979)			
		/gb=U09820			
1		/gi=606832	NM_000489;		
		/ug=Hs.96264	NM_138270;		
seob0047	U09820	/len=6115	NM_138271	Hs.96264	NP 612115
-		hypothetical protein		<u> </u>	
		BC013035			
		(LOC114926),			
		mRNA			
	:	/cds=(128,430)			
		/gb=NM_138436			
		/gi=19923964			
		/ug=Hs.10018			
seoc1948	NM 138436	/len=836	NM 138436	Hs.10018	NP 612445
30001040	14111_100400	clone MGC:20208	1401_100400	113.10010	012443
		IMAGE:3936339,			
		mRNA, complete			
		cds			
		/cds=(330,1832)			
		1			
		/gb=BC014000			
		/gi=15559281			
	D0044000	/ug=Hs.58461		50404	
ncr5529	BC014000	/len=2733		Hs.58461	NP_612456
		collagen triple helix			
		repeat containing 1			
		(CTHRC1), mRNA			
		/cds=(109,840)			
		/gb=NM_138455			
		/gi=19923988			
		/ug=Hs.283713			
fcrb5507	NM_138455	/len=1245	NM_138455	Hs.283713	NP_612464
	j	kinesin family			
		member 23 (KIF23),			
		transcript variant 1,			
		mRNA			
		/cds=(118,3000)			
		/gb=NM_138555			
		/gi=20143966		ļ	
		/ug=Hs.270845	NM_004856;		i
fcrb5705	NM_138555	/len=3636	NM_138555	Hs.270845	NP_612565
		hypothetical protein			
		BC014320			
		(LOC116254),			
		mRNA			
		/cds=(28,1020)			
		/gb=NM_138785			
		/gi=20302037			
		/ug=Hs.240767			
fcrb5164	NM_138785	/len=1143	NM_138785	Hs.240767	NP_620140
		******	<u> </u>		

Figure 6	a Conta.		Y		,
		peptidylglycine			
1		alpha-amidating			
		monooxygenase			
		(PAM), transcript			
		variant 1, mRNA			
		/cds=(374,3298)			
		1 ' ' '	NIM 000010:		
		/gb=NM_000919	NM_000919;		
		/gi=21070983	NM_138766;		
		/ug=Hs.83920	NM_138821;		
mioa4326	NM_000919	/len=3960	NM_138822	Hs.83920	NP_620177
		SON DNA binding			
1		protein (SON),			
1		transcript variant e,			
		mRNA '	NM_003103;		
i		/cds=(50,6376)	NM_032195;		
		/gb=NM_058183	NM_058183;		
		_	. –		
		/gi=21040317	NM_138925;		
		/ug=Hs.92909	NM_138926;		
seoa5894	NM_058183	/len=8482	NM_138927	Hs.92909	NP_620305
		splicing factor,			
		arginine/serine-rich			
		12 (SFRS12),			
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(FLJ25005), mRNA /cds=(166,1467) /gb=NM_152334 /gi=22748728 /ug=Hs.181426 /len=2109 NM_152334 Hs.181426 NP_689547					•	
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Mig Hs.181426 Mig	ł	•	_		:	
miod1450 NM_152334	İ					
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		F-box only protein			
	İ	29 (FBXO29),			İ
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		/ug=Hs.7299			
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		/gb=NM_172240			
1		/gi=26665868	1		
		1 ~	1		
michOFOC	NIM 470040	/ug=Hs.25130	NNA 470040	112 05400	ND 750440
miob9506	NM_172240	/len=2984	NM_172240	Hs.25130	NP_758440
1		nuclear factor of			
		activated T-cells,			
		cytoplasmic,			
		calcineurin-		}	
		dependent 3			
1		(NFATC3),			
		1,	1		
		transcript variant 2,			
		mRNA			
		/cds=(211,3417)	ļ		
		/gb=NM_004555	NM_004555;		
		/gi=27886542	NM 173163;		
1		/ug=Hs.172674	NM_173164;		
ncrc4907	NM_004555	/len=4005	NM_173165	Hs.172674	NP 775188
106701	LIAIN OUTOOD	Me11-4000	1100 TO 100	[115.172074	00100

_ rigure o	a Conta.		,		·
		hypothetical protein			
		LOC119504			
		(LOC119504),			
	1	mRNA			
1		/cds=(119,451)			
j		/gb=NM 173473			
		/gi=27735038			1
		/ug=Hs.426296			
ncrb8134	NIM 472472	/len=1177	NINA 472472	11- 400000	ND 775744
110100134	NM_173473		NM_173473	Hs.426296	NP_775744
		hypothetical protein			
		LOC119504			
		(LOC119504),			
		mRNA			
		/cds=(119,451)			
		/gb=NM_173473			
		/gi=27735038		1	
		/ug=Hs.426296		1	
mioc7700	NM_173473	/len=1177	NM 173473	Hs.426296	NP 775744
		cDNA FLJ90504 fis,	_ _		
		clone			
		NT2RP3004090,			
]	weakly similar to			
		GOLIATH			
1		PROTEIN.			
	1	/cds=(103,1305)			
		/gb=AK074985			
		1 —			
		/gi=22760786			
	11/07/005	/ug=Hs.171802		l	
ncr2861	AK074985	/len=2452	NM_173647	Hs.171802	NP_775918
ł		keratinocytes			
1		associated protein 2			
1		(KCP2), mRNA	,		
		/cds=(1,489)			
		/gb=NM_173852			
		/gi=27777660			
		/ug=Hs.374854		1	
seob9694	NM_173852	/len=489	NM_173852	Hs.374854	NP 776251
		isocitrate	-		
		dehydrogenase 3			
		(NAD) gamma			
		(IDH3G), nuclear			
		gene encoding			
		mitochondrial			
	1	protein, transcript	NM_004135;		
hfcr1694	NM 004135	variant 1, mRNA		He 75252	ND 777250
1101 1094	INIVI_UU4 133	Ivaniant I, MKINA	NM_174869	Hs.75253	NP_777358

1 19010 0	a Conta.				
mioc1117	NM_174890	hypothetical protein LOC93550 (LOC93550), mRNA /cds=(217,2400) /gb=NM_174890 /gi=28376663 /ug=Hs.377945 /len=3256	NM_174890	Hs.377945	NP 777550
		hypothetical protein LOC153339	_		
		(LOC153339),			
		mRNA			
		/cds=(21,239)			:
		/gb=NM_174909 /gi=28372532			
		/ug=Hs.374538			
mioc0621	NM_174909	/len=726	NM_174909	Hs.374538	NP_777569
		melanoma antigen, family D, 2			
		(MAGED2), mRNA			
		/cds=(97,1917)			
		/gb=NM_014599			
		/gi=21264316 /ug=Hs.4943	NM_014599;		
fcrb3285	NM 014599	/len=2077	NM 177433	Hs.4943	NP 803182
		111 11 511011 45			
		UI-H-EU0-azI-k-15- 0-UI.s1			
		NCI_CGAP_Car1			
		cDNA clone			
		IMAGE: 5850374 3',			
		mRNA sequence /clone=IMAGE:_585			
		0374 /clone_end=3'	i		
		/gb=BQ181216			
		/gi=20356708			
miod6500	BQ181216	/ug=Hs.442170 /len=1044		Hs.442170	NP 835228
	24101210	AD037 protein	·	113.772170	111 _000220
		(AD037), mRNA			
		/cds=(107,1072)			
		/gb=NM_032023 /gi=23510359			
		/ug=Hs.296162			
miod0500	NM_032023	/len=2481	NM_032023	Hs.296162	NP_835281

<u>Figure o</u>	d Cont'd.				
miod4216	BC041375	clone IMAGE:5274527, mRNA /gb=BC041375 /gi=27370608 /ug=Hs.11700 /len=3905	NM_178314	Hs.11700	NP_847884
fcrb6483	NM 020830	WD40 and FYVE domain containing 1 (WDFY1), mRNA /cds=(30,1262) /gb=NM_020830 /gi=18482372 /ug=Hs.44743 /len=4585	NM_020830	Hs.44743	NP 848127
miob9458	Al377292	te65d01.x1 Soares_NFL_T_GB C_S1 cDNA clone IMAGE:2091553 3', mRNA sequence /clone=IMAGE:2091 553 /clone_end=3' /gb=Al377292 /gi=4187145 /ug=Hs.410753 /len=238		Hs.410753	NP_848642
mioc2216	NM_006814	proteasome (prosome, macropain) inhibitor subunit 1 (PI31) (PSMF1), mRNA /cds=(127,942) /gb=NM_006814 /gi=5803122 /ug=Hs.405813 /len=3188 component of	NM_006814	Hs.405813	NP_848694
ncrc3073	NM_006348	oligomeric golgi complex 5 (COG5), mRNA /cds=(52,2571) /gb=NM_006348 /gi=5453669 /ug=Hs.239631 /len=3105	NM_006348	Hs.239631	NP_859422

rigule o	d Cont'd.	T DATA BOSS (SE		· · · · · · · · · · · · · · · · · · ·	
		cDNA PSEC0152 fis, clone PLACE1007885. /cds=(20,1144) /gb=AK075459 /gi=22761560			
fcrb7072	AK075459	/ug=Hs.350475 /len=2130		Hs.350475	NP_877437
		engulfment and cell motility 2 (ced-12 C. elegans) (ELMO2), transcript variant 1, mRNA /cds=(141,2303) /gb=NM_133171 /gi=19718768 /ug=Hs.96560	NM_022086;		
ncr1692	NM_133171	/len=3630	NM_133171	Hs.96560	NP_877496
h5a-4.422	NNA 046240	scavenger receptor class A, member 3 (SCARA3), mRNA /cds=(142,1962) /gb=NM_016240 /gi=7705335 /ug=Hs.128856	NNA 040040	U. 100050	ND 070405
hfcr1433	NM_016240	/len=3636 procollagen-lysine, 2-oxoglutarate 5- dioxygenase (lysine hydroxylase) 2 (PLOD2), mRNA /cds=(1,2214) /gb=NM_000935 /gi=4505888 /ug=Hs.41270	NM_016240	Hs.128856	NP_878185
seoa3752	NM_000935	/len=3503 PRO0461 protein	NM_000935	Hs.41270	NP_891988
seob5748	NM_031268	(PRO0461), mRNA /gb=NM_031268 /gi=20588827 /ug=Hs.25063 /len=1100	NM_031268	Hs.25063	NP_112558
seob7984	AF094481	trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds	NM_003663		NP_003654

riguici	oa Conta.	Ter e En	1.114 000000		IND 000047.
4054	V07740	fibronectin gene ED-	. –		NP_002017;
seoc4654	X07718	A region	NM_054034		NP_473375
		hypothetical protein			
		FLJ20015			
		(FLJ20015), mRNA			
		/cds=(32,523)			
		/gb=NM_018996			
		/gi=9506648			
		/ug=Hs.375614			
ncrb2544	NM_018996	/len=1457	NM_018996	Hs.375614	NP_061869
		1 11- 11- 1-			
		hypothetical gene			
		supported by			
		U79248; AK056929;			
	1	BC041875			
4040		(LOC339290),			
ncrc1316	XM_294901	mRNA			XP_294901
		PTS gene for 6-			
		pyruvoyltetrahydropt			
		erin synthase,			
ncr1954	AB042297	complete cds	NM_031938		NP_114144

	Figure 7a: Mild	OA stage-spec	ific markers	<u></u>	
Gene name	Common name	Genbank	Description	RefSeq	UniGene
			gb:NM_001063.1		
			/DEF=Homo		
			sapiens transferrin		
			(TF), mRNA.		
			/FEA=mRNA		
			/GEN=TF		•
			/PROD=transferrin		
			precursor /DB_XREF=gi:4557		
	1		1870		
			/UG=Hs.284176		
			transferrin		
			/FL=gb:M12530.1		
203400_s_at		NM_001063	gb:NM_001063.1		
			ubiquitin specific		
214674_at	USP19	AW451502	protease 19		Hs.301373
			Consensus		
			includes		
			gb:AF119863.1		
			/DEF=Homo		
			sapiens PRO2160		
			mRNA, complete		
			cds. /FEA=mRNA		
			/PROD=PRO2160		
			/DB_XREF=gi:7770		
			162		
			/UG=Hs.112844		1
			maternally		
			expressed 3		
210794_s_at		AF119863	/FL=gb:AF119863.1		

Figure 7a Co	nta.		
		Consensus includes gb:Z95331 /DEF=Human DNA sequence from clone CTA-941F9 on chromosome 22q13 Contains the 3 end of the FBLN1 gene for Fibulin 1 isoforms B, C and D, the first exon of the gene for a novel protein (the ortholog of mouse brain protein E46), ESTs, STSs, GSSs and two /FEA=mRNA_1 /DB_XREF=gi:6572 282 /UG=Hs.79732 fibulin 1 /FL=gb:U01244.1	
202994_s_at	Z953	gb:NM_017777.1 /DEF=Homo sapiens hypothetical protein FLJ20345 (FLJ20345), mRNA.	
218630_at	NM_	/FEA=mRNA /GEN=FLJ20345 /PROD=hypothetica I protein FLJ20345 /DB_XREF=gi:8923 323 /UG=Hs.20558 hypothetical protein FLJ20345 /FL=gb:NM_017777 .1	

Figure 7a Cont.d.			
222186_at AL	in gl /E si le cl E 2' /F /E 80 /L H min E	consensus icludes b:AL109684.1 DEF=Homo apiens mRNA full ength insert cDNA lone :UROIMAGE 7080. FEA=mRNA DB_XREF=gi:5689 05 JG=Hs.306329 lomo sapiens inRNA full length insert cDNA clone :UROIMAGE 7080 b:NM_001360.1	
	/[DEF=Homo apiens 7-	
		ehydrocholesterol	
		eductase	
		DHCR7), mRNA.	
		EA=mRNA	
		GEN=DHCR7	
		PROD=7-	
	· · · · · · · · · · · · · · · · · · ·	ehydrocholesterol eductase	
		DB_XREF=gi:4503	
		20 /UG=Hs.11806	
	7-	_	
		ehydrocholesterol	
	i	eductase	
		FL=gb:BC000054.1	
	10	b:AF034544.1 b:AF067127.1	
	1.	b:AF096305.1	
201791_s_at NN	10	b:NM_001360.1	

Figure /a Co	nit a.		
		Consensus	
		includes	
		gb:Al375919	
		/FEA=EST	
		/DB_XREF=gi:4175	
		909	
		/DB_XREF=est:tc1	
		4d04.x1	
		/CLONE=IMAGE:20	
İ		63815	
		/UG=Hs.110637	
		homeo box A10	i
		i i	
	NINA 040054	/FL=gb:NM_018951	
213147_at	NM_018951		
		-b-NNA 000405.4	
		gb:NM_002405.1	
		/DEF=Homo	
		sapiens manic	
	[fringe (Drosophila)	
		homolog (MFNG),	
		mRNA.	
		/FEA=mRNA	
		/GEN=MFNG	
		/PROD=manic	
		fringe (Drosophila)	
		homolog	
		/DB_XREF=gi:4505	
		158 /UG=Hs.31939	
		manic fringe	
		(Drosophila)	
ł		homolog	
		/FL=gb:U94352.1	
204153_s_at	NM_002405	gb:NM_002405.1	
20+100_3_al	[1414]_002403	195.1111 002-100.1	

Figure 7a Co	nicu.			
205702_at		NM_006608	gb:NM_006608.1 /DEF=Homo sapiens putative homeodomain transcription factor (PHTF1), mRNA. /FEA=mRNA /GEN=PHTF1 /PROD=putative homeodomain transcription factor /DB_XREF=gi:5729 975 /UG=Hs.123637 putative homeodomain transcription factor /FL=gb:NM_006608 .1	
210355_at		J03580	gb:J03580.1 /DEF=Human, parathyroid-like protein (associated with humoral hypercalcemia of malignancy) mRNA, complete cds. /FEA=mRNA /GEN=PTHLH /DB_XREF=gi:1907 05 /UG=Hs.89626 parathyroid hormone-like hormone /FL=gb:J03580.1	

			7		
211252_x_at		U36759	gb:U36759.1 /DEF=Human pre- T cell receptor alpha-type chain precursor, mRNA, complete cds. /FEA=mRNA /PROD=pre-T cell receptor alpha-type chain precursor /DB_XREF=gi:1127 580 /UG=Hs.169002 Human pre TCR alpha mRNA, partial cds /FL=gb:U36759.1		
211252_X_at		030739	ESTs, Moderately		
			similar to S71105 protein-glutamine gamma- glutamyltransferase (EC 2.3.2.13) 4, prostate specific -		
217566_s_at		BF222018	human [H.sapiens]		Hs.289803
			p21(CDKN1A)-		
33814_at	PAK4	AF005046	activated kinase 4	NM_005884	Hs.20447
			This sequence comes from Fig. 1; author's translation differs from conceptual translation; Homo sapiens T-cell receptor alpha chain-c6.1A fusion protein (c6.1A-TCRC) gene, partial		
216521_s_at	c6.1A-TCRC	S72931	cds.		

Figure 7a CC	THE G.				
219961_s_at		NM 018474	gb:NM_018474.1 /DEF=Homo sapiens uncharacterized hypothalamus protein HT013 (HT013), mRNA. /FEA=mRNA /GEN=HT013 /PROD=uncharacte rized hypothalamus protein HT013 /DB_XREF=gi:8923 814 /UG=Hs.173515 uncharacterized hypothalamus protein HT013 /FL=gb:AF220187.1 gb:NM_018474.1		
				-	
		·	gb:NM_000809.1 /DEF=Homo sapiens gamma- aminobutyric acid (GABA) A receptor, alpha 4 (GABRA4), mRNA. /FEA=CDS /GEN=GABRA4 /PROD=gamma- aminobutyric acid A receptor, alpha 4precursor /DB_XREF=gi:4557 604 /UG=Hs.248112 gamma- aminobutyric acid (GABA) A receptor, alpha 4 /FL=gb:NM_000809		
208463_at		NM_000809	.1 gb:U30461.1		

Figure 7a Co	intu.			
218743_at		NM_024591	gb:NM_024591.1 /DEF=Homo sapiens hypothetical protein FLJ11749 (FLJ11749), mRNA. /FEA=mRNA /GEN=FLJ11749 /PROD=hypothetica I protein FLJ11749 /DB_XREF=gi:1337 5782 /UG=Hs.22897 hypothetical protein FLJ11749 /FL=gb:NM_024591 .1	
			gb:NM_013337.1 /DEF=Homo	
			sapiens translocase of inner mitochondrial membrane 22 (yeast) homolog (TIM22), mRNA.	
		·	/FEA=mRNA /GEN=TIM22 /PROD=translocase of inner mitochondrial	
			membrane 22(yeast) homolog /DB_XREF=gi:7019 552 /UG=Hs.87595	
			translocase of inner mitochondrial membrane 22 (yeast) homolog /FL=gb:BC002324.1	
219184_x_at		NM_013337	gb:AF155330.1 gb:NM_013337.1	

gb:NM_001231.1 /DEF=Homo sapiens calsequestrin 1 (fast-twitch, skeletal muscle) (CASQ1), nuclear gene encoding mitochondrial protein, mRNA. /FEA=mRNA /GEN=CASQ1 /PROD=skeletal muscle calsequestrin 1 /DB_XREF=gi:4557 406 /UG=Hs.60708 calsequestrin 1 (fast-twitch, skeletal muscle) /FL=gb:NM 001231 NM_001231 .1 gb:S73775.1 219645_at gb:NM 012383.1 /DEF=Homo sapiens osteoclast stimulating factor 1 (OSTF1), mRNA. /FEA=mRNA /GEN=OSTF1 /PROD=osteoclast stimulating factor 1 /DB_XREF=gi:6912 563 /UG=Hs.95821 osteoclast stimulating factor 1 /FL=gb:U63717.1 gb:NM_012383.1 204479_at NM_012383

Figure /a Co	int d.				
			Consensus includes gb:N25546 /FEA=EST /DB_XREF=gi:1139 894 /DB_XREF=est:yx7 6e05.s1 /CLONE=IMAGE:26 7680 /UG=Hs.181461 ariadne (Drosophila) homolog, ubiquitin-conjugating enzyme E2-binding protein, 1 /FL=gb:AF072832.1		
201878_at	NN	/_005744	gb:NM_005744.2		
212729_at	AE	3033058	Consensus includes gb:Al916274 /FEA=EST /DB_XREF=gi:5636 129 /DB_XREF=est:wg9 9e04.x1 /CLONE=IMAGE:23 79390 /UG=Hs.11101 KIAA1232 protein		
212726 at	٨	3014562	Consensus includes gb:AB014562.1 //DEF=Homo sapiens mRNA for KIAA0662 protein, partial cds. //FEA=mRNA //GEN=KIAA0662 //PROD=KIAA0662 //PROD=KIAA0662 protein //DB_XREF=gi:3327 137 //UG=Hs.93868 KIAA0662 gene product		
212726_at	Į AŁ	3014562	[product	l	

- rigare ra oc	717¢ GI.				
			gb:NM_006246.1		
		,	/DEF=Homo		
	-		sapiens protein		
	ı		phosphatase 2,		
			regulatory subunit		
]			B (B56), epsilon		
			isoform		
			(PPP2R5E),		
		:	mRNA.		
			/FEA=mRNA		
			/GEN=PPP2R5E		
			/PROD=protein		
			phosphatase 2,		
			regulatory subunit		
			B(B56), epsilon		
			isoform		
			/DB_XREF=gi:5453		
			955		
			/UG=Hs.173328		
			protein		
			phosphatase 2,		
			regulatory subunit		
			B (B56), epsilon		
			isoform		
			/FL=gb:L76703.1	·	
203338 at		NM 006246	gb:NM_006246.1		
			Consensus		
			includes		
			gb:X92110.1		
			/DEF=H.sapiens		
			mRNA for hcgVIII		
			protein.		
			/FEA=mRNA		
			/DB_XREF=gi:1216		
			163		
			/UG=Hs.153618		
215985_at	:	X92110	HCGVIII-1 protein		,
	I			L	L

Figure /a Contra	·	1	 ···
201511 at	NM_001087	gb:NM_001087.1 /DEF=Homo sapiens angio- associated, migratory cell protein (AAMP), mRNA. /FEA=mRNA /GEN=AAMP /PROD=angio- associated, migratory cell protein /DB_XREF=gi:4557 228 /UG=Hs.83347 angio-associated, migratory cell protein /FL=gb:NM_001087 .1 gb:M95627.1	
		ab.NM 005670.4	
		gb:NM_005670.1 /DEF=Homo	
		sapiens epilepsy,	
		progressive	
		myoclonus type 2,	
		Lafora disease	
		(laforin) (EPM2A),	
		mRNA. /FEA=mRNA	
		/GEN=EPM2A	
		/PROD=epilepsy,	
		progressive	
		myoclonus type 2,	
		Laforadisease	
		(laforin)	
		/DB_XREF=gi:1132 1612	
		/UG=Hs.22464	
		epilepsy,	
		progressive	
	ł	myoclonus type 2,	
		Lafora disease (laforin)	
		/FL=gb:AF284580.1	
		gb:NM_005670.1	
205231_s_at	NM_005670	gb:AF084535.2	
212337_at	Al687738	ESTs	Hs.409222

Figure /a Co	711. 4.			
219920 s at		NM 021971	gb:NM_021971.1 /DEF=Homo sapiens GDP- mannose pyrophosphorylase B (GMPPB), transcript variant 2, mRNA. /FEA=mRNA /GEN=GMPPB /PROD=GDP- mannose pyrophosphorylase B, isoform 2 /DB_XREF=gi:1176 1620 /UG=Hs.28077 GDP-mannose pyrophosphorylase B /FL=gb:NM_021971 .1 gb:BC001141.1 gb:AF135421.1	
			gb:AF045452.1 /DEF=Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds. /FEA=mRNA /PROD=transcriptio nal regulatory protein p54 /DB_XREF=gi:3282 824 /UG=Hs.107474 NGFI-A binding protein 1 (ERG1 binding protein 1)	
211139_s_at		AF045452		

Figure 7a Co	Jiii G.	,		
209984_at		AB037901	gb:AB037901.1 /DEF=Homo sapiens GASC-1 mRNA, complete cds. /FEA=mRNA /GEN=GASC-1 /DB_XREF=gi:1056 7163 /UG=Hs.149918 gene amplified in squamous cell carcinoma 1; KIAA0780 protein /FL=gb:AB037901.1	
218761_at		NM_017610	gb:NM_017610.1 /DEF=Homo sapiens hypothetical protein DKFZp761D081 (DKFZp761D081), mRNA. /FEA=mRNA /GEN=DKFZp761D 081 /PROD=hypothetica I protein DKFZp761D081 /DB_XREF=gi:8922 164 /UG=Hs.12504 hypothetical protein DKFZp761D081 /FL=gb:NM_017610 .1	
			epidermal growth factor receptor (erythroblastic	
201983_s_at	EGFR	AW157070	leukemia viral (v- erb-b) oncogene homolog, avian) mitogen-activated	Hs.77432
215499_at	MAP2K3	AA780381	protein kinase kinase 3	 Hs.180533

I iguio ra oc			
		gb:NM_024597.1 /DEF=Homo sapiens hypothetical protein FLJ12649 (FLJ12649), mRNA. /FEA=mRNA /GEN=FLJ12649 /PROD=hypothetica I protein FLJ12649 /DB_XREF=gi:1337 5794 /UG=Hs.24078 hypothetical protein FLJ12649 /FL=gb:NM_024597	
219626_at	NM_02459	7 .1	
	AK000684	Consensus includes gb:AK000684.1 /DEF=Homo sapiens cDNA FLJ20677 fis, clone KAIA4183. /FEA=mRNA /DB_XREF=gi:7020 930 /UG=Hs.183887 hypothetical protein	
222209_s_at	JANUU0664	17LJZZ 104	

	Fig	ure	7a	Cor	ıt'd.	
--	-----	-----	----	-----	-------	--

1 19410 74 00			T		
203300_x_at		NM_003916	gb:NM_003916.1 /DEF=Homo sapiens adaptor- related protein complex 1, sigma 2 subunit (AP1S2), mRNA. /FEA=mRNA /GEN=AP1S2 /PROD=adaptor- related protein complex 1, sigma 2subunit /DB_XREF=gi:4506 956 /UG=Hs.40368 adaptor-related protein complex 1, sigma 2 subunit /FL=gb:AF251295.1 gb:BC001117.1 gb:AB015320.1 gb:NM_003916.1		
203300_x_at		NM_003916	protein complex 1, sigma 2 subunit /FL=gb:AF251295.1 gb:BC001117.1 gb:AB015320.1		
203269_at		NM_003580	/FL=gb:NM_003580 .1		
214151_s_at	PIGB	AU144243	phosphatidylinositol glycan, class B	_	Hs.247118
	<u> </u>	 	101		·

tubulin, gamma complex associated protein 2 ### TUBGCP2 Al377497 ### TUBGCP2 Al377497 ### TUBGCP2 Al377497 ### TUBGCP2 ### TUBGCP2 ### TUBGCP2 Al377497 ### TUBGCP2 ### TUBCCPC	Figure 7a Ci	one a.	r	· · · · · · · · · · · · · · · · · · ·	
/DEF=Homo sapiens fatty-acid-Coenzyme A ligase, long-chain 3 (FACL3), mRNA. //FEA=mRNA //GEN=FACL3 //PROD=long-chain fatty-acid-Coenzyme A ligase 3 //DB_XREF=gi:1266 9907 //UG=Hs.268012 fatty-acid-Coenzyme A ligase, long-chain 3 //FL=gb:NM_004457 .2 gb:D89053.1 gb:AF116690.1	212989_at	TUBGCP2	Al377497	complex associated	Hs.13386
/DEF=Homo sapiens mRNA; cDNA	201661_s_at		NM_004457	/DEF=Homo sapiens fatty-acid-Coenzyme A ligase, long-chain 3 (FACL3), mRNA. /FEA=mRNA /GEN=FACL3 /PROD=long-chain fatty-acid-Coenzyme A ligase 3 /DB_XREF=gi:1266 9907 /UG=Hs.268012 fatty-acid-Coenzyme A ligase, long-chain 3 /FL=gb:NM_004457 .2 gb:D89053.1	
DKFZp434F205 (from clone DKFZp434F205); complete cds. /FEA=mRNA /GEN=DKFZp434F 205 /PROD=hypothetica I protein /DB_XREF=gi:6807 670 /UG=Hs.50758 SMC4 (structural maintenance of chromosomes 4, yeast)-like 1 /FL=gb:AB019987.1 gb:NM_005496.1 gb:NM_005496.1 gb:AL136877.1				/DEF=Homo sapiens mRNA; cDNA DKFZp434F205 (from clone DKFZp434F205); complete cds. /FEA=mRNA /GEN=DKFZp434F 205 /PROD=hypothetica I protein /DB_XREF=gi:6807 670 /UG=Hs.50758 SMC4 (structural maintenance of chromosomes 4, yeast)-like 1 /FL=gb:AB019987.1 gb:NM_005496.1	

Application of: Liew, et. al. Our Docket #: 4231/2042 Figure 7a Cont'd.

Consensus includes gb:AB011155.1 /DEF=Homo sapiens mRNA for KIAA0583 protein, partial cds. /FEA=mRNA /GEN=KIAA0583 /PROD=KIAA0583 protein /DB_XREF=gi:3043 689 /UG=Hs.170290 discs, large (Drosophila) homolog 5 /FL=gb:U61843.1 gb:NM_004747.1 AB011155 201681_s_at gb:M55575.1 /DEF=Human branched chain alpha-keto acid dehydrogenase (BCKDHB) E1-beta subunit mRNA, complete cds. /FEA=mRNA /GEN=BCKDHB /PROD=branched chain alpha-keto acid dehydrogenaseE1beta subunit /DB_XREF=gi:1793 61 /UG=Hs.1265 branched chain keto acid dehydrogenase E1, beta polypeptide (maple syrup urine disease) /FL=gb:M55575.1 210653_s_at M55575

210691_s_at	AF275803	gb:AF275803.1 /DEF=Homo sapiens PNAS-107 mRNA, complete cds. /FEA=mRNA /PROD=PNAS-107 /DB_XREF=gi:1083 4769 /UG=Hs.27258 calcyclin binding protein /FL=gb:AF275803.1	
2 1003 1_3_dt	 7.1 27 0000	77 E 95.7 (1 2 7 0 0 0 0 . 1	
		gb:D45421.1 /DEF=Human mRNA for phosphodiesterase I alpha, complete cds. /FEA=mRNA /PROD=phosphodie sterase I alpha /DB_XREF=gi:6622 89 /UG=Hs.174185 ectonucleotide pyrophosphataseph osphodiesterase 2 (autotaxin) /FL=gb:NM_006209	
210839_s_at	D45421	.1 gb:D45421.1	

Application of: Liew, et. al. Our Docket #: 4231/2042 Figure 7a Cont'd.

gb:NM_005697.2 /DEF=Homo sapiens secretory carrier membrane protein 2 (SCAMP2), mRNA. /FEA=mRNA /GEN=SCAMP2 /PROD=secretory carrier membrane protein 2 /DB_XREF=gi:5730 030 /UG=Hs.238030 secretory carrier membrane protein /FL=gb:BC001376.1 gb:BC004385.1 gb:AF005038.2 gb:NM_005697.2 NM 005697 218143_s_at gb:NM_024590.1 /DEF=Homo sapiens hypothetical protein FLJ23548 (FLJ23548), mRNA. /FEA=mRNA /GEN=FLJ23548 /PROD=hypothetica I protein FLJ23548 /DB_XREF=gi:1337 5780 /UG=Hs.22895 hypothetical protein FLJ23548 /FL=gb:NM_024590 NM 024590 .1 219973_at

Figure /a Co	nitu.				
203460_s_at			gb:NM_007318.1 /DEF=Homo sapiens presenilin 1 (Alzheimer disease 3) (PSEN1), transcript variant I-463, mRNA. /FEA=mRNA /GEN=PSEN1 /PROD=presenilin 1 isoform I-463 /DB_XREF=gi:7549 812 /UG=Hs.3260 presenilin 1 (Alzheimer disease 3) /FL=gb:U40379.1 gb:L76517.1 gb:NM_007318.1		
			gb:NM_003348.1 //DEF=Homo sapiens ubiquitin- conjugating enzyme E2N (homologous to yeast UBC13) (UBE2N), mRNA. //FEA=mRNA //GEN=UBE2N //PROD=ubiquitin- conjugating enzyme E2N (homologous toyeast UBC13) //DB_XREF=gi:4507 792 //UG=Hs.75355 ubiquitin- conjugating enzyme E2N (homologous toyeast UBC13) //FL=gb:D83004.1 gb:BC000396.1 gb:BC0003365.1		
201524_x_at		NM_003348	gb:NM_003348.1	l	l

Figure 7a Co	iii u.		ECTa Mastelli	 1	
216005_at		BF434846	ESTs, Weakly similar to hypothetical protein FLJ20234 [Homo sapiens] [H.sapiens]	· · · · · · · · · · · · · · · · · · ·	Hs.392339
201519_at		NM_014820	gb:NM_014820.1 /DEF=Homo sapiens translocase of outer mitochondrial membrane 70 (yeast) homolog A (TOMM70A), mRNA. /FEA=mRNA /GEN=TOMM70A /PROD=translocase of outer mitochondrial membrane 70(yeast) homolog A /DB_XREF=gi:7662 672 /UG=Hs.21198 translocase of outer mitochondrial membrane 70 (yeast) homolog A /FL=gb:BC003633.1 gb:AB018262.1 gb:NM_014820.1		
201824_at		AB022663	gb:AB022663.1 /DEF=Homo sapiens HFB30 mRNA, complete cds. /FEA=mRNA /GEN=HFB30 /DB_XREF=gi:5019 617 /UG=Hs.215857 ring finger protein 14 /FL=gb:AF060544.1 gb:NM_004290.1 gb:AB022663.1		

Tigure 7a s	1		zinc finger protein	· · · · · · · · · · · · · · · · · · ·
219540_at	ZNF267	AU150728	267	Hs.145498
219540_at	ZINFZOI	A0130720	201	113.143490
			-b-NIM 004906 4	
			gb:NM_004896.1	
			/DEF=Homo	
			sapiens vacuolar	
			protein sorting 26	
			(yeast homolog)	
			(VPS26), mRNA.	
			/FEA=mRNA	
	l		/GEN=VPS26	
			/PROD=vacuolar	
	1		protein sorting 26	
			(yeast homolog)	
			/DB XREF=gi:4758	
	ļ		509 /UG=Hs.67052	
	ł		vacuolar protein	
			sorting 26 (yeast	-
			homolog)	
			/FL=gb:AF054179.1	
i	i		1 -	
004007		NII 4 00 4000	gb:NM_004896.1	
201807_at		NM_004896	gb:AF175266.1	
			gb:NM_004503.1	
			/DEF=Homo	
			sapiens homeo	
			box C6 (HOXC6),	1
			mRNA.	
			/FEA=mRNA	
			/GEN=HOXC6	
			/PROD=homeo	
			box C6	
			/DB_XREF=gi:4758	
	ľ		553 /UG=Hs.820	
	1		homeo box C6	
	1		/FL=gb:NM_004503	
206858 s at		NM 004503	1.1	
			L'	

1 iguic 7a coi			
210993 s at	U54826	gb:U54826.1 /DEF=Human mad- related protein MADR1 mRNA, complete cds. /FEA=mRNA /PROD=mad- related protein MADR1 /DB_XREF=gi:1332 713 /UG=Hs.79067 MAD (mothers against decapentaplegic, Drosophila) homolog 1 /FL=gb:U54826.1 gb:U59912.1	
209099_x_at	U73936	gb:U73936.1 /DEF=Homo sapiens Jagged 1 (HJ1) mRNA, complete cds. /FEA=mRNA /GEN=HJ1 /PROD=Jagged 1 /DB_XREF=gi:1695 273 /UG=Hs.91143 jagged 1 (Alagille syndrome) /FL=gb:U61276.1 gb:U73936.1 gb:AF003837.1 gb:AF028593.1 gb:NM_000214.1	

Figure 7a CC	nit a.				
210944_s_at		BC003169	gb:BC003169.1 /DEF=Homo sapiens, Similar to calpain 3, (p94), clone MGC:4403, mRNA, complete cds. /FEA=mRNA /PROD=Similar to calpain 3, (p94) /DB_XREF=gi:1311 1992 /UG=Hs.40300 calpain 3, (p94) /FL=gb:BC003169.1		
216941_s_at		AK026521	Consensus includes gb:AK026521.1 /DEF=Homo sapiens cDNA: FLJ22868 fis, clone KAT02340, highly similar to HUMTFSL1C Homo sapiens transcription factor SL1 mRNA. /FEA=mRNA /DB_XREF=gi:1043 9398 /UG=Hs.121044 TATA box binding protein (TBP)-associated factor, RNA polymerase I, B, 63kD	NM 045420:	
36030_at	DKFZP586l222 3	AL080214	intermediate filament-like MGC:2625	NM_015438; NM_080730; NM_080731	Hs.408973
201736_s_at	TEB4	BF000409	similar to S. cerevisiae SSM4		Hs.380875
201752_s_at	ADD3	AI763123	adducin 3 (gamma)		Hs.98834

Figure 7a Co	Jillu.			
205554_s_at		NM_004944	gb:NM_004944.1 /DEF=Homo sapiens deoxyribonuclease I-like 3 (DNASE1L3), mRNA. /FEA=mRNA /GEN=DNASE1L3 /PROD=deoxyribon uclease I-like 3 /DB_XREF=gi:4826 697 /UG=Hs.88646 deoxyribonuclease I-like 3 /FL=gb:U56814.1 gb:AF047354.1 gb:NM_004944.1	
20000+_5_ut			ribosomal protein	
213350_at	RPS11	BF680255	S11	Hs.182740
202876_s_at		NM_002586	gb:NM_002586.1 /DEF=Homo sapiens pre-B-cell leukemia transcription factor 2 (PBX2), mRNA. /FEA=mRNA /GEN=PBX2 /PROD=pre-B-cell leukemia transcription factor 2 /DB_XREF=gi:4505 624 /UG=Hs.93728 pre-B-cell leukemia transcription factor 2 /FL=gb:NM_002586 .1	

Figure 7a Co			<u> </u>		
214805_at		U79273	Consensus includes gb:U79273.1 /DEF=Human clone 23933 mRNA sequence. /FEA=mRNA /DB_XREF=gi:1710 239 /UG=Hs.239483 Human clone 23933 mRNA sequence		
212535_at	MEF2A	AA142929	MADS box transcription enhancer factor 2, polypeptide A (myocyte enhancer factor 2A)		Hs.277806
221865_at	DKFZp547P23	BF969986	hypothetical protein DKFZp547P234		Hs.170226
218957_s_at		NM_025155	gb:NM_025155.1 /DEF=Homo sapiens hypothetical protein FLJ11848 (FLJ11848), mRNA. /FEA=mRNA /GEN=FLJ11848 /PROD=hypothetica I protein FLJ11848 /DB_XREF=gi:1337 6750 /UG=Hs.289031 hypothetical protein FLJ11848 /FL=gb:NM_025155 .1		
2 10001_3_at	1	1020 100	1	<u> </u>	

Application of: Liew, et. al. Our Docket #: 4231/2042 Figure 7a Cont'd.

	 	,	
218124_at	NM_017750	gb:NM_017750.1 /DEF=Homo sapiens hypothetical protein FLJ20296 (FLJ20296), mRNA. /FEA=mRNA /GEN=FLJ20296 /PROD=hypothetica I protein FLJ20296 /DB_XREF=gi:8923 274 /UG=Hs.6603 hypothetical protein FLJ20296 /FL=gb:NM_017750 .1 gb:NM_017976.1 /DEF=Homo sapiens	
205511_at	NM_017976	hypothetical protein FLJ10038 (FLJ10038), mRNA. /FEA=mRNA /GEN=FLJ10038 /PROD=hypothetica I protein FLJ10038 /DB_XREF=gi:8922 197 /UG=Hs.181202 hypothetical protein FLJ10038 /FL=gb:NM_017976 .1	

Figure 7a Ci	one a.	·	· · · · · · · · · · · · · · · · · · ·	,	
221617_at		AF077053	Consensus includes gb:AF077053.1 //DEF=Homo sapiens neuronal cell death-related protein mRNA, complete cds. //FEA=mRNA //PROD=neuronal cell death-related protein //DB_XREF=gi:4689 153 //UG=Hs.171723 neuronal cell death-related protein //FL=gb:AF077053.1 gb:NM_015975.1 gb:AF220509.1		
	MCLC		Mid-1-related		Hs.93121
221922_at	MCLC	AW195581	gb:AF008442.1 /DEF=Homo sapiens RNA polymerase I subunit hRPA39 mRNA, complete cds. /FEA=mRNA /PROD=RNA polymerase I subunit hRPA39 /DB_XREF=gi:2266 928 /UG=Hs.5409 RNA polymerase I subunit /FL=gb:AF008442.1		ПS.93 IZ1

Figure	7a	Cont'	d.

Figure /a Conti	u	Lab.NM 005174.1
	1	gb:NM_005174.1
		/DEF=Homo
1		sapiens ATP
		synthase, H+
		transporting,
		mitochondrial F1
		complex, gamma
		polypeptide 1
		(ATP5C1), mRNA.
		/FEA=mRNA
		/GEN=ATP5C1
1	·	/PROD=ATP
		synthase, H+
ļ.		transporting,
ļ .		mitochondrial
		I I
		F1complex,
	ł	gamma
		polypeptide 1
		/DB_XREF=gi:4885
1		078
ļ l		/UG=Hs.155433
		ATP synthase, H+
		transporting,
		mitochondrial F1
		complex, gamma
		polypeptide 1
		/FL=gb:D16563.1
205711_x_at	NM 005174	gb:NM_005174.1
200711_X_ax	11111_000111	
		gb:NM_017810.1
		/DEF=Homo
	1	sapiens
	İ	, ·
		hypothetical protein
		FLJ20417
	1	(FLJ20417),
		mRNA.
	1	/FEA=mRNA
		/GEN=FLJ20417
		/PROD=hypothetica
	1	protein FLJ20417
	[/DB_XREF=gi:8923
	1	385 /UG=Hs.10710
	1	hypothetical protein
<u> </u>	1	FLJ20417
	1	/FL=gb:NM_017810
218937_at	NM_017810	1.1

I igure ra ce	711C GI.				
221731_x_at 214695_at	NICE-4	J02814 AW051361	Consensus includes gb:BF218922 /FEA=EST /DB_XREF=gi:1111 2418 /DB_XREF=est:601 885091F1 /CLONE=IMAGE:41 03447 /UG=Hs.81800 chondroitin sulfate proteoglycan 2 (versican) NICE-4 protein Consensus includes gb:BE538424 /FEA=EST /DB_XREF=gi:9767 069 /DB_XREF=est:601 068256F1 /CLONE=IMAGE:34 54693 /UG=Hs.288283	-	Hs.8127
221745_at		AK026008			
202656_s_at	TRIP-Br2	BG107456	transcriptional regulator interacting with the PHS-bromodomain 2		Hs.77293

Figure	7a	Conf	ľd.

	gb:AF005774.1 //DEF=Homo sapiens caspase- like apoptosis regulatory protein (clarp) mRNA, alternatively spliced, complete cds. /FEA=mRNA //GEN=clarp //PROD=caspase- like apoptosis regulatory protein //DB_XREF=gi:2286 144 //UG=Hs.195175 CASP8 and FADD- like apoptosis regulator //FL=gb:BC001602.1 gb:U97074.1 gb:AF010127.1 gb:AF009618.1 gb:U85059.1 gb:AF041458.1 gb:AF041458.1 gb:AF041460.1
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I Iguic /u Oc				
202529_at		NM_002766	gb:NM_002766.1 /DEF=Homo sapiens phosphoribosyl pyrophosphate synthetase- associated protein 1 (PRPSAP1), mRNA. /FEA=mRNA /GEN=PRPSAP1 /PROD=phosphorib osyl pyrophosphatesynth etase-associated protein 1 /DB_XREF=gi:4506 130 /UG=Hs.77498 phosphoribosyl pyrophosphate synthetase- associated protein 1 /FL=gb:D61391.1 gb:NM_002766.1 H2A histone family,	
213344_s_at	H2AFX	H51429	member X	Hs.147097

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1 iguie 7a Ci	JII. G.			
209523_at		AK001618	Consensus includes gb:AK001618.1 //DEF=Homo sapiens cDNA FLJ10756 fis, clone NT2RP3004572, highly similar to Homo sapiens cofactor of initiator function mRNA. //FEA=mRNA //DB_XREF=gi:7022 983 //UG=Hs.122752 TATA box binding protein (TBP)-associated factor, RNA polymerase II, B, 150kD //FL=gb:AF026445.1 gb:AF040701.1 gb:AF057694.1 gb:NM_003184.1	
202621_at		NM_001571	gb:NM_001571.1 /DEF=Homo sapiens interferon regulatory factor 3 (IRF3), mRNA. /FEA=mRNA /GEN=IRF3 /PROD=interferon regulatory factor 3 /DB_XREF=gi:4504 724 /UG=Hs.75254 interferon regulatory factor 3 /FL=gb:NM_001571 .1	

gb:NM_014785.1 //DEF=Homo sapiens KIAA0258 gene product (KIAA0258), mRNA. //ECN=KIAA0258 //PROD=KIAA0258 gene product //DB_XREF=gi:7662 029 //UG=Hs.47313 KIAA0258 gene product //EL=gb.BC001725.1 gb:D87447.1 gb:D87447.1 gb:NM_014785.1 novel putative protein similar to YIL091C yeast hypothetical 84 kD protein from SGA1- KTR7 gb:BC005122.1 //DEF=Homo sapiens, ADP- ribosylation factor GTPase activating protein 1, clone MGC:10272, mRNA, complete cds. //EA=mRNA //PROD=ADP- ribosylation factor GTPase activatingprotein 1 //DB_XREF=gi:1347 7296 //UG=Hs.13014 ADP-ribosylation factor GTPase activating protein 1 //DB_XREF=gi:1347 7296 //UG=Hs.13014 ADP-ribosylation factor GTPase activating protein 1 //FL=gb.BC005122.1 gb:AB4711 gb:AB4711 gb:AB4711 gb:AB4711 gb:AB4711 gb:AB471	Figure 7a Co	Jiica.			· · · · · · · · · · · · · · · · · · ·	
214193_s_at DJ434O14.5 Al770084 KTR7 Hs.194754 gb:BC005122.1 /DEF=Homo sapiens, ADP- ribosylation factor GTPase activating protein 1, clone MGC:10272, mRNA, complete cds. /FEA=mRNA /PROD=ADP- ribosylation factor GTPase activatingprotein 1 /DB_XREF=gi:1347 7296 /UG=Hs.13014 ADP-ribosylation factor GTPase activating protein 1 /FL=gb:BC005122.1			NM_014785	/DEF=Homo sapiens KIAA0258 gene product (KIAA0258), mRNA. /FEA=mRNA /GEN=KIAA0258 gene product /DB_XREF=gi:7662 029 /UG=Hs.47313 KIAA0258 gene product /FL=gb:BC001725.1 gb:D87447.1 gb:NM_014785.1 novel putative protein similar to YIL091C yeast hypothetical 84 kD		
gb:BC005122.1 //DEF=Homo sapiens, ADP- ribosylation factor GTPase activating protein 1, clone MGC:10272, mRNA, complete cds. //FEA=mRNA //PROD=ADP- ribosylation factor GTPase activatingprotein 1 //DB_XREF=gi:1347 7296 //UG=Hs.13014 ADP-ribosylation factor GTPase activating protein 1 //FL=gb:BC005122.1	214193 s at	D.I434O14 5	A1770084	1.7		Hs.194754
202211_at BC005122 gb:NM_014570.1				gb:BC005122.1 /DEF=Homo sapiens, ADP- ribosylation factor GTPase activating protein 1, clone MGC:10272, mRNA, complete cds. /FEA=mRNA /PROD=ADP- ribosylation factor GTPase activatingprotein 1 /DB_XREF=gi:1347 7296 /UG=Hs.13014 ADP-ribosylation factor GTPase activating protein 1 /FL=gb:BC005122.1 gb:AF111847.1		

gb:NM_014223.2 /DEF=Homo sapiens nuclear transcription factor Y. gamma (NFYC), mRNA. /FEA=mRNA /GEN=NFYC /PROD=nuclear transcription factor Y. gamma //DB_XREF=gi:1149 6977 //UG=Hs.168157 nuclear transcription factor Y. gamma //FL=gb:NM_014223 2. gb:D85425.1 gb:BC005003.1 gb:BE005003.1 gb:BE005003.1 gb:BE966540 //FEA=EST //DB_XREF=gi:1233 3755 //DB_XREF=gi:1233 3755 //DB_XREF=gi:1233 3755 //DB_XREF=gi:1233 37558 //UG=Hs.267819 protein phosphatase 1, regulatory (inhibitor) subunit 2 //FL=gb:NM_006241 .1 .1 .1 .1 .1	1 igure 7a Oc	iii d.	
sapiens nuclear transcription factor Y, gamma (NFYC), mRNA. //FEA=mRNA //GEN=NFYC //PROD=nuclear transcription factor Y, gamma //DB_XREF=gi:1149 //6977 //UG=Hs.168157 nuclear transcription factor Y, gamma //FL=gb:NM_014223 2 gb:D85425.1 gb:D605003.1 gb:D89486.1 Consensus includes gb:BF966540 //FEA=EST //DB_XREF=gi:1233 3755 7/DB_XREF=gi:1233 3755 7/DB_XREF=gi:1233 3755 8/DB_XREF=gi:1233 375586 7/UG=Hs.267819 protein phosphatase 1, regulatory (inhibitor) subunit 2 //FL=gb:NM_006241			
transcription factor Y, gamma (NFYC), mRNA. //FEA=mRNA //GEN=NFYC //PROD=nuclear transcription factor Y, gamma //DB_XREF=gi:1149 6977 //UG=Hs.168157 nuclear transcription factor Y, gamma //FL=gb:NM_014223 .2 gb:D85425.1 gb:BC005003.1 gb:BC005003.1 gb:BC005003.1 gb:BC986540 //FEA=EST //DB_XREF=gi:1233 3755 //DB_XREF=gi:1233 3755 //DB_XREF=gi:1233 375586 //UG=Hs.267819 protein phosphatase 1, regulatory (inhibitor) subunit 2 //FL=gb:NM_006241			
Y, gamma (NFYC), mRNA. //EA=mRNA //GEN=NFYC //PROD=nuclear transcription factor Y, gamma //DB_XREF=gi:1149 6977 //UG=Hs.168157 nuclear transcription factor Y, gamma //FL=gb:NM_014223 2. gb:D85425.1 gb:BC005003.1 gb:D89986.1 Consensus includes gb:BF966540 //FEA=EST //DB_XREF=gi:1233 3755 //DB_XREF=gi:1233 3755 //DB_XREF=gi:1233 375586 //UG=Hs.267819 protein phosphatase 1, regulatory (inhibitor) subunit 2 //FL=gb:NM_006241			
(NFYC), mRNA. //FEA=mRNA //GEN=NFYC //PROD=nuclear transcription factor Y, gamma //DB_XREF=gi:1149 6977 //UG=Hs.168157 nuclear transcription factor Y, gamma //FL=gb:NM_014223 .2 gb:D85425.1 gb:BC005003.1 gb:D89986.1 Consensus includes gb:BF966540 //FEA=EST //DB_XREF=gi:1233 3755 //DB_XREF=gi:1233 3755 //DB_XREF=gi:1233 3755 //DB_XREF=st:602 2287009T1 //CLONE=IMAGE:43 75586 //UG=Hs.267819 protein phosphatase 1, regulatory (inhibitor) subunit 2 //FL=gb:NM_006241			
/FEA=mRNA /GEN=NFYC //PROD=nuclear transcription factor Y, gamma //DB_XREF=gi:1149 6977 //UG=Hs.168157 nuclear transcription factor Y, gamma //FL=gb:NM_014223 2. gb:D85425.1 gb:BC005003.1 gb:BC005003.1 gb:BC005003.1 Consensus includes gb:BF966540 //FEA=EST //DB_XREF=gi:1233 3755 //DB_XREF=gi:1233 3755 //DB_XREF=est:602 287009T1 //CLONE=IMAGE:43 75586 //UG=Hs.267819 protein phosphatase 1, regulatory (inhibitor) subunit 2 //FL=gb:NM_006241			
/GEN=NFYC //PROD=nuclear transcription factor Y, gamma //DB_XREF=gi:1149 6977 //UG=Hs.168157 nuclear transcription factor Y, gamma //FL=gb:NM_014223 2 gb:D85425.1 gb:BC005003.1 gb:BC005003.1 gb:BC9586540 //FEA=EST //DB_XREF=gi:1233 3755 //DB_XREF=gi:1233 3755 //DB_XREF=est:602 287009T1 //CLONE=IMAGE:43 75586 //UG=Hs.267819 protein phosphatase 1, regulatory (inhibitor) subunit 2 //FL=gb:NM_006241		1	
/PROD=nuclear transcription factor Y, gamma //DB_XREF=gi:1149 6977 //UG=Hs.168157 nuclear transcription factor Y, gamma //FL=gb:NM_014223 .2 gb:D85425.1 gb:BC005003.1 gb:D89986.1 202215_s_at NM_014223 DB_XREF=gi:1233 3755 //DB_XREF=gi:1233 3755 //DB_XREF=est:602 287009T1 //CLONE=IMAGE:43 75586 //UG=Hs.267819 protein phosphatase 1, regulatory (inhibitor) subunit 2 //FL=gb:NM_006241			
transcription factor Y, gamma //DB_XREF=gi:1149 6977 //UG=Hs.168157 nuclear transcription factor Y, gamma //FL=gb:NM_014223 .2 gb:D85425.1 gb:BC005003.1 gb:D89986.1 Consensus includes gb:BF966540 //FEA=EST //DB_XREF=gi:1233 3755 //DB_XREF=gi:1233 3755 //DB_XREF=est:602 287009T1 //CLONE=IMAGE:43 75586 //UG=Hs.267819 protein phosphatase 1, regulatory (inhibitor) subunit 2 //FL=gb:NM_006241			/GEN=NFYC
Y, gamma //DB_XREF=gi:1149 6977 //UG=Hs.168157 nuclear transcription factor Y, gamma //FL=gb:NM_014223 .2 gb:D85425.1 gb:B605003.1 gb:D89986.1 Consensus includes gb:BF966540 //FEA=EST //DB_XREF=gi:1233 3755 //DB_XREF=est:602 287009T1 //CLONE=IMAGE:43 75586 //UG=Hs.267819 protein phosphatase 1, regulatory (inhibitor) subunit 2 //FL=gb:NM_006241			
/DB_XREF=gi:1149 6977 //UG=Hs.168157 nuclear transcription factor Y, gamma /FL=gb:NM_014223 .2 gb:D85425.1 gb:BC005003.1 gb:D89986.1 Consensus includes gb:BF966540 /FEA=EST //DB_XREF=gi:1233 3755 //DB_XREF=est:602 287009T1 //CLONE=IMAGE:43 75586 //UG=Hs.267819 protein phosphatase 1, regulatory (inhibitor) subunit 2 //FL=gb:NM_006241			transcription factor
6977 //UG=Hs.168157 nuclear transcription factor Y, gamma //FL=gb:NM_014223 .2 gb:D85425.1 gb:BC005003.1 gb:D89986.1 Consensus includes gb:BF966540 //FEA=EST //DB_XREF=gi:1233 3755 //DB_XREF=est:602 287009T1 //CLONE=IMAGE:43 75586 //UG=Hs.267819 protein phosphatase 1, regulatory (inhibitor) subunit 2 //FL=gb:NM_006241			
/UG=Hs.168157 nuclear transcription factor Y, gamma /FL=gb:NM_014223 2 gb:D85425.1 gb:BC005003.1 gb:D89986.1 Consensus includes gb:BF966540 /FEA=EST /DB_XREF=gi:1233 3755 /DB_XREF=est:602 287009T1 /CLONE=IMAGE:43 75586 /UG=Hs.267819 protein phosphatase 1, regulatory (inhibitor) subunit 2 /FL=gb:NM_006241			
nuclear transcription factor Y, gamma //FL=gb:NM_014223 .2 gb:D85425.1 gb:BC005003.1 gb:BC005003.1 gb:BS9986.1 Consensus includes gb:BF966540 //FEA=EST //DB_XREF=gi:1233 3755 //DB_XREF=est:602 287009T1 //CLONE=IMAGE:43 75586 //UG=Hs.267819 protein phosphatase 1, regulatory (inhibitor) subunit 2 //FL=gb:NM_006241			6977
transcription factor Y, gamma //FL=gb:NM_014223 .2 gb:D85425.1 gb:BC005003.1 gb:D89986.1 Consensus includes gb:BF966540 //FEA=EST //DB_XREF=gi:1233 3755 //DB_XREF=est:602 287009T1 //CLONE=IMAGE:43 75586 //UG=Hs.267819 protein phosphatase 1, regulatory (inhibitor) subunit 2 //FL=gb:NM_006241			/UG=Hs.168157
Y, gamma /FL=gb:NM_014223 .2 gb:D85425.1 gb:BC005003.1 gb:D89986.1 Consensus includes gb:BF966540 /FEA=EST /DB_XREF=gi:1233 3755 /DB_XREF=est:602 287009T1 /CLONE=IMAGE:43 75586 /UG=Hs.267819 protein phosphatase 1, regulatory (inhibitor) subunit 2 /FL=gb:NM_006241			nuclear
/FL=gb:NM_014223 .2 gb:D85425.1 gb:BC005003.1 202215_s_at NM_014223 Domesting the provided HTML of the provided			transcription factor
.2 gb:D85425.1 gb:BC005003.1 202215_s_at NM_014223 gb:D89986.1 Consensus includes gb:BF966540 /FEA=EST /DB_XREF=gi:1233 3755 /DB_XREF=est:602 287009T1 /CLONE=IMAGE:43 75586 /UG=Hs.267819 protein phosphatase 1, regulatory (inhibitor) subunit 2 /FL=gb:NM_006241			Y, gamma
gb:BC005003.1 gb:D89986.1 Consensus includes gb:BF966540 /FEA=EST /DB_XREF=gi:1233 3755 /DB_XREF=est:602 287009T1 /CLONE=IMAGE:43 75586 /UG=Hs.267819 protein phosphatase 1, regulatory (inhibitor) subunit 2 /FL=gb:NM_006241			/FL=gb:NM_014223
202215_s_at NM_014223			.2 gb:D85425.1
Consensus includes gb:BF966540 /FEA=EST /DB_XREF=gi:1233 3755 /DB_XREF=est:602 287009T1 /CLONE=IMAGE:43 75586 /UG=Hs.267819 protein phosphatase 1, regulatory (inhibitor) subunit 2 /FL=gb:NM_006241			gb:BC005003.1
Consensus includes gb:BF966540 /FEA=EST /DB_XREF=gi:1233 3755 /DB_XREF=est:602 287009T1 /CLONE=IMAGE:43 75586 /UG=Hs.267819 protein phosphatase 1, regulatory (inhibitor) subunit 2 /FL=gb:NM_006241	202215 s at	NM_014223	gb:D89986.1
gb:BF966540 //FEA=EST //DB_XREF=gi:1233 3755 //DB_XREF=est:602 287009T1 //CLONE=IMAGE:43 75586 //UG=Hs.267819 protein phosphatase 1, regulatory (inhibitor) subunit 2 //FL=gb:NM_006241			Consensus
/FEA=EST //DB_XREF=gi:1233 3755 //DB_XREF=est:602 287009T1 //CLONE=IMAGE:43 75586 //UG=Hs.267819 protein phosphatase 1, regulatory (inhibitor) subunit 2 //FL=gb:NM_006241			includes
/DB_XREF=gi:1233 3755 /DB_XREF=est:602 287009T1 /CLONE=IMAGE:43 75586 /UG=Hs.267819 protein phosphatase 1, regulatory (inhibitor) subunit 2 /FL=gb:NM_006241			gb:BF966540
3755 //DB_XREF=est:602 287009T1 //CLONE=IMAGE:43 75586 //UG=Hs.267819 protein phosphatase 1, regulatory (inhibitor) subunit 2 //FL=gb:NM_006241	•		/FEA=EST
/DB_XREF=est:602 287009T1 /CLONE=IMAGE:43 75586 /UG=Hs.267819 protein phosphatase 1, regulatory (inhibitor) subunit 2 /FL=gb:NM_006241			/DB_XREF=gi:1233
287009T1 /CLONE=IMAGE:43 75586 /UG=Hs.267819 protein phosphatase 1, regulatory (inhibitor) subunit 2 /FL=gb:NM_006241			3755
/CLONE=IMAGE:43 75586 /UG=Hs.267819 protein phosphatase 1, regulatory (inhibitor) subunit 2 /FL=gb:NM_006241	1		/DB_XREF=est:602
75586 /UG=Hs.267819 protein phosphatase 1, regulatory (inhibitor) subunit 2 /FL=gb:NM_006241			287009T1
/UG=Hs.267819 protein phosphatase 1, regulatory (inhibitor) subunit 2 /FL=gb:NM_006241			/CLONE=IMAGE:43
protein phosphatase 1, regulatory (inhibitor) subunit 2 /FL=gb:NM_006241			75586
phosphatase 1, regulatory (inhibitor) subunit 2 /FL=gb:NM_006241			/UG=Hs.267819
regulatory (inhibitor) subunit 2 /FL=gb:NM_006241			protein
regulatory (inhibitor) subunit 2 /FL=gb:NM_006241			phosphatase 1,
(inhibitor) subunit 2 /FL=gb:NM_006241			
2 /FL=gb:NM_006241			1 - 1
, , , , , , , , , , , , , , , , , , ,			11.
, , , , , , , , , , , , , , , , , , ,			/FL=gb:NM_006241
	202165 at	NM_006241	

Figure 7a CC	 		 =
203136 at	NM_006423	gb:NM_006423.1 /DEF=Homo sapiens Rab acceptor 1 (prenylated) (RABAC1), mRNA. /FEA=mRNA /GEN=RABAC1 /PROD=Rab acceptor 1 (prenylated) /DB_XREF=gi:5453 959 /UG=Hs.11417 Rab acceptor 1 (prenylated) /FL=gb:NM_006423 .1 gb:AF112202.1	
203130_at	 14101_000423	.1 gb.Al 112202.1	
		gb:NM_006599.1 /DEF=Homo sapiens nuclear factor of activated T-cells 5, tonicity- resonsive (NFAT5), mRNA. /FEA=mRNA /GEN=NFAT5 /PROD=nuclear factor of activated T-cells 5,tonicity- resonsive /DB_XREF=gi:5729 944 /UG=Hs.86998 nuclear factor of activated T-cells 5, tonicity-responsive /FL=gb:AB020634.1 gb:AF163836.1	
208003_s_at	NM_006599	gb:NM_006599.1	

Figure /a C		· · · · · · · · · · · · · · · · · · ·			
202113_s_at		AF043453	gb:AF043453.1 /DEF=Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds. /FEA=mRNA /GEN=SNX2 /PROD=sorting nexin 2 /DB_XREF=gi:2827 433 /UG=Hs.11183 sorting nexin 2 /FL=gb:BC003382.1 gb:AF043453.1 gb:AF065482.1 gb:NM_003100.1		
202069 s at	BG1	AI826060	lipidosin		Hs.277543
213217_at	ADCY2	AU149572	adenylate cyclase 2 (brain)		Hs.2352
		ADOUTOO	gb:AB005289.1 /DEF=Homo sapiens mRNA for ABC transporter 7 protein, complete cds. /FEA=mRNA /GEN=hABC7 /PROD=ABC transporter 7 protein /DB_XREF=gi:3228 278 /UG=Hs.125856 ATP-binding cassette, sub-family B (MDRTAP), member 7 /FL=gb:AB005289.1 gb:AF038950.1 gb:AF133659.1		
209620_s_at		AB005289	gb:NM_004299.2	1	

I igule 7a Oc	711 G.			
i igare i a es	mu.		gb:NM_021212.1 /DEF=Homo sapiens HCF- binding transcription factor Zhangfei (ZF), mRNA. /FEA=mRNA /GEN=ZF /PROD=HCF- binding transcription factor Zhangfei /DB_XREF=gi:1086 4024 /UG=Hs.29417 HCF-binding transcription factor Zhangfei /FL=gb:NM_021212	
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			/FEA=mRNA /GEN=TTC3 /PROD=tetratricope ptide repeat domain 3 /DB_XREF=gi:1083 5036 /UG=Hs.118174	
208073_x_at		NM_003316	tetratricopeptide repeat domain 3 /FL=gb:NM_003316 .1 gb:D84295.1	

Figure /a Co	Jiica.			
			gb:NM_001934.1 /DEF=Homo sapiens distal-less homeobox 4 (DLX4), mRNA. /FEA=mRNA /GEN=DLX4 /PROD=distal-less homeobox 4 /DB_XREF=gi:4503 342 /UG=Hs.172648 distal-less homeobox 4 /FL=gb:U73328.1	
208216_at		NM_001934	gb:NM_001934.1	
214934_at	ATP9B	AW411030	ATPase, Class II, type 9B	Hs.91471
214749_s_at		AK000818	Consensus includes gb:AK000818.1 /DEF=Homo sapiens cDNA FLJ20811 fis, clone ADSE01435. /FEA=mRNA /DB_XREF=gi:7021 128 /UG=Hs.83530 hypothetical protein	
208424_s_at		NM_020313	gb:NM_020313.1 /DEF=Homo sapiens hypothetical protein (LOC57019), mRNA. /FEA=mRNA /GEN=LOC57019 /PROD=hypothetica I protein /DB_XREF=gi:1009 2672 /UG=Hs.4900 hypothetical protein /FL=gb:NM_020313 .1	

gb:NM_003920.1 //DEF=Homo sapiens timeless (Drosophila) homolog (TIMELESS), mRNA. //FEA=mRNA //FEA=mRNA //GEN=TIMELESS //PROD=timeless (Drosophila) homolog //DB_XREF=gi:4507 506 //UG=Hs.118631 timeless (Drosophila) homolog	Figure /a Co	JIILU.			
/GEN=TIMELESS /PROD=timeless (Drosophila) homolog /DB_XREF=gi:4507 506 /UG=Hs.118631 timeless (Drosophila) homolog			BF340083	1 (glutamate/neutral amino acid transporter), member 4 gb:NM_003920.1 /DEF=Homo sapiens timeless (Drosophila) homolog (TIMELESS), mRNA.	Hs.323878
gb:AB015597.1 203046_s_at	203046 s at		NM_003920	/GEN=TIMELESS /PROD=timeless (Drosophila) homolog /DB_XREF=gi:4507 506 /UG=Hs.118631 timeless (Drosophila) homolog /FL=gb:AF098162.1 gb:AB015597.1	
gb:NM_021030.1 /DEF=Homo sapiens zinc finger protein 14 (KOX 6) (ZNF14), mRNA. /FEA=mRNA /GEN=ZNF14 /PROD=zinc finger protein 14 (KOX 6) /DB_XREF=gi:1113 9306 /UG=Hs.197219 zinc finger protein 14 (KOX 6) /FL=gb:NM_021030 219854_at NM_021030 .1 gb:AB021644.1				gb:NM_021030.1 /DEF=Homo sapiens zinc finger protein 14 (KOX 6) (ZNF14), mRNA. /FEA=mRNA /GEN=ZNF14 /PROD=zinc finger protein 14 (KOX 6) /DB_XREF=gi:1113 9306 /UG=Hs.197219 zinc finger protein 14 (KOX 6) /FL=gb:NM_021030	
NM_021030 1 gb:AB021644.1		SCAMP5		secretory carrier membrane protein	Hs.7934

Application of: Liew, et. al. Our Docket #: 4231/2042 Figure 7a Cont'd.

Figure 7a Co	JIIC G.				
			zinc finger protein		
			45 (a Kruppel-		
			associated box		
			(KRAB) domain		11 11700
222028_at	ZNF45	AI967981	polypeptide)		Hs.41728
			Homo sapiens		
			cDNA FLJ34103 fis,		
			clone		
			FCBBF3007859,		
			moderately similar		
			to Human putative		
214319_at		W58342	protein B2 mRNA		Hs.406809
			G protein-coupled		
	CNR1; CB1;		receptor; Human		
	CB-R; CB1A;		CB1 cannabinoid	NM 001840;	
			receptor (CNR1)	NM_016083;	
242426 et	CANN6; CB1K5	U73304			
213436_at	CBIKS	073304	gene, complete cds.	14141_033101	
			gb:BC005247.1		
			/DEF=Homo		
			sapiens,		
			isopentenyl-		
		1	diphosphate delta		
			isomerase, clone		
			MGC:12281,		
			mRNA, complete		
			cds. /FEA=mRNA		
			/PROD=isopentenyl-		
			diphosphate delta		
		Ì	lisomerase		
1			/DB_XREF=gi:1352		
			8899		
			/UG=Hs.76038		
			isopentenyl-		
		}	diphosphate delta		
			isomerase		
208881_x_at		BC005247	/FL=gb:BC005247.1		

Application of: Liew, et. al. Our Docket #: 4231/2042 Figure 7a Cont'd.

I iguie 7a CO			
200886 s_at	NM 002629	gb:NM_002629.1 /DEF=Homo sapiens phosphoglycerate mutase 1 (brain) (PGAM1), mRNA. /FEA=mRNA /GEN=PGAM1 /PROD=phosphogly cerate mutase 1 (brain) /DB_XREF=gi:4505 752 /UG=Hs.181013 phosphoglycerate mutase 1 (brain) /FL=gb:BC000455.1 gb:NM_002629.1 gb:J04173.1	
212018_s_at	AK025446	Consensus includes gb:AK000822.1 //DEF=Homo sapiens cDNA FLJ20815 fis, clone ADSE01038, highly similar to AJ007398 Homo sapiens mRNA for PBK1 protein. //FEA=mRNA //DB_XREF=gi:7021 134 //UG=Hs.85963 DKFZP564M182 protein	

gb:NM_005345.3 //DEF=Homo sapiens heat shock 70kD protein 1A (HSPA1A), mRNA. //FEA=mRNA //GEN=HSPA1A //PROD=heat shock 70kD protein 1A //DB_XREF=gi:5579 469 /UG=Hs.8997 heat shock 70kD protein 1A //FL=gb:BC002453.1 gb:NM_005345.3 peptidylproly isomerase D (cyclophilin D) 204186_s_at PPID Al014573 (consensus includes gb:Al745225 //FEA=EST //DB_XREF=gi:5113 513 //DB_XREF=gi:5113 513 //DB_XREF=set:wg1 0d12_x1 //CLONE=IMAGE:23 64695 //UG=Hs.127649 KIAA0414 protein //FI=gb:NM_014007 1 Consensus includes gb:AU152088 //FEA=EST //DB_XREF=gi:101 3609 //DB_XREF=gi:101 3609 //DB_XREF=gi:101 3609 //DB_XREF=est:AU 152088	Figure 7a Co	onica.			
Somerase D			NM_005345	/DEF=Homo sapiens heat shock 70kD protein 1A (HSPA1A), mRNA. /FEA=mRNA /GEN=HSPA1A /PROD=heat shock 70kD protein 1A /DB_XREF=gi:5579 469 /UG=Hs.8997 heat shock 70kD protein 1A /FL=gb:BC002453.1 gb:NM_005345.3	
204186_s_at PPID AI014573 (cyclophilin D) Hs.143482 Consensus includes gb:AI745225 /FEA=EST /DB_XREF=gi:5113 513 /DB_XREF=est:wg1 0d12.x1 /CLONE=IMAGE:23 64695 /UG=Hs.127649 KIAA0414 protein /FL=gb:NM_014007 .1 204180_s_at NM_014007 .1 Consensus includes gb:AU152088 /FEA=EST /DB_XREF=gi:1101 3609 /DB_XREF=est:AU					
includes gb:Al745225 //FEA=EST //DB_XREF=gi:5113 513 //DB_XREF=est:wg1 0d12.x1 //CLONE=IMAGE:23 64695 //UG=Hs.127649 KIAA0414 protein //FL=gb:NM_014007 1 Consensus includes gb:AU152088 //FEA=EST //DB_XREF=gi:1101 3609 //DB_XREF=est:AU	204186_s_at	PPID	AI014573	(cyclophilin D)	 Hs.143482
Consensus includes gb:AU152088 /FEA=EST /DB_XREF=gi:1101 3609 /DB_XREF=est:AU				includes gb:Al745225 /FEA=EST /DB_XREF=gi:5113 513 /DB_XREF=est:wg1 0d12.x1 /CLONE=IMAGE:23 64695 /UG=Hs.127649 KIAA0414 protein /FL=gb:NM_014007	
includes gb:AU152088 /FEA=EST /DB_XREF=gi:1101 3609 /DB_XREF=est:AU	204180_s_at		NM_014007		
/CLONE=NT2RP30 00162 /UG=Hs.7976 212060_at AB002330 KIAA0332 protein			ADGGGGG	includes gb:AU152088 /FEA=EST /DB_XREF=gi:1101 3609 /DB_XREF=est:AU 152088 /CLONE=NT2RP30 00162 /UG=Hs.7976	

Figure /a Co	illu.			
64418_at		Al472320	ESTs, Weakly similar to I38022 hypothetical protein human [H.sapiens]	Hs.48504
			gb:NM_006311.1 /DEF=Homo sapiens nuclear receptor co- repressor 1 (NCOR1), mRNA. /FEA=mRNA /GEN=NCOR1 /PROD=nuclear receptor co- repressor 1 /DB_XREF=gi:5454 137 /UG=Hs.144904 nuclear receptor co-repressor 1 /FL=gb:AF044209.1	
200857_s_at		NM_006311	gb:NM_006311.1	
217925_s_at		NM_022758	gb:NM_022758.1 /DEF=Homo sapiens hypothetical protein FLJ22195 (FLJ22195), mRNA. /FEA=mRNA /GEN=FLJ22195 /PROD=hypothetica I protein FLJ22195 /DB_XREF=gi:1223 2426 /UG=Hs.25999 hypothetical protein FLJ22195 /FL=gb:NM_022758 .1	
200002 04	חחה	1160567	progestin induced	Uc 278429
208883_at	DD5	U69567	protein	 Hs.278428

Figure /a Contro.				
İ		gb:NM_016061.1		ŀ
		/DEF=Homo		
		sapiens CGI-127		
		protein		
	1	(LOC51646),		
		mRNA.		
İ		/FEA=mRNA		
		/GEN=LOC51646		
		/PROD=CGI-127		
		protein		
		/DB_XREF=gi:7706		
<u> </u>		340		
ł l		/UG=Hs.184542		
		CGI-127 protein		
		/FL=gb:BC000836.1		
		gb:AF151885.1		
1,,,,,,	NINA 040004	1~]
217783_s_at	NM_016061	gb:NM_016061.1		
		gb:NM_005642.1	•	
		/DEF=Homo		
		sapiens TATA box		
		binding protein		
		(TBP)-associated		
İ		factor, RNA		
		polymerase II, F,		ı
		55kD (TAF2F),		
		mRNA.		
		/FEA=mRNA		
1		1		
		/GEN=TAF2F		
		/PROD=TATA box		
		binding protein		
		(TBP)-		
		associatedfactor,	:	
1		RNA polymerase		
		II, F, 55kD		
		/DB_XREF=gi:5032		
		148		
		/UG=Hs.155188		
]		TATA box binding		
		protein (TBP)-		
]				
] 1		associated factor,		
1		RNA polymerase		
		II, F, 55kD		
		/FL=gb:NM_005642		
201023_at	NM_005642	1.1 gb:U18062.1		1

Figure 7a Cont'd.	ıt'd.
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	Jittu.		, 	·	
205053_at		NM_000946	gb:NM_000946.1 /DEF=Homo sapiens primase, polypeptide 1 (49kD) (PRIM1), mRNA. /FEA=mRNA /GEN=PRIM1 /PROD=primase, polypeptide 1 (49kD) /DB_XREF=gi:4506 050 /UG=Hs.82741 primase, polypeptide 1 (49kD) /FL=gb:BC005266.1 gb:NM_000946.1		
204038_s_at		NM_001401	gb:NM_001401.1 /DEF=Homo sapiens endothelial differentiation, lysophosphatidic acid G-protein- coupled receptor, 2 (EDG2), mRNA. /FEA=mRNA /GEN=EDG2 /PROD=endothelial differentiation, lysophosphatidicaci d G-protein- coupled receptor, 2 /DB_XREF=gi:4503 456 /UG=Hs.75794 endothelial differentiation, lysophosphatidic acid G-protein- coupled receptor, 2 /FL=gb:U78192.1 gb:U80811.1 gb:NM_001401.1		

Tigule 7a Oc	11. 4.	,			
			Consensus		
			includes		
		ļ.	gb:N29889		
			/FEA=EST		
			/DB_XREF=gi:1148		
			409		
		i	/DB_XREF=est:yy1		
			1e11.s1		
			/CLONE=IMAGE:27		
			0956		
			/UG=Hs.77495		i
			UBX domain-		
212008_at		D87684	containing 1		
			hypothetical protein		
51146_at	FLJ20477	AA203365	FLJ20477		Hs.26994
			gb:NM_021632.1		
			/DEF=Homo		·
			sapiens zinc-finger		
			protein ZBRK1		1
			(ZBRK1), mRNA.		
			/FEA=mRNA		
			/GEN=ZBRK1		
			/PROD=zinc-finger		
			protein ZBRK1		
		•	/DB_XREF=gi:1105		
			6003		
			/UG=Hs.130965		:
			zinc-finger protein		
			ZBRK1		
			/FL=gb:AF295096.1		
			gb:AF309561.1	,	1
219266_at		NM 021632	gb:NM_021632.1		
			zinc-finger protein		
204556_s_at	DZIP1	AL568422	DZIP1		Hs.60177
			SET translocation		
1					
	SET	AV702810	(myeloid leukemia- associated)		Hs.145279

F	iau	re	7a	Cor	nt'd.
	u		, u	\sim	16 0.

			gb:NM_004544.1 /DEF=Homo sapiens NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10 (42kD) (NDUFA10), mRNA. /FEA=mRNA /GEN=NDUFA10 /PROD=NADH dehydrogenase (ubiquinone) 1 alphasubcomplex, 10 (42kD) /DB_XREF=gi:4758 767 /UG=Hs.198271 NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10 in the second seco	
			10 (42kD)	
			/FL=gb:BC003417.1	
			gb:AF087661.1	
217860_at		NM_004544	gb:NM_004544.1	 11 100000
213650_at	GOLGIN-67	AW006438	golgin-67	 Hs.182982

Figure 7a Co	mica.			 <u> </u>
220287_at		NM_020249	gb:NM_020249.1 /DEF=Homo sapiens disintegrin metalloproteinase with thrombospondin repeats (ADAMTS9), mRNA. /FEA=mRNA /GEN=ADAMTS9 /PROD=a disintegrin and metalloproteinase withthrombospondin motifs-9 preproprotein /DB_XREF=gi:9910 121 /UG=Hs.126855 disintegrin metalloproteinase with thrombospondin repeats /FL=gb:AF261918.1 gb:NM_020249.1	
			gb:D89729.1 /DEF=Homo sapiens mRNA for CRM1 protein, complete cds. /FEA=mRNA /PROD=CRM1 protein /DB_XREF=gi:2626 839 /UG=Hs.79090 exportin 1 (CRM1, yeast, homolog) /FL=gb:D89729.1 gb:NM_003400.2	
213684_s_at	LIM	BF671400	LIM protein (similar to rat protein kinase C-binding enigma)	Hs.154103

Figure /a Co	incu.			
212086 x at			Consensus includes gb:AK026584.1 /DEF=Homo sapiens cDNA: FLJ22931 fis, clone KAT07501, highly similar to HSLAMAR Human mRNA for nuclear envelope protein lamin A precursor. /FEA=mRNA /DB_XREF=gi:1043 9468 /UG=Hs.77886 lamin AC	
			gb:NM_000610.1 /DEF=Homo	
			sapiens CD44	
			antigen (homing	
1			function and	
			Indian blood group	
			system) (CD44),	
			mRNA.	
			/FEA=mRNA	
			/GEN=CD44	
1			/PROD=CD44	
			antigen (homing	
			function and Indian bloodgroup	
			system)	
			/DB XREF=gi:1083	
			5162	
			/UG=Hs.169610	
	ļ		CD44 antigen	
	ĺ		(homing function	
			and Indian blood	
			group system)	
			/FL=gb:NM_000610 .1 gb:U40373.1	
			gb:M59040.1	
204489_s_at	}	NM_000610	gb:M24915.1	
	4		·	 · · · · · · · · · · · · · · · · · · ·

Figure 7a Co	one a.			
208734_x_at		M28213	gb:M28213.1 /DEF=Homo sapiens GTP- binding protein (RAB2) mRNA, complete cds. /FEA=mRNA /GEN=RAB2 /PROD=GTP- binding protein /DB_XREF=gi:5500 61 /UG=Hs.78305 RAB2, member RAS oncogene family /FL=gb:NM_002865 .1 gb:M28213.1	
	SERPINB1	AI554300	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 1	Hs.183583
213572_s_at	SERFINDI	A1354300	splicing factor 30, survival of motor	118.103303
200071_at	SPF30	BF224259	neuron-related	 Hs.79968
200060_s_at		BC001659	gb:BC001659.1 /DEF=Homo sapiens, RNA- binding protein S1, serine-rich domain, clone MGC:1125, mRNA, complete cds. /FEA=mRNA /PROD=RNA- binding protein S1, serine-rich domain /DB_XREF=gi:1280 4496 /UG=Hs.75104 RNA-binding protein S1, serine- rich domain /FL=gb:BC001659.1 gb:BC001838.1	

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	 	·	 · · · · · · · · · · · · · · · · · · ·
220261_s_at	NM_018106	gb:NM_018106.1 /DEF=Homo sapiens hypothetical protein FLJ10479 (FLJ10479), mRNA. /FEA=mRNA /GEN=FLJ10479 /PROD=hypothetica I protein FLJ10479 /DB_XREF=gi:8922 447 /UG=Hs.5268 hypothetical protein FLJ10479 /FL=gb:AL136674.1 gb:BC001239.1 gb:NM_018106.1	
		gb:AF182645.1 /DEF=Homo sapiens chondrosarcoma- associated protein 2 (CSA2) mRNA, complete cds. /FEA=mRNA /GEN=CSA2	
		/PROD=chondrosar coma-associated protein 2 /DB_XREF=gi:5901 877 /UG=Hs.8024 IK cytokine, down-	
200066_at	AF182645	regulator of HLA II /FL=gb:NM_006083 .2 gb:AF182645.1	

Figure	7a	Cor	าt'd.

		gb:NM_003016.1 /DEF=Homo sapiens splicing factor, arginineserine-rich 2 (SFRS2), mRNA. /FEA=mRNA /GEN=SFRS2 /PROD=splicing factor, arginineserine-rich 2 /DB_XREF=gi:4506 898 /UG=Hs.73965 splicing factor, arginineserine-rich 2 /FL=gb:BC000339.1 gb:BC001303.1 gb:M90104.1	
200754_x_at	NM_003016	gb:NM_003016.1 gb:NM_021930.1 /DEF=Homo sapiens hypothetical protein FLJ11785 (FLJ11785), mRNA. /FEA=mRNA /GEN=FLJ11785 /PROD=hypothetica I protein FLJ11785 /DB_XREF=gi:1134 5465 /UG=Hs.44625 Rad50-interacting protein 1 /FL=gb:NM_021930 .1 gb:AF317622.1	

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Figure 7a CC	r -		T	
200744_s_at		NM_002074	Consensus includes gb:AI741124 /FEA=EST /DB_XREF=gi:5109 412 /DB_XREF=est:wg1 9c04.x1 /CLONE=IMAGE:23 65542 /UG=Hs.215595 guanine nucleotide binding protein (G protein), beta polypeptide 1 /FL=gb:NM_002074.1 gb:BC004186.1 qb80a04.x1 Soares_fetal_heart _NbHH19W Homo sapiens cDNA clone IMAGE:1706382 3' similar to TR:O21123 O21123 CYTOCHROME OXIDASE I;, mRNA sequence.	
200770_s_at		J03202	gb:J03202.1 /DEF=Human laminin B2 chain mRNA, complete cds. /FEA=mRNA /GEN=LAMB2 /DB_XREF=gi:1869 16 /UG=Hs.214982 laminin, gamma 1 (formerly LAMB2) /FL=gb:J03202.1 gb:NM_002293.2	
54632_at	FLJ21877	AI286226	hypothetical protein FLJ21877	Hs.16063
217798_at	CNOT2	AI123426	CCR4-NOT transcription complex, subunit 2	Hs.239720

gb:BC002923.1 //DEF=Homo sapiens, clone MGC:10280, mRNA, complete cds. /FEA=mRNA //PROD=Unknown (protein for MGC:10280) //DB_XREF=gi:1280 4138 //UG=Hs.31968 DKFZP586D211 protein //FL=gb:BC002923.1 gb:NM_015450.1 gb:AB034747.1 //DEF=Homo sapiens SIMPLE mRNA for small integral membrane protein of lysosomelate endosome, complete cds. //FEA=mRNA //GEN=SIMPLE //ROD=small integral membrane protein of lysosomelateendos ome //DB_XREF=gi:1286 2475 //UG=Hs.76507 LPS-induced TNF- alpha factor //PL=gb:AB034747.1 gb:U77396.1 gb:AF010312.1 gb:MF004862.1	Figure /a CC		-	
/DEF=Homo sapiens SIMPLE mRNA for small integral membrane protein of lysosomelate endosome, complete cds. //EA=mRNA //GEN=SIMPLE //PROD=small integral membrane protein of lysosomelateendos ome //DB_XREF=gi:1286 2475 //UG=Hs.76507 LPS-induced TNF- alpha factor //EL=gb:AB034747.1 gb:U77396.1 gb:AF010312.1	204353_s_at	BC002923	/DEF=Homo sapiens, clone MGC:10280, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:10280) /DB_XREF=gi:1280 4138 /UG=Hs.31968 DKFZP586D211 protein /FL=gb:BC002923.1	
- CARLANA AV 1 - 10-100 AVA 1 - 10-1			gb:AB034747.1 /DEF=Homo sapiens SIMPLE mRNA for small integral membrane protein of lysosomelate endosome, complete cds. /FEA=mRNA /GEN=SIMPLE /PROD=small integral membrane protein of lysosomelateendos ome /DB_XREF=gi:1286 2475 /UG=Hs.76507 LPS-induced TNF- alpha factor /FL=gb:AB034747.1 gb:U77396.1 gb:AF010312.1	

1 19410 74 04					
			gb:NM_006826.1 /DEF=Homo sapiens tyrosine 3- monooxygenasetryp tophan 5- monooxygenase activation protein, theta polypeptide (YWHAQ), mRNA. /FEA=mRNA /GEN=YWHAQ /PROD=tyrosine 3- monooxygenase activation protein, theta polypeptide /DB_XREF=gi:5803 226 /UG=Hs.74405 tyrosine 3- monooxygenasetryp tophan 5- monooxygenasetryp tophan 5- monooxygenase activation protein, theta polypeptide /FL=gb:NM_006826	·	
200693 at		NM_006826	.1		
<u> </u>	····		hypothetical protein		
217795_s_at	MGC3222	W74580	MGC3222		Hs.323193

Figure /a C	ont u.				
208810_at		AF080569	gb:AF080569.1 //DEF=Homo sapiens DnaJ-like 2 protein (HSJ2) mRNA, complete cds. /FEA=mRNA //GEN=HSJ2 //PROD=DnaJ-like 2 protein //DB_XREF=gi:4322 314 //UG=Hs.181195 DnaJ (Hsp40) homolog, subfamily B, member 6 //FL=gb:AL136707.1 gb:BC000177.2 gb:AB014888.1 gb:AF080569.1 gb:NM_005494.1 gb:AF075601.1 gb:AF075601.1 gb:AF07599.1 microtubule- associated protein, RP/EB family,		
200712_s_at	MAPRE1	Al633566	member 1		Hs.234279
200712 a at		NIM 042225	gb:NM_012325.1 /DEF=Homo sapiens microtubule- associated protein, RPEB family, member 1 (MAPRE1), mRNA. /FEA=mRNA /GEN=MAPRE1 /PROD=microtubule associated protein, RPEB family,member 1 /DB_XREF=gi:6912 493 /UG=Hs.234279 microtubule- associated protein, RPEB family, member 1 /FL=gb:NM_012325 .1 gb:U24166.1		
200713_s_at	<u></u>	NM_012325	1. 1 gb.024100.1	L	

211569_s_at	AF001903	gb:AF001903.1 /DEF=Human 3- hydroxyacyl-CoA dehydrogenase, isoform 2 mRNA, complete cds. /FEA=mRNA /PROD=3- hydroxyacyl-CoA dehydrogenase, isoform 2 /DB_XREF=gi:2078 328 /UG=Hs.8110 L-3-hydroxyacyl- Coenzyme A dehydrogenase, short chain /FL=gb:AF001903.1 gb:NM_006201.1 /DEF=Homo sapiens PCTAIRE protein kinase 1 (PCTK1), mRNA. /FEA=mRNA /GEN=PCTK1 /PROD=PCTAIRE protein kinase 1 /DB_XREF=gi:5453 859 /UG=Hs.171834	
207239_s_at	NM_006201	PCTAIRE protein kinase 1 /FL=gb:NM_006201	

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Tigure 7a Conta.				
1		gb:AB049113.1		
		/DEF=Homo		ļ
		sapiens DUT		
1		mRNA for dUTP		
		pyrophosphatase,		
		complete cds.		
		/FEA=mRNA		
		/GEN=DUT		
İ		/PROD=dUTP		
		pyrophosphatase		
		/DB_XREF=gi:1025		
		7384		
1		/UG=Hs.82113		
		dUTP		
		pyrophosphatase		
		/FL=gb:AB049113.1		
		gb:U31930.1		
		gb:U62891.1		
		gb:M89913.1		
208955_at	AB049113	gb:NM_001948.1		
20000_01				
		gb:NM_018507.1		
		/DEF=Homo		
		sapiens		
		hypothetical protein		
		PRO1843		
		(PRO1843),		
		mRNA.	ļ	
		/FEA=mRNA		
		/GEN=PRO1843		
		/PROD=hypothetica		
		I protein PRO1843		
		/DB_XREF=gi:8924		
		082		
		/UG=Hs.283330		
1		hypothetical protein		
		PRO1843		
		/FL=gb:AF119854.1		
219599_at	NM 018507	gb:NM_018507.1	I	1

Figure /a Co	illu.			
218532_s_at	nicu.	NM_019000	gb:NM_019000.1 /DEF=Homo sapiens hypothetical protein (FLJ20152), mRNA. /FEA=mRNA /GEN=FLJ20152 /PROD=hypothetica I protein /DB_XREF=gi:9506 660 /UG=Hs.82273 hypothetical protein /FL=gb:NM_019000 .1 gb:NM_001356.2 /DEF=Homo sapiens DEADH (Asp-Glu-Ala-AspHis) box polypeptide 3 (DDX3), transcript variant 2, mRNA. /FEA=mRNA	
	·		variant 2, mRNA. /FEA=mRNA /GEN=DDX3 /PROD=DEADH (Asp-Glu-Ala-AspHis) box polypeptide 3 /DB_XREF=gi:1351 4812 /UG=Hs.147916 DEADH (Asp-Glu-	
201210_at		NM_001356	Ala-AspHis) box polypeptide 3 /FL=gb:NM_001356 .2 gb:U50553.1 gb:AF000982.1 gb:AF061337.1	

Figure	7a	Cont'd.
1 Igui C	, 4	OUTIL G.

- riguic ra oc	 		
218347_at	NM_018264	gb:NM_018264.1 /DEF=Homo sapiens hypothetical protein FLJ10900 (FLJ10900), mRNA. /FEA=mRNA /GEN=FLJ10900 /PROD=hypothetica I protein FLJ10900 /DB_XREF=gi:8922 751 /UG=Hs.16277 hypothetical protein FLJ10900 /FL=gb:NM_018264 .1 gb:NM_005110.1 /DEF=Homo sapiens glutamine- fructose-6- phosphate transaminase 2 (GFPT2), mRNA.	
		phosphate transaminase 2	
		transaminase 2 /DB_XREF=gi:4826 741 /UG=Hs.30332 glutamine-fructose- 6-phosphate transaminase 2 /FL=gb:BC000012.1 gb:AB016789.1	
205100_at	NM_005110	gb:NM_005110.1	

Figure 7a Co	 	· · · · · · · · · · · · · · · · · · ·	
218696 at	NM_004836	gb:NM_004836.1 /DEF=Homo sapiens eukaryotic translation initiation factor 2-alpha kinase 3 (EIF2AK3), mRNA. /FEA=mRNA /GEN=EIF2AK3 /PROD=eukaryotic translation initiation factor 2- alphakinase 3 /DB_XREF=gi:4758 891 /UG=Hs.102506 eukaryotic translation initiation factor 2-alpha kinase 3 /FL=gb:AF110146.1 gb:NM_004836.1 gb:AF193339.1	
205091_x_at	NM_002907	gb:NM_002907.1 /DEF=Homo sapiens RecQ protein-like (DNA helicase Q1-like) (RECQL), mRNA. /FEA=mRNA /GEN=RECQL /PROD=RecQ protein-like (DNA helicase Q1-like) /DB_XREF=gi:4506 468 /UG=Hs.235069 RecQ protein-like (DNA helicase Q1-like) /FL=gb:NM_002907 .1 gb:L36140.1	

Figure 7a CC	iii u.				
			gb:NM_004528.1		
			/DEF=Homo		
			sapiens		
			microsomal		
			glutathione S-	•	
			transferase 3		
			(MGST3), mRNA.		
			/FEA=mRNA		
			/GEN=MGST3		
			/PROD=microsomal		
			glutathione S-		
			transferase 3		
			/DB_XREF=gi:4758		
			713		
			/UG=Hs.111811		
			microsomal		
			glutathione S-		
			transferase 3		
:			/FL=gb:BC000505.1		
			gb:BC003034.1		
			gb:AF026977.1		
201403_s_at		NM_004528	gb:NM_004528.1		
			gb:AB009010.1		
			/DEF=Homo		
			sapiens mRNA for		
			polyubiquitin UbC,		
			complete cds.	:	
			/FEA=mRNA		
			/GEN=UbC1		
			/PROD=polyubiquiti		
]	n UbC		
			/DB_XREF=gi:2647		
			407		
		1	/UG=Hs.183704		
			ubiquitin C		
			/FL=gb:BC000449.1		
		T.	gb:AB009010.1	1	

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Figure 7a Co	mica.			
201381_x_at		AF057356	gb:AF057356.1 //DEF=Homo sapiens calcyclin binding protein mRNA, complete cds. /FEA=mRNA //PROD=calcyclin binding protein //DB_XREF=gi:3063 652 /UG=Hs.27258 calcyclin binding protein //FL=gb:AF314752.1 gb:AF057356.1 gb:NM_014412.1 thyroid hormone	
			receptor-associated	
	TD 4 D05		protein, 95-kD	LI- 24050
43544_at	TRAP95	AA314406	subunit	Hs.31659
211509_s_at		AB015639	gb:AB015639.1 /DEF=Homo sapiens ASY mRNA, complete cds. /FEA=mRNA /GEN=ASY /DB_XREF=gi:5821 139 /UG=Hs.65450 reticulon 4 /FL=gb:AB015639.1	
201190_s_at	PITPN	 H15647	phosphotidylinositol transfer protein	Hs.409367
201218_at		NM_001329	Consensus includes gb:N23018 /FEA=EST /DB_XREF=gi:1137 168 /DB_XREF=est:yx6 5d12.s1 /CLONE=IMAGE:26 6615 /UG=Hs.171391 C-terminal binding protein 2 /FL=gb:AF016507.1 gb:NM_001329.1	

			gb:NM_001628.1 /DEF=Homo sapiens aldo-keto reductase family 1, member B1 (aldose reductase) (AKR1B1), mRNA. /FEA=mRNA /GEN=AKR1B1 /PROD=aldo-keto reductase family 1, member B1 (aldosereductase) /DB_XREF=gi:4502 048 /UG=Hs.75313 aldo-keto reductase family 1, member B1 (aldose reductase) /FL=gb:BC000260.1 gb:BC005387.1 gb:J054795.1 gb:J05474.1 gb:M34720.1	
			gb:J05474.1	
201272_at		NM 001628	gb:NM_001628.1	
			hypothetical protein	
201245_s_at	FLJ20113	AL523776	FLJ20113	Hs.108504

Figure 7a Cont'd. Consensus includes gb:AL157398 /DEF=Human DNA sequence from clone RP11-56H7 on chromosome 10. Contains ESTs, STSs and GSSs. Contains the gene for the nebulette protein (NEBL, actinbinding Z-disc protein) /FEA=mRNA_1 /DB_XREF=gi:1004 5326 /UG=Hs.5025 nebulette /FL=gb:NM_006393 AL157398 203961_at gb:NM_018281.1 /DEF=Homo sapiens hypothetical protein FLJ10948 (FLJ10948), mRNA. /FEA=mRNA /GEN=FLJ10948 /PROD=hypothetica I protein FLJ10948 /DB_XREF=gi:8922 786 /UG=Hs.9670 hypothetical protein FLJ10948

/FL=gb:NM_018281

NM_018281

218552_at

Figure 7a Co	onta.			
218656_s_at		NM_005780	gb:NM_005780.1 /DEF=Homo sapiens lipoma HMGIC fusion partner (LHFP), mRNA. /FEA=mRNA /GEN=LHFP /PROD=lipoma HMGIC fusion partner /DB_XREF=gi:5031 864 /UG=Hs.93765 lipoma HMGIC fusion partner /FL=gb:AF098807.1 gb:NM_005780.1 ESTs, Weakly similar to PRO0478	
213413_at		BG434174	protein [Homo sapiens] [H.sapiens] zinc finger protein	Hs.409046
213916_at	ZNF20	AU154474	20 (KOX 13)	 Hs.110956
218430_s_at		NM_022841	gb:NM_022841.1 /DEF=Homo sapiens hypothetical protein FLJ12994 (FLJ12994), mRNA. /FEA=mRNA /GEN=FLJ12994 /PROD=hypothetica I protein FLJ12994 /DB_XREF=gi:1238 3091 /UG=Hs.126908 hypothetical protein FLJ12994 /FL=gb:NM_022841 .1	

Figure 7a Co	ont a.			
	int d.	NIM 006474	gb:NM_006474.1 /DEF=Homo sapiens lung type-I cell membrane- associated glycoprotein (T1A- 2), transcript variant 2, mRNA. /FEA=mRNA /GEN=T1A-2 /PROD=lung type-I cell membrane- associatedglycoprot ein, isoform 2 precursor /DB_XREF=gi:5454 097 /UG=Hs.135150 lung type-I cell membrane- associated glycoprotein /FL=gb:AF030428.1 gb:NM_006474.1	
204879_at		NM_006474	gb:NM_006474.1	
			ESTs, Highly similar to FRIL_HUMAN Ferritin light chain (Ferritin L subunit)	
213813_x_at		AI345238	[H.sapiens]	 Hs.356834
		NIM 005229	gb:NM_005338.3 /DEF=Homo sapiens huntingtin interacting protein 1 (HIP1), mRNA. /FEA=mRNA /GEN=HIP1 /PROD=huntingtin interacting protein 1 /DB_XREF=gi:1254 5385 /UG=Hs.97206 huntingtin interacting protein 1 /FL=gb:NM_005338 3 gb:179734.1	
205425_at	l,	NM_005338	.3 gb:U79734.1	<u> </u>

Figure 7a CC	mica.			
		Consensus		
		includes		
		gb:U90030.1		
		/DEF=Homo		
		sapiens bicaudal-D		
		(BICD) mRNA,		
		alternatively		
		spliced, partial		
		cds. /FEA=mRNA		
		/GEN=BICD		
		/PROD=bicaudal-D		
		/DB_XREF=gi:2745		
		977		
		/UG=Hs.164975		
		Bicaudal D		
	1	(Drosophila)		
214806_at	U90030	homolog 1		
İ	}	`		
1		gb:NM_005079.1		
		/DEF=Homo		
		sapiens tumor		
		protein D52		
		(TPD52), mRNA.		
:		/FEA=mRNA		
		/GEN=TPD52		
		/PROD=tumor		
		protein D52		
		/DB_XREF=gi:4827		
		037 /UG=Hs.2384		
		tumor protein D52	•	
		/FL=gb:NM_005079		
201691_s_at	NM 005079	.1 gb:U18914.1		
201031_S_at	1411_003079	.1 gb.010314.1		
		ESTs, Highly similar		
		to IF5A HUMAN		
		Initiation factor 5A		
		(eIF-5A) (eIF-4D)		
040750	DE544557	(Rev-binding factor)		11- 204005
213753_x_at	BF541557	[H.sapiens]		Hs.381005

Figure 7a Co	int u.				
			gb:NM_015590.1		
			/DEF=Homo		
			sapiens		
			DKFZP434F1735		
			protein		
			(DKFZP434F1735),		
			mRNA.		
			/FEA=mRNA		
			/GEN=DKFZP434F		
			1735		
			/PROD=DKFZP434		
			F1735 protein		
			/DB_XREF=gi:7661		
			571		
			1		
			/UG=Hs.306189		
			DKFZP434F1735		[
			protein		
			/FL=gb:NM_015590		
220596_at		NM_015590	.1		
			gb:NM_020366.1		
			/DEF=Homo		
			sapiens retinitis		
			pigmentosa		
			GTPase regulator		İ
			interacting protein		
			1 (RPGRIP1),		
	-	1	mRNA.		
	ŕ		/FEA=mRNA		
			/GEN=RPGRIP1		1
		ļ	/PROD=retinitis		
		1	pigmentosa		
			GTPase		
			regulatorinteracting		
			protein 1		
		1	/DB_XREF=gi:9966		
					1
			834		
			/UG=Hs.131917		
			retinitis pigmentosa		
			GTPase regulator		
			interacting protein		
			1		
	İ		/FL=gb:AF260257.1	1	
	}	1	gb:AF227257.1		
206608 5 5		NM_020366	gb:NM_020366.1		
206608_s_at	<u> </u>	TIMINI_020300	190.14W_020000.1	L	<u> </u>

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Figure /a Cont d.			
riguic 7a dointa.		gb:NM_016583.1 /DEF=Homo sapiens LUNX protein; PLUNC (palate lung and nasal epithelium clone); tracheal epithelium enriched protein (LOC51297), mRNA. /FEA=mRNA /GEN=LOC51297 /PROD=LUNX protein; PLUNC (palate lung and nasalepithelium clone); tracheal epithelium enriched protein /DB_XREF=gi:7706 118 /UG=Hs.211092 LUNX protein; PLUNC (palate lung and nasal epithelium clone); tracheal epithelium	
220542_s_at	NM 016583	enriched protein /FL=gb:AB024937.1 gb:NM_016583.1 gb:AF172993.1	
		gb:M85289.1 /DEF=Human heparan sulfate proteoglycan (HSPG2) mRNA, complete cds. /FEA=mRNA /GEN=HSPG2 /PROD=heparan sulfate proteoglycan /DB_XREF=gi:1844 26 /UG=Hs.211573 heparan sulfate proteoglycan 2 (perlecan) /FL=gb:M85289.1	
201655_s_at	M85289	gb:NM_005529.2	l

1 iguio 7 a oc					
221728_x_at	·	AK025198	Consensus includes gb:AA628440 /FEA=EST /DB_XREF=gi:2540 827 /DB_XREF=est:af2 6f02.s1 /CLONE=IMAGE:10 32795 /UG=Hs.83623 nuclear receptor subfamily 1, group I, member 3		
			gb:NM_017905.1 /DEF=Homo		
			sapiens hypothetical protein		
			FLJ20623 (FLJ20623),		
			mRNA. /FEA=mRNA		
			/GEN=FLJ20623 /PROD=hypothetica		
			I protein FLJ20623 /DB_XREF=gi:8923		
			574 /UG=Hs.27337 hypothetical protein		
			FLJ20623 /FL=gb:NM_017905		
220241_at		NM_017905	.1	·	

219993_at	NM 022454	gb:NM_022454.1 /DEF=Homo sapiens hypothetical protein FLJ22252 similar to SRY-box containing gene 17 (FLJ22252), mRNA. /FEA=mRNA /GEN=FLJ22252 /PROD=hypothetica I protein FLJ22252 similar to SRY-boxcontaining gene 17 /DB_XREF=gi:1196 7990 /UG=Hs.97984 hypothetical protein FLJ22252 similar to SRY-box containing gene 17 /FL=gb:NM_022454 .1	
206003_at	_ NM_014645	gb:NM_014645.1 /DEF=Homo sapiens KIAA0635 gene product (KIAA0635), mRNA. /FEA=mRNA /GEN=KIAA0635 /PROD=KIAA0635 gene product /DB_XREF=gi:7662 215 /UG=Hs.185091 KIAA0635 gene product /FL=gb:AB014535.1 gb:NM_014645.1	

Figure 7a Co	Jittu.			· · · · · · · · · · · · · · · · · · ·	
209408_at		U63743	gb:U63743.1 /DEF=Homo sapiens mitotic centromere- associated kinesin mRNA, complete cds. /FEA=mRNA /PROD=mitotic centromere- associated kinesin /DB_XREF=gi:1695 881 /UG=Hs.69360 kinesin-like 6 (mitotic centromere- associated kinesin) /FL=gb:NM_006845 .2 gb:U63743.1 phospholipase D1, phophatidylcholine-		
177_at	PLD1	NM_019108	gb:NM_019108.1 /DEF=Homo sapiens hypothetical protein F17127_1 (F17127_1), mRNA. /FEA=CDS /GEN=F17127_1 /PROD=hypothetica I protein F17127_1 /DB_XREF=gi:1009 2658 /UG=Hs.10116 hypothetical protein F17127_1 /FL=gb:NM_019108		Hs.82587

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rigule /a CC	mea.			
205995_x_at			gb:NM_014642.1 /DEF=Homo sapiens KIAA0036 gene product (KIAA0036), mRNA. /FEA=mRNA /GEN=KIAA0036 /PROD=KIAA0036 gene product /DB_XREF=gi:7661 875 /UG=Hs.169387 KIAA0036 gene product /FL=gb:D25278.1 gb:NM_014642.1	
205215_at		NM_007212	gb:NM_007212.1 /DEF=Homo sapiens ring finger protein 2 (RNF2), mRNA. /FEA=mRNA /GEN=RNF2 /PROD=ring finger protein 2 /DB_XREF=gi:6005 746 /UG=Hs.124186 ring finger protein 2 /FL=gb:AF141327.1 gb:NM_007212.1	

Figure 7a Co	nita.			
201206_s_at		NM 004587	gb:NM_004587.1 /DEF=Homo sapiens ribosome binding protein 1 (dog 180kD homolog) (RRBP1), mRNA. /FEA=mRNA /GEN=RRBP1 /PROD=ribosome binding protein 1 /DB_XREF=gi:4759 055 /UG=Hs.98614 ribosome binding protein 1 (dog 180kD homolog) /FL=gb:AF006751.1 gb:NM_004587.1	
201200_5_dt			gb:NM_024308.1 /DEF=Homo sapiens hypothetical protein MGC4172 (MGC4172), mRNA. /FEA=mRNA /GEN=MGC4172 /PROD=hypothetica	
218756_s_at		NM_024308	I protein MGC4172 /DB_XREF=gi:1323 6541 /UG=Hs.8949 hypothetical protein MGC4172 /FL=gb:BC002731.1 gb:NM_024308.1	

Figure 7a CC			The state of the s	
204572_s_at		gb:NM_00622 /DEF=Homo sapiens prote (peptidyl-proly cistrans isomerase) N interacting, 4 (parvulin) (PI mRNA. /FEA=mRNA /GEN=PIN4 /PROD=prote (peptidyl-proly cistrans isomerase) NI interacting, 4 (parvulin) /DB_XREF=g 901 /UG=Hs. protein (pepti prolyl cistrans isomerase) N interacting, 4 (parvulin) /FL=gb:BC00 gb:AF143096 gb:AB009690 gb:NM_00622	ein /I IIMA- N4), in /I MA- i:5453 11774 idyl- s IIMA- 5234.1 .1	
		gb:AF311312 /DEF=Homo sapiens infer related spern protein mRN complete cds /FEA=mRNA /PROD=infert related spern protein /DB_XREF=g 3767 /UG=Hs.1530 sperm associ antigen 1 /FL=gb:AF31 gb:NM_0031	tility- n A, s. iility- n ii:1086	
210117_at	IMF3	1312	17.1	

Figure /a Cor	<u> </u>			·
204819_at	NM_004463	gb:NM_004463.1 /DEF=Homo sapiens faciogenital dysplasia (Aarskog-Scott syndrome) (FGD1), mRNA. /FEA=mRNA /GEN=FGD1 /PROD=faciogenital dysplasia protein /DB_XREF=gi:4758 357 /UG=Hs.1572 faciogenital dysplasia (Aarskog-Scott syndrome) /FL=gb:NM_004463 .1 gb:U11690.1		

202762 04	NINA OOAQAQ	gb:NM_004346.1 /DEF=Homo sapiens caspase 3, apoptosis- related cysteine protease (CASP3), mRNA. /FEA=mRNA /GEN=CASP3 /PROD=caspase 3, apoptosis-related cysteine protease /DB_XREF=gi:4757 911 /UG=Hs.74552 caspase 3, apoptosis-related cysteine protease /FL=gb:NM_004346 .1 gb:U13737.1 gb:U13738.1		
202763_at 222341_x_at	NM_004346 AW973235	gb:U26943.1 ESTs		Hs.293697
222341_X_dl	[Avva73235	[E313	L	115.233031

Figure 7a Co	Jii G.				
215293_s_at		AL049261	Consensus includes gb:AL049261.1 /DEF=Homo sapiens mRNA; cDNA DKFZp564E053 (from clone DKFZp564E053). /FEA=mRNA /DB_XREF=gi:4500 009 /UG=Hs.133968 FGF receptor activating protein 1 sarcoma amplified		
203226_s_at	SAS	AL514076	sequence	•	Hs.50984
		NM 001340	gb:NM_001340.1 /DEF=Homo sapiens cylicin, basic protein of sperm head cytoskeleton 2 (CYLC2), mRNA. /FEA=mRNA /GEN=CYLC2 /PROD=cylicin 2 /DB_XREF=gi:4557 508 /UG=Hs.3232 cylicin, basic protein of sperm head cytoskeleton 2 /FL=gb:NM_001340 .1		
207780_at	[[NIVI_001340			

Figure 7a Cont'd.		10		·
		Consensus		
		includes		
		gb:BE646414		
1		/FEA=EST		
1		/DB_XREF=gi:9970		
		725		
		/DB_XREF=est:7e8		
		6d08.x1		
		1		
		/CLONE=IMAGE:32		
		92047		
		/UG=Hs.155546		
		KIAA1080 protein;		
		Golgi-associated,		
		gamma-adaptin		
		ear containing,		
]		ARF-binding		
		protein 2		
		/FL=gb:AF190863.1		
		gb:AF233522.1		
		1 -		
000044 -4	245044	gb:AF165531.1		
208914_at	NM_015044	gb:NM_015044.1	 	
		ESTs, Weakly		
		similar to T45117		
ļ :		hU1-70K protein		
		(286 AA) [imported]		
		human (fragment)		
214920_at	R33964	[H.sapiens]		Hs.23799
		Consensus		
		includes		
	1	gb:AK024677.1		
		/DEF=Homo		
		sapiens cDNA:		
		FLJ21024 fis,		
		clone CAE06651,		
		1		
[highly similar to		
		HUMPLT Human		
		LTR mRNA.		
		/FEA=mRNA		
		/DB_XREF=gi:1043		
į į		7016		
		/UG=Hs.264330 N-		
		acylsphingosine		ļ .
		amidohydrolase		
		(acid ceramidase)-		
214765_s_at	AK024677	like		

Figure /a CC	TICU.			
201294_s_at		NM_015626	Consensus includes gb:N24643 /FEA=EST /DB_XREF=gi:1138 793 /DB_XREF=est:yx8 9f11.s1 /CLONE=IMAGE:26 8941 /UG=Hs.187991 DKFZP564A122 protein /FL=gb:AF106684.1 gb:NM_015626.1	
		NNA 002000	gb:NM_003060.1 /DEF=Homo sapiens solute carrier family 22 (organic cation transporter), member 5 (SLC22A5), mRNA. /FEA=mRNA /GEN=SLC22A5 /PROD=solute carrier family 22 (organic cationtransporter), member 5 /DB_XREF=gi:4507 004 /UG=Hs.15813 solute carrier family 22 (organic cation transporter), member 5 /FL=gb:AB015050.1 gb:AF057164.1	
205074_at		NM_003060	gb:NM_003060.1	

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i igaio ra ot	, , , , , , , , , , , , , , , , , , ,			
203119 at		NM 024098	gb:NM_024098.1 /DEF=Homo sapiens hypothetical protein MGC2574 (MGC2574), mRNA. /FEA=mRNA /GEN=MGC2574 /PROD=hypothetica I protein MGC2574 /DB_XREF=gi:1312 9103 /UG=Hs.4253 hypothetical protein MGC2574 /FL=gb:BC001378.1 gb:NM_024098.1	
217212_s_at 201085_s_at	SON	Z84723 AA664291	Human DNA sequence from phage LAW2 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3 Contains Interleukin 9 receptor pseudogene. SON DNA binding protein	Hs.92909
214060_at	SSBP1	BE220360	single-stranded DNA binding protein	Hs.923

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Tigare 74 conta.	1	Consensus		
		includes		1
		gb:AK025267.1		
		1-		
		/DEF=Homo		
		sapiens cDNA:		
		FLJ21614 fis,		
		clone COL07391,		
		highly similar to		
		AB020625 Homo		
		sapiens mRNA for		i
		butyrophilin like		
		receptor.		
		/FEA=mRNA]
		/DB_XREF=gi:1043		
		7746		
		/UG=Hs.225949	•	
217207_s_at	AK025267	butyrophilin-like 3		
		fatty acid		
208963_x_at FADS1	BE540552	desaturase 1		Hs.132898
		gb:NM_004082.2		
		/DEF=Homo		
		sapiens dynactin 1		
		(p150, Glued		
		(Drosophila)		
		homolog)		
	1	(DCTN1),		
		transcript variant		
		1, mRNA.		
		/FEA=mRNA		ĺ
		/GEN=DCTN1		
		/PROD=dynactin 1,		
		isoform 1		
		/DB_XREF=gi:1325]
		9509		
		/UG=Hs.74617		
		dynactin 1 (p150,		
		Glued (Drosophila)		
		homolog)		
		/FL=gb:NM_023019		
		1.1		
201082_s_at	NM_004082	gb:NM_004082.2		

Figure 7a Co		r -		
217253_at	L37198	Consensus includes gb:L37198.1 //DEF=Homo sapiens (clone B3B3E13) Huntingtons disease candidate region mRNA fragment. //FEA=mRNA //DB_XREF=gi:6005 19 //UG=Hs.233617 Homo sapiens (clone B3B3E13) Huntingtons disease candidate region mRNA fragment		
		gb:NM_015836.1 /DEF=Homo sapiens tryptophanyl tRNA synthetase 2 (mitochondrial) (WARS2), nuclear gene encoding mitochondrial protein, mRNA. /FEA=mRNA /GEN=WARS2 /PROD=tryptophanyl tRNA synthetase 2 (mitochondrial) /DB_XREF=gi:7710 153 /UG=Hs.227274 tryptophanyl tRNA synthetase 2 (mitochondrial) /FL=gb:NM_015836		
218766_s_at	NM_015836	1.1	L	l <u> </u>

Tigure 7a C	OTIC G.	T	T		
209073_s_at		AF015040	gb:AF015040.1 //DEF=Homo sapiens NUMB protein (NUMB) mRNA, complete cds. /FEA=mRNA //GEN=NUMB //PROD=NUMB protein //DB_XREF=gi:4102 704 /UG=Hs.78890 numb (Drosophila) homolog //FL=gb:AF015040.1 gb:AF108092.1 gb:AF171939.1		
			BMP-2 inducible		
37170_at	BIKE	AB015331	kinase	NM_017593	Hs.198642
52837_at	KIAA1644	AL047020	KIAA1644 protein		Hs.6829
209431 s at		AF254083	gb:AF254083.1 /DEF=Homo sapiens zinc finger sarcoma gene long A isoform (ZSG) mRNA, complete cds. /FEA=mRNA /GEN=ZSG /PROD=zinc finger sarcoma gene long A isoform /DB_XREF=gi:9954 374 /UG=Hs.27801 zinc finger protein 278 /FL=gb:NM_014323 .1 gb:AF254083.1		

1 iguie ra oc	JITE G.			
209994_s_at		AF016535	gb:AF016535.1 /DEF=Homo sapiens P- glycoprotein (mdr1) mRNA, complete cds. /FEA=mRNA /GEN=mdr1 /PROD=P- glycoprotein /DB_XREF=gi:2353 263 /UG=Hs.21330 ATP-binding cassette, sub- family B (MDRTAP), member 1 /FL=gb:M14758.1 gb:AF016535.1 gb:NM_000927.2	
216210_x_at	HRIHFB2122	AA046650	Tara-like protein	Hs.40342
207338_s_at		NM_003454	gb:NM_003454.1 /DEF=Homo sapiens zinc finger protein 200 (ZNF200), mRNA. /FEA=mRNA /GEN=ZNF200 /PROD=zinc finger protein 200 /DB_XREF=gi:4508 012 /UG=Hs.88219 zinc finger protein 200 /FL=gb:AF060866.1 gb:NM_003454.1	

Figure /a CC	nit d.			
218883 s at			gb:NM_024629.1 /DEF=Homo sapiens hypothetical protein FLJ23468 (FLJ23468), mRNA. /FEA=mRNA /GEN=FLJ23468 /PROD=hypothetica I protein FLJ23468 /DB_XREF=gi:1337 5855 /UG=Hs.38178 hypothetical protein FLJ23468 /FL=gb:NM_024629 .1	
218883_s_at		NM_024629	gb:NM_018316.1 /DEF=Homo sapiens hypothetical protein FLJ11078 (FLJ11078), mRNA. /FEA=mRNA /GEN=FLJ11078	
219354_at		NM_018316	/PROD=hypothetica I protein FLJ11078 /DB_XREF=gi:8922 853 /UG=Hs.250632 hypothetical protein FLJ11078 /FL=gb:NM_018316	

Figure /a Cont'd.				
		Consensus		
		includes		
		gb:AL161999.1		
		/DEF=Homo		
		sapiens mRNA;		
		cDNA		
		DKFZp761H087		
		(from clone		·
		DKFZp761H087);		
		partial cds.	-	
		/FEA=mRNA		
		/GEN=DKFZp761H		
		087		
		/PROD=hypothetica		
		I protein		
		/DB_XREF=gi:7328		
		000		
1 1 .		/UG=Hs.258503		
		p53 inducible		
215785_s_at	AL161999	protein		
		<u>• </u>		
1		gb:AF165520.1	Į	
		/DEF=Homo		
		sapiens phorbolin I		
		protein (PBI)		
		mRNA, complete		
		cds. /FEA=mRNA		
		/GEN=PBI		
		/PROD=phorbolin I		
		protein		
		/DB_XREF=gi:9294		
		746 /UG=Hs.8583		
		similar to	-	
		APOBEC1		
209584_x_at	AF165520	/FL=gb:AF165520.1		
		ESTs, Moderately		
		similar to cytokine	1	
		receptor-like factor		
		2; cytokine receptor		
		CRL2 precusor		
		[Homo sapiens]		
214082_at	AW003516	[H.sapiens]		Hs.13503

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gb:BC005961.1 /DEF=Homo sapiens, parathyroid hormone-like hormone, clone MGC:14611, mRNA, complete cds. /FEA=mRNA /PROD=parathyroid hormone-like hormone /DB XREF=gi:1354 3620 BC005961 /FL=gb:BC005961.1 211756_at guanine nucleotide binding protein (G protein), alpha activating activity Hs.296184 204762_s_at GNA01 BE670563 polypeptide O gb:NM_003810.1 /DEF=Homo sapiens tumor necrosis factor (ligand) superfamily, member 10 (TNFSF10), mRNA. /FEA=mRNA /GEN=TNFSF10 /PROD=tumor necrosis factor (ligand) superfamily,membe r 10 /DB_XREF=gi:4507 592 /UG=Hs.83429 tumor necrosis factor (ligand) superfamily, member 10 /FL=gb:U37518.1 gb:U57059.1 202688_at NM_003810 gb:NM_003810.1 Hs.355264 209163_at CYB561 AL514271 cytochrome b-561

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1 19470 74 04			
		Consensus includes gb:AL031290 //DEF=Human DNA sequence from clone 774124 on chromosome 1q24.1-24.3 Contains protein similar to pregnancy-associated plasma protein A precursor neuronal migration protein astrotactin, ESTs, STS and GSS //FEA=mRNA_1 //DB_XREF=gi:3550 114 //UG=Hs.9654 similar to pregnancy-associated plasma	
213332_at 219818_s_at	AL031290 NM_018025	gb:NM_018025.1 /DEF=Homo sapiens hypothetical protein FLJ10206 (FLJ10206), mRNA. /FEA=mRNA /GEN=FLJ10206 /PROD=hypothetica I protein FLJ10206 /DB_XREF=gi:8922 282 /UG=Hs.55014 hypothetical protein FLJ10206 /FL=gb:NM_018025	

gb:NM_005774.1 //DEF=Homo sapiens zinc finger protein 255 (ZNF255), mRNA. //EA=mRNA //GEN=ZNF255 //PR_OD=zinc finger protein 255 //DB_XREF=gi:5031 614 //UG=Hs.181696 zinc finger protein 255 //EL-gb:AF067164.1 gb:NM_005774 AU159276 THYRO1 Homo sapiens cDNA clone THYRO101262 3', mRNA sequence. gb:NM_018700.1 //DEF=Homo sapiens zinc- binding protein Rbcc728 //RCD=zinc- binding protein Rbcc728 //PROD=zinc- binding protein Rbcc728 //PROD=zinc- binding protein Rbcc728 //PROD=zinc- binding protein Rbcc728 //PROD=zinc- binding protein Rbcc728 //PROD=zinc- binding protein Rbcc728 //PROD=zinc- binding protein Rbcc728 //PROD=zinc- binding protein Rbcc728 //PROD=zinc- binding protein Rbcc728 //PROD=zinc- binding protein Rbcc728 //BS_XREF=gi:8924 237 //UG=Hs.121429 zinc-binding protein Rbcc728 //EL-gb:NM_018700 1 cell division cycle 2, G1 to S and G2 to M Hs.334562	Figure 7a Co	orica.			· · · · · · · · · · · · · · · · · · ·
216288_at AU159276 mRNA sequence. gb:NM_018700.1 //DEF=Homo sapiens zinc- binding protein Rbcc728 (Rbcc728), mRNA. //FEA=mRNA //GEN=Rbcc728 //PROD=zinc- binding protein Rbcc728 //DB_XREF=gi:8924 237 //UG=Hs.121429 zinc-binding protein Rbcc728 //PL=gb:NM_018700 219736_at NM_018700 1 cell division cycle 2, G1 to S and G2 to	220019_s_at		NM_005774	/DEF=Homo sapiens zinc finger protein 255 (ZNF255), mRNA. /FEA=mRNA /GEN=ZNF255 /PROD=zinc finger protein 255 /DB_XREF=gi:5031 614 /UG=Hs.181696 zinc finger protein 255 /FL=gb:AF067164.1 gb:NM_005774.1 AU159276 THYRO1 Homo sapiens cDNA clone	
gb:NM_018700.1 //DEF=Homo sapiens zinc- binding protein Rbcc728 (Rbcc728), mRNA. //FEA=mRNA //GEN=Rbcc728 //PROD=zinc- binding protein Rbcc728 //PROD=zinc- binding protein Rbcc728 //DB_XREF=gi:8924 237 //UG=Hs.121429 zinc-binding protein Rbcc728 //FL=gb:NM_018700 219736_at NM_018700 I cell division cycle 2, G1 to S and G2 to	216288 at		AU159276		
cell division cycle 2, G1 to S and G2 to				gb:NM_018700.1 /DEF=Homo sapiens zinc- binding protein Rbcc728 (Rbcc728), mRNA. /FEA=mRNA /GEN=Rbcc728 /PROD=zinc- binding protein Rbcc728 /DB_XREF=gi:8924 237 /UG=Hs.121429 zinc-binding protein Rbcc728 /FL=gb:NM_018700	
	219/36_at		NM_018/00		
	203213 at	CDC2	AL524035		Hs.334562

Figure 7a Co	illed.			· · · · · · · · · · · · · · · · · · ·	
			Consensus includes gb:AK022669.1 /DEF=Homo sapiens cDNA FLJ12607 fis, clone NT2RM4001489, highly similar to Homo sapiens mRNA for KIAA0685 protein. /FEA=mRNA /DB_XREF=gi:1043 4196 /UG=Hs.296406 KIAA0685 gene product /FL=gb:AB014585.1		
202791_s_at		AK022669	gb:NM_014678.1 Consensus		
215916_at		AL157418	Consensus includes gb:AL157418.1 /DEF=Homo sapiens mRNA; cDNA DKFZp761K18121 (from clone DKFZp761K18121). /FEA=mRNA /DB_XREF=gi:7018 439 /UG=Hs.112028 MisshapenNIK- related kinase		
∠ 159 16_at	L	AL 10/418	pelateu kinase	l	

Figure 7a Co	JITE G.			
221155_x_at		NM_018603	gb:NM_018603.1 /DEF=Homo sapiens hypothetical protein PRO1496 (PRO1496), mRNA. /FEA=mRNA /GEN=PRO1496 /PROD=hypothetica I protein PRO1496 /DB_XREF=gi:8924 053 /UG=Hs.283617 hypothetical protein PRO1496 /FL=gb:AF116665.1 gb:NM_018603.1	
52255_s_at	COL5A3	Al984221	collagen, type V, alpha 3	Hs.235368
	COLOAS		Consensus includes gb:AK025276.1 /DEF=Homo sapiens cDNA: FLJ21623 fis, clone COL07915. /FEA=mRNA /DB_XREF=gi:1043 7759 /UG=Hs.306791 Homo sapiens cDNA: FLJ21623 fis, clone	113.233300
216175_at		AK025276	COL07915	

I igule /a Ci	511t d.				
213105_s_at			Consensus includes gb:AI799802 /FEA=EST /DB_XREF=gi:5365 274 /DB_XREF=est:wc4 3d09.x1 /CLONE=IMAGE:23 21393 /UG=Hs.134846 Human DNA sequence from clone 316G12 on chromosome 16. Contains the gene for C2 domain protein KIAA0734, the gene for a novel protein similar to predicted yeast, worm and archae-bacterial proteins, a novel gene and the 3 part of the gene for a novel protein ARP1 actin-related	·	
			protein 1 homolog	:	
000700	LAGERAA	1, 500044	A, centractin alpha		
200720_s_at	ACTR1A	AL532341	(yeast)		Hs.153961

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i iguie ra co	med.	*			
208299_at		NM_021096	gb:NM_021096.1 /DEF=Homo sapiens calcium channel, voltage- dependent, alpha 11 subunit (CACNA1I), mRNA. /FEA=mRNA /GEN=CACNA1I /PROD=calcium channel, voltage- dependent, alpha 11subunit /DB_XREF=gi:1086 3882 /UG=Hs.125116 calcium channel, voltage-dependent, alpha 11 subunit /FL=gb:NM_021096 .1 gb:AF129133.1 gb:NM_005401.1 /DEF=Homo sapiens protein tyrosine phosphatase, non-		
			receptor type 14 (PTPN14), mRNA. /FEA=mRNA /GEN=PTPN14 /PROD=protein tyrosine phosphatase, non- receptor type14 /DB_XREF=gi:4885 566		
205503_at		NM_005401	/UG=Hs.159238 protein tyrosine phosphatase, non- receptor type 14 /FL=gb:NM_005401 .1 erythropoietin		
396_f_at	EPOR	X97671	receptor	NM_000121	Hs.127826

Figure 7a Co	one a.			
221815_at		BE671816	Homo sapiens, Similar to hypothetical protein PRO2831, clone MGC:23813 IMAGE:4273837, mRNA, complete cds	Hs.351935
220777_at		NM_022113	gb:NM_022113.1 /DEF=Homo sapiens kinesin family member 13A (KIF13A), mRNA. /FEA=mRNA /GEN=KIF13A /PROD=kinesin family member 13A /DB_XREF=gi:1154 5828 /UG=Hs.146286 kinesin family member 13A /FL=gb:NM_022113	
220111_at		INIVI_UZZ I 13	1	
212997_s_at	TLK2	AU119586	tousled-like kinase 2	Hs.57553

Figure 7a Co	iica.			
205288_at		NM_003672	gb:NM_003672.1 /DEF=Homo sapiens CDC14 (cell division cycle 14, S. cerevisiae) homolog A (CDC14A), mRNA. /FEA=mRNA /GEN=CDC14A /PROD=CDC14 (cell division cycle 14, S. cerevisiae)homolog A /DB_XREF=gi:4502 696 /UG=Hs.65993 CDC14 (cell division cycle 14, S. cerevisiae) homolog A /FL=gb:AF000367.1 gb:NM_003672.1 gb:AF122013.1 gb:U16996.1 /DEF=Human protein tyrosine phosphatase	-
209457_at		U16996	mRNA, complete cds. /FEA=mRNA /PROD=protein tyrosine phosphatase /DB_XREF=gi:6420 12 /UG=Hs.2128 dual specificity phosphatase 5 /FL=gb:NM_004419 .2 gb:U15932.2	

gb:NM_004848.1 //DEF=Homo sapiens basement membrane-induced gene (ICB-1), mRNA. //FEA=mRNA //GEN=ICB-1 //PROD=basement membrane-induced gene //DB_XREF=gi:4758	
579 /UG=Hs.10649 basement membrane-induced gene /FL=gb:AF044896.1 207571_x_at NM_004848 gb:NM_004848.1	
guanine nucleotide binding protein (G protein), beta 222034_at GNB2L1 AA443762 polypeptide 2-like 1 Hs.5662	2
Consensus includes gb:AK026682.1 //DEF=Homo sapiens cDNA: FLJ23029 fis, clone LNG01883. //FEA=mRNA //DB_XREF=gi:1043 9589 //UG=Hs.306864 Homo sapiens cDNA: FLJ23029 fis, clone 215651 at AK026682 LNG01883	

	 	, , , , , , , , , , , , , , , , , , , 	
219470_x_at	NM_019084	gb:NM_019084.1 /DEF=Homo sapiens hypothetical protein FLJ10895 (FLJ10895), mRNA. /FEA=mRNA /GEN=FLJ10895 /PROD=hypothetica I protein FLJ10895 /DB_XREF=gi:9506 628 /UG=Hs.281348 hypothetical protein FLJ10895 /FL=gb:NM_019084 .1 gb:M34055.1	
208911 s at	M34055	/DEF=Human pyruvate dehydrogenase E1- beta subunit mRNA, complete cds. /FEA=mRNA /GEN=PDHB /DB_XREF=gi:1907 91 /UG=Hs.979 pyruvate dehydrogenase (lipoamide) beta /FL=gb:BC000439.1 gb:BC001924.1 gb:J03576.1 gb:M34479.1 gb:M34479.1 gb:M34055.1 gb:NM_000925.1	

1 igure 7a Ct	Jine G.	· · · · · · · · · · · · · · · · · · ·	,		
203970_s_at		NM 003630	gb:NM_003630.1 /DEF=Homo sapiens peroxisomal biogenesis factor 3 (PEX3), mRNA. /FEA=mRNA /GEN=PEX3 /PROD=peroxisoma I biogenesis factor 3 /DB_XREF=gi:4505 726 /UG=Hs.7277 peroxisomal biogenesis factor 3 /FL=gb:NM_003630 .1 gb:AB035307.1		
203910_S_at		14141_003030	. i gu.Abusssur. i		
			gb:NM_016194.1 /DEF=Homo sapiens hypothetical protein (DKFZp586O1922), mRNA. /FEA=mRNA /GEN=DKFZp586O 1922 /PROD=hypothetica I protein /DB_XREF=gi:7705 366 /UG=Hs.155090 hypothetical protein /FL=gb:AL117471.1		
204000_at		NM_016194	gb:NM_016194.1		
			KIAA0763 gene		100101
203906_at	KIAA0763	AI652645	product		Hs.409124
213398_s_at	HCDI	Al347090	HCDI protein	L	Hs.7911

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Figure /a Co	nta.			
201117_s_at		NM_001873	gb:NM_001873.1 /DEF=Homo sapiens carboxypeptidase E (CPE), mRNA. /FEA=mRNA /GEN=CPE /PROD=carboxypeptidase E precursor /DB_XREF=gi:4503 008 /UG=Hs.75360 carboxypeptidase E /FL=gb:NM_001873 .1 gb:NM_003438.1 /DEF=Homo	
•			sapiens zinc finger protein 137 (clone pHZ-30) (ZNF137), mRNA. /FEA=mRNA /GEN=ZNF137 /PROD=zinc finger protein 137 (clone pHZ-30)	
207394_at		NM_003438	/DB_XREF=gi:4507 988 /UG=Hs.151689 zinc finger protein 137 (clone pHZ- 30) /FL=gb:NM_003438 .1 gb:U09414.1	

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rigule 7a CO	ii. G.		gb:BC004904.1		
			/DEF=Homo		
			sapiens, nuclear		
			RNA export factor		
			1, clone		
			MGC:4612, mRNA,		
			complete cds.		
		:	/FEA=mRNA	i	
			/PROD=nuclear		
			RNA export factor		
			1		
			/DB_XREF=gi:1343		
			6184		
			/UG=Hs.323502		
	,		nuclear RNA		
			export factor 1		
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			gb:U80073.1		
			gb:AF126246.1		
			gb:AF112880.1	:	!
208922_s_at		BC004904	gb:NM_006362.1		
			Consensus		
			includes		
			gb:X74070.1		
			/DEF=H.sapiens		
			mRNA for		
			transcription factor]
			BTF 3.		
			/FEA=mRNA		
			/PROD=transcriptio		
			n factor BTF3		
	•		/DB_XREF=gi:3950		
			86 /UG=Hs.101025		
			basic transcription		
211939_x_at		X74070	factor 3		

Figure 7a Cont'd.			
	NM 001967	gb:NM_001967.2 /DEF=Homo sapiens eukaryotic translation initiation factor 4A, isoform 2 (EIF4A2), mRNA. /FEA=mRNA /GEN=EIF4A2 /PROD=eukaryotic translation initiation factor 4A,isoform 2 /DB_XREF=gi:9945 313 /UG=Hs.173912 eukaryotic translation initiation factor 4A, isoform 2 /FL=gb:D30655.1 gb:NM_001967.2	
200912_s_at	MM_00 1967	gb.NW_001907.2	
208880_s_at	AB019219	gb:AB019219.1 /DEF=Homo sapiens mRNA, complete cds, similar to yeast pre-mRNA splicing factors, Prp1Zer1 and Prp6. /FEA=mRNA /DB_XREF=gi:4164 165 /UG=Hs.31334 putative mitochondrial outer membrane protein import receptor /FL=gb:BC001666.1 gb:AF026031.1 gb:AB019219.1 gb:AF221842.1	

nitu.		
Y09703	Consensus includes gb:BF508848 /FEA=EST /DB_XREF=gi:1159 2146 /DB_XREF=est:UI- H-BI4-aor-e-06-0- UI.s1 /CLONE=IMAGE:30- 85907 /UG=Hs.44499 pinin, desmosome associated protein	
NM 005476	gb:NM_005476.2 /DEF=Homo sapiens UDP-N- acetylglucosamine- 2-epimeraseN- acetylmannosamine kinase (GNE), mRNA. /FEA=mRNA /GEN=GNE /PROD=UDP-N- acetylglucosamine- 2-epimeraseN- acetylmannosamine kinase /DB_XREF=gi:6382 074 /UG=Hs.5920 UDP-N- acetylglucosamine- 2-epimeraseN- acetylglucosamine- 2-epimeraseN- acetylglucosamine- kinase /FL=gb:AF051852.1 gb:AF155663.1 gb:NM_005476.2	
NM_005476	gb:NM_005476.2	
	Y09703 NM_005476	Consensus includes gb:BF508848 //FEA=EST //DB_XREF=gi:1159 2146 //DB_XREF=est:UI- H-BI4-aor-e-06-0- UI.s1 //CLONE=IMAGE:30- 85907 //UG=Hs.44499 pinin, desmosome associated protein gb:NM_005476.2 //DEF=Homo sapiens UDP-N- acetylglucosamine- 2-epimeraseN- acetylmannosamine kinase (GNE), mRNA. //FEA=mRNA //GEN=GNE //PROD=UDP-N- acetylglucosamine- 2-epimeraseN- acetylmannosamine kinase //DB_XREF=gi:6382 074 //UG=Hs.5920 UDP-N- acetylglucosamine- 2-epimeraseN- acetylglucosamine- acetylglucosamine- acetylglucosamine- acetylglucosamine- acetylglucosamine- acetylglucosamine- acetylglucosamine- acetylglucosamine- acetylglucosam

Figure 7a Co				-	
			Consensus		
			includes		
			gb:AW007532		
			/FEA=EST		
	1		/DB_XREF=gi:5856		
			310		
			/DB_XREF=est:ws5		
i			2h07.x1		
			/CLONE=IMAGE:25		
			00861		
			/UG=Hs.103391		
			Human insulin-like		
			growth factor		
			binding protein 5		
211959_at		L27560	(IGFBP5) mRNA		
		· ·	KIAA0471 gene		
213982_s_at	KIAA0471	BG107203	product		Hs.242271
			gb:NM 001425.1		
			/DEF=Homo		
			sapiens epithelial		
			membrane protein		
			3 (EMP3), mRNA.		
			/FEA=mRNA		
			/GEN=EMP3		
			/PROD=epithelial		
		1	membrane protein		
			3		
]		/DB_XREF=gi:4503		
			562 /UG=Hs.9999	•	
			epithelial		
			membrane protein		
	1		3 /FL=gb:U52101.1		
	1		gb:U87947.1]
203729_at	1	NM 001425	gb:NM_001425.1		
200.20_00			3		
			gb:AF267856.1		
			/DEF=Homo		
	1		sapiens HT033		1
•	1		mRNA, complete		
			cds. /FEA=mRNA	•	
			/PROD=HT033		
			/DB_XREF=gi:1200		
			6038 /UG=Hs.8084		
			hypothetical protein		
			dJ465N24.2.1		
200007		A E 26 7 9 F 6	/FL=gb:AF247168.1		
209007_s_at	L	AF267856	gb:AF267856.1		<u> </u>

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rigule /a Ci	<u> </u>		gb:NM_005585.1		
			/DEF=Homo		
1			sapiens MAD		
			(mothers against		
			decapentaplegic,		
			Drosophila)		
			homolog 6		
			(MADH6), mRNA.		
			/FEA=mRNA		
			/GEN=MADH6 /PROD=MAD		
1			(mothers against		
			decapentaplegic,Dr		
	1		osophila) homolog		
			6 VDE VDEE:		
			/DB_XREF=gi:5031		
			898		
			/UG=Hs.153863		
		:	MAD (mothers		
			against		
			decapentaplegic,		
			Drosophila)		
			homolog 6		
			/FL=gb:U59914.1		
207069_s_at		NM_005585	gb:NM_005585.1		
			neuronal PAS		
39549_at	NPAS2	AI743090	domain protein 2		Hs.321164
			Consensus		
			includes		
		1	gb:AB029025.1		
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			sapiens mRNA for		
			KIAA1102 protein,		
			partial cds.		
			/FEA=mRNA		
			/GEN=KIAA1102		
			/PROD=KIAA1102		
			protein		
		1	/DB_XREF=gi:5689		
			540		
·			/UG=Hs.202949		
212328_at		AK027231	KIAA1102 protein		

	T	<u> </u>	Canadana	· · · · · · · · · · · · · · · · · · ·	
			Consensus		
			includes		
			gb:AL512687.1	•	
			/DEF=Homo		
			sapiens mRNA;		
			cDNA		
1			DKFZp547A1913	1	
			(from clone		
			DKFZp547A1913).		
1			/FEA=mRNA		
1			/GEN=DKFZp547A		
			1913		
			/PROD=hypothetica	:	
			I protein		
			/DB_XREF=gi:1222		
			14839		
047005		41.540007	/UG=Hs.227823		
217225_x_at		AL512687	pM5 protein	<u> </u>	
			-1-114 0044004		
		,	gb:NM_021130.1		
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			sapiens		
			peptidylprolyl		
			isomerase A		
			(cyclophilin A)		
			(PPIA), mRNA.		
			/FEA=mRNA		
			/GEN=PPIA		
			/PROD=peptidylprol		
			yl isomerase A		
			(cyclophilin A)		
			/DB_XREF=gi:1086		
			3926		
			/UG=Hs.182937		
			peptidylprolyl		
			isomerase A		
			(cyclophilin A)		
			/FL=gb:NM_021130		
			.1 gb:BC000689.1		
201293 x at		NM 021130	_		
201293_x_at		NM_021130	gb:BC005320.1		

nt a.		·		
	AK026678	stromal antigen 2 /FL=gb:BC001765.1		He 225767
IDN3	BF221673	IDN3 protein		Hs.225767
		(A.nidulans) homolog (NUDC), mRNA. /FEA=mRNA /GEN=NUDC /PROD=nuclear distribution gene C (A.nidulans)homolo g /DB_XREF=gi:5729 952 /UG=Hs.263812 nuclear distribution gene C (A.nidulans) homolog /FL=gb:BC002399.1 gb:BC003132.1	-	
	NM_006600	gb:AF125465.1 gb:AF100760.1 gb:NM_006600.1		
	IDN3	AK026678 IDN3 BF221673	Consensus includes gb:AK026678.1 //DEF=Homo sapiens cDNA: FLJ23025 fis, clone LNG01702, highly similar to HUMAUTOND Human autonomously replicating sequence (ARS) mRNA. //FEA=mRNA //DB_XREF=gi:1043 9584 /UG=Hs.8217 stromal antigen 2 /FL=gb:BC001765.1 IDN3 BF221673 IDN3 protein IDN3 BF221673 IDN3 protein gb:NM_006600.1 //DEF=Homo sapiens nuclear distribution gene C (A.nidulans) homolog (NUDC), mRNA. //FEA=mRNA //GEN=NUDC //PROD=nuclear distribution gene C (A.nidulans)homolo g //DB_XREF=gi:5729 952 //UG=Hs.263812 nuclear distribution gene C (A.nidulans)homolog //FL=gb:BC002399.1 gb:BC003132.1 gb:AB019408.1 gb:AF130736.1 gb:AF125465.1 gb:AF100760.1	Consensus includes gb:AK026678.1 //DEF=Homo sapiens cDNA: FLJ23025 fis, clone LNG01702, highly similar to HUMAUTOND Human autonomously replicating sequence (ARS) mRNA. //FEA=mRNA //DB_XREF=gi:1043 9584 /UG=Hs.8217 stromal antigen 2 AK026678 /FL=gb:BC001765.1 IDN3 BF221673 IDN3 protein gb:NM_006600.1 //DEF=Homo sapiens nuclear distribution gene C (A.nidulans) homolog (NUDC), mRNA. //FEA=mRNA //GEN=NUDC //PROD=nuclear distribution gene C (A.nidulans)homolo g //DB_XREF=gi:5729 952 //UG=Hs.263812 nuclear distribution gene C (A.nidulans) homolog //FL=gb:BC002399.1 gb:AB019408.1 gb:AF130736.1 gb:AF130736.1 gb:AF130736.1 gb:AF130760.1

85022 7973
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Figure 7a C	Ont u.	y	1	
			Consensus	
			includes	ļ
			gb:AK026589.1	
			/DEF=Homo	
			sapiens cDNA:	
			FLJ22936 fis,	
			clone KAT07936.	
			/FEA=mRNA	
			/DB_XREF=gi:1043	
			9473	
			/UG=Hs.90998	
			KIAA0128 protein;	
213666_at		AK026589	septin 2	
		[Sec23 homolog A	
212887_at	SEC23A	AI753659	(S. cerevisiae)	Hs.272927
			gb:NM_004859.1	
			/DEF=Homo	
		}	sapiens clathrin,	
			heavy polypeptide	
	1		(Hc) (CLTC),	
		•	mRNA.	
			/FEA=mRNA	
			/GEN=CLTC	
			/PROD=clathrin	
	,			
			heavy chain	
		-	/DB_XREF=gi:4758	
	•	1	011	
			/UG=Hs.178710	
			clathrin, heavy	
			polypeptide (Hc)	
1				
			/FL=gb:D21260.1	
200614_at	<u></u>	NM_004859	gb:NM_004859.1	
	}			
t			gb:NM_025182.1	
			/DEF=Homo	
			sapiens	
			hypothetical protein	
	1		FLJ11560	
			(FLJ11560),	
			mRNA.	
			/FEA=mRNA	
			/GEN=FLJ11560	
	1		/PROD=hypothetica	
Ì	1		I protein FLJ11560	
			/DB_XREF=gi:1337	
			8154	
	1		/UG=Hs.301696	
	1		hypothetical protein	
			FLJ11560	
	1		/FL=gb:NM_025182	
207765_s_at		NM_025182	1.1]
	·		<u> </u>	•

Application of: Liew, et. al. Our Docket #: 4231/2042 Figure 7a Cont'd.

Figure 7a CO	iii u.				
			Consensus		
		'	includes		
			gb:AK024896.1		
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			FLJ21243 fis,		
			clone COL01164.		
			/FEA=mRNA		
			/DB XREF=gi:1043		•
			7310		
			/UG=Hs.268016		
			Homo sapiens		
			cDNA: FLJ21243		
			fis, clone		
212944_at		AK024896	COL01164		
			ESTs, Weakly		
1			similar to		
			hypothetical protein		
			FLJ20234 [Homo		
ļ			sapiens]		
213469 at		AV705244	[H.sapiens]		Hs.409229
210-100_ut		7.00211	[,]		
			gb:NM_005767.1		
			/DEF=Homo		
1			sapiens purinergic		
			receptor (family A		
			group 5) (P2Y5),		
			mRNA.		
			/FEA=mRNA	İ	
			/GEN=P2Y5		
			/PROD=purinergic		
			receptor (family A		
			group 5)		
			/DB_XREF=gi:5031	i	
			968		
			/UG=Hs.189999		
			purinergic receptor		
			(family A group 5)		
		1	/FL=gb:AF000546.1		
218589_at		NM 005767	gb:NM_005767.1		
2 10009_at		[14141_003707	[95.14W]_000707.1	L	L

1 19410 74 00			
204524_at	NM_002613	gb:NM_002613.1 /DEF=Homo sapiens 3- phosphoinositide dependent protein kinase-1 (PDPK1), mRNA. /FEA=mRNA /GEN=PDPK1 /PROD=3- phosphoinositide dependent protein kinase-1 /DB_XREF=gi:4505 694 /UG=Hs.154729 3- phosphoinositide dependent protein kinase-1 /FL=gb:AF017995.1 gb:NM_002613.1 gb:BC003005.1 /DEF=Homo sapiens, unactive progesterone receptor, 23 kD, clone MGC:4004, mRNA, complete cds. /FEA=mRNA /PROD=unactive progesterone receptor, 23 kD /DB_XREF=gi:1280 4292	
		/PROD=unactive progesterone receptor, 23 kD	
		. – •	
200627_at	BC003005	/FL=gb:BC003005.1 gb:L24804.1 gb:NM_006601.1	

Application of: Liew, et. al. Our Docket #: 4231/2042 Figure 7a Cont'd.

gb:NM_003406.1 //DEF=Homo sapiens tyrosine 3- monooxygenasetryp tophan 5- monooxygenase activation protein, zeta polypeptide (YWHAZ), mRNA, //EA=mRNA //GEN=YWHAZ //PROD=tyrosine 3- monooxygenasetryp tophan5- monooxygenase activation protein, zeta polypeptide //DB_XREF=gi:4507 952 /L/G=Hs.75103 tyrosine 3- monooxygenasetryp tophan 5- monooxygenasetryp tophan 5- monooxygenasetryp tophan 5- monooxygenasetryp tophan 5- monooxygenase activation protein, zeta polypeptide //FL=gb:BC003623.1 gb:M86400.1 gb:NM_003406.1 gb:NM_0003406.1 gb:NM_0003406.1 gb:NM_0003406.1 gb:NM_0003406.1 gb:NM_0003406.1 gb:NM_0003406.1 gb:NM_0003406.1	Figure 7a Co	1100.			
gb:NM_000130.2 //DEF=Homo sapiens coagulation factor V (proaccelerin, labile factor) (F5), mRNA. //FEA=mRNA //GEN=F5 //PROD=coagulation factor V precursor //DB_XREF=gi:1051 8500 //UG=Hs.30054 coagulation factor V (proaccelerin, labile factor) //FL=gb:NM_000130	200640 04		NIM 003406	/DEF=Homo sapiens tyrosine 3-monooxygenasetryp tophan 5-monooxygenase activation protein, zeta polypeptide (YWHAZ), mRNA. /FEA=mRNA /GEN=YWHAZ /PROD=tyrosine 3-monooxygenasetryp tophan5-monooxygenase activation protein, zeta polypeptide /DB_XREF=gi:4507 952 /UG=Hs.75103 tyrosine 3-monooxygenasetryp tophan 5-monooxygenase activation protein, zeta polypeptide /FL=gb:BC003623.1 gb:M86400.1 gb:NM_003406.1	
				gb:NM_000130.2 /DEF=Homo sapiens coagulation factor V (proaccelerin, labile factor) (F5), mRNA. /FEA=mRNA /GEN=F5 /PROD=coagulation factor V precursor /DB_XREF=gi:1051 8500 /UG=Hs.30054 coagulation factor V (proaccelerin, labile factor) /FL=gb:NM_000130 .2 gb:M16967.1	

Figure 7a CC	71.0.		·	
217906 at	NM 014315	gb:NM_014315.1 /DEF=Homo sapiens host cell factor homolog (LCP), mRNA. /FEA=mRNA /GEN=LCP /PROD=host cell factor homolog /DB_XREF=gi:7657 300 /UG=Hs.20597 host cell factor homolog /FL=gb:BC002335.1 gb:AF113131.1 gb:NM_014315.1 gb:AF244137.1		
217300_at	14111_014010	33 2		
		gb:NM_022494.1 //DEF=Homo sapiens hypothetical protein FLJ21952 (FLJ21952), mRNA. //FEA=mRNA //GEN=FLJ21952 //PROD=hypothetica I protein FLJ21952 //DB_XREF=gi:1196 8052 //UG=Hs.22353 hypothetical protein FLJ21952 //FL=gb:NM_022494		
218249_at	NM_022494	.1		

Figure /a Co	iii u.			· · · · · · · · · · · · · · · · · · ·	
			Consensus		
			includes		
			gb:AL577322		
			/FEA=EST		
			/DB_XREF=gi:1294		
			0338		
			/DB_XREF=est:AL5		
			77322		
			/CLONE=CS0DI085		
			YI06 (3 prime)		
			/UG=Hs.1501		
			1		
			syndecan 2		
			(heparan sulfate		
l			proteoglycan 1,		
			cell surface-		
			associated,		
212158_at		J04621	fibroglycan)		
212130_at		004021	gb:NM_004501.1		
			/DEF=Homo		
			sapiens		
}			heterogeneous		
	•		nuclear		
1			ribonucleoprotein U		
			(scaffold	,	
		•	attachment factor		
			A) (HNRPU),		
			mRNA.		
			/FEA=mRNA		
			/GEN=HNRPU		
			/PROD=heterogene		
			ous nuclear		
			ribonucleoprotein		
			U(scaffold		
	*		attachment factor		
			A)		
			/DB_XREF=gi:4758		
			545		
			/UG=Hs.103804		
			heterogeneous		
			nuclear		
			ribonucleoprotein U		
			•		
			(scaffold		
]			attachment factor		
			(A)		
			/FL=gb:BC003367.1		
			gb:BC003621.1		
200594_x_at		NM 004501	gb:NM_004501.1		
at		14141_004001	192.1111007001.1	L	l

gb:NM_003563.1 /DEF=Homo sapiens speckle- type POZ protein (SPOP), mRNA. /FEA=mRNA /FEA=mRNA /GEN=SPOP /PROD=speckle- type POZ protein /DB_XREF=gi:4507 182 /UG=Hs.129951 speckle-type POZ protein /FL=gb:BC003385.1 gb:NM_003563.1 DEF=Homo sapiens RNA polymerase I 16 kDa subunit (LOC51082), mRNA /FEA=mRNA /GEN=LOC51082 /PROD=RNA polymerase I 16 kDa subunit /FL=gh:BC00389.1 gb:NM_015972.7 RNA polymerase I 16 kDa subunit /FEA=mRNA /GEN=LOC51082 /PROD=RNA polymerase I 16 kDa subunit /BS_XREF=gi:7705 739 /UG=Hs.106127 RNA polymerase I 16 kDa subunit /FL=gb:BC000899.1 gb:NF077044.1 gb:NM_015972.1 Consensus includes gb:AP001745 /DEF=Homo sapiens genomic DNA, chromosome 21q, section 89105 /FEA=mRNA_3 /DB_XREF=gi:7768 737 /UG=Hs.16007	Figure 7a Co	ico.		
gb:NM_015972.1 //DEF=Homo sapiens RNA polymerase I 16 kDa subunit (LOC51082), mRNA. //FEA=mRNA //GEN=LOC51082 //PROD=RNA polymerase I 16 kDa subunit //DB_XREF=gi:7705 739 //UG=Hs.106127 RNA polymerase I 16 kDa subunit //FL=gb:BC000889.1 gb:AF077044.1 gb:NM_015972 Consensus includes gb:AP001745 //DEF=Homo sapiens genomic DNA, chromosome 21q, section 89105 //FEA=mRNA_3 //DB_XREF=gi:7768	204640 s at	NM 00356	/DEF=Homo sapiens speckle-type POZ protein (SPOP), mRNA. /FEA=mRNA /GEN=SPOP /PROD=speckle-type POZ protein /DB_XREF=gi:4507 182 /UG=Hs.129951 speckle-type POZ protein /FL=gb:BC003385.1	
/DEF=Homo sapiens RNA polymerase I 16 kDa subunit (LOC51082), mRNA. /FEA=mRNA /GEN=LOC51082 /PROD=RNA polymerase I 16 kDa subunit /DB_XREF=gi:7705 739 /UG=Hs.106127 RNA polymerase I 16 kDa subunit /FL=gb:BC000889.1 gb:AF077044.1 gb:NM_015972.1 Consensus includes gb:AP001745 /DEF=Homo sapiens genomic DNA, chromosome 21q, section 89105 /FEA=mRNA_3 /DB_XREF=gi:7768	204040_S_at			
218258_at NM_015972 gb:NM_015972.1 Consensus includes gb:AP001745 //DEF=Homo sapiens genomic DNA, chromosome 21q, section 89105 //FEA=mRNA_3 //DB_XREF=gi:7768			/DEF=Homo sapiens RNA polymerase I 16 kDa subunit (LOC51082), mRNA. /FEA=mRNA /GEN=LOC51082 /PROD=RNA polymerase I 16 kDa subunit /DB_XREF=gi:7705 739 /UG=Hs.106127 RNA polymerase I 16 kDa subunit /FL=gb:BC000889.1	
Consensus includes gb:AP001745 //DEF=Homo sapiens genomic DNA, chromosome 21q, section 89105 //FEA=mRNA_3 //DB_XREF=gi:7768	218258_at	NM_01597	1 - 1	
chromosome 21 open reading 212875_s_at AP001745 frame 25		ΔΡΩ01745	includes gb:AP001745 /DEF=Homo sapiens genomic DNA, chromosome 21q, section 89105 /FEA=mRNA_3 /DB_XREF=gi:7768 737 /UG=Hs.16007 chromosome 21 open reading	

I igure ra oc			,	
218610_s_at		NM_018340	gb:NM_018340.1 /DEF=Homo sapiens hypothetical protein FLJ11151 (FLJ11151), mRNA. /FEA=mRNA /GEN=FLJ11151 /PROD=hypothetica I protein FLJ11151 /DB_XREF=gi:8922 900 /UG=Hs.14992 hypothetical protein FLJ11151 /FL=gb:NM_018340 .1	
		,	gb:NM_012103.1 /DEF=Homo sapiens ancient ubiquitous protein 1 (AUP1), mRNA. /FEA=mRNA /GEN=AUP1 /PROD=ancient ubiquitous protein 1 /DB_XREF=gi:6912 259	
220525_s_at 65438_at	KIAA1609	NM_012103 AA195124	/UG=Hs.173736 ancient ubiquitous protein 1 /FL=gb:AF100754.1 gb:NM_012103.1 KIAA1609 protein	Hs.14449

Application of: Liew, et. al. Our Docket #: 4231/2042 Figure 7a Cont'd.

Tigure 74 O	 		
204137_at	NM_003272	gb:NM_003272.1 /DEF=Homo sapiens transmembrane 7 superfamily member 1 (upregulated in kidney) (TM7SF1), mRNA. /FEA=mRNA /GEN=TM7SF1 /PROD=transmemb rane 7 superfamily member 1(upregulated in kidney) /DB_XREF=gi:4507 544 /UG=Hs.15791 transmembrane 7 superfamily member 1 (upregulated in kidney) /FL=gb:AF027826.1 gb:NM_003272.1	
212221_x_at	AL117536	Consensus includes gb:AV703259 /FEA=EST /DB_XREF=gi:1072 0588 /DB_XREF=est:AV7 03259 /CLONE=ADBCRE 12 /UG=Hs.303154 popeye protein 3	

Tigure 74 Oc		
		gb:NM_015450.1 /DEF=Homo sapiens DKFZP586D211 protein (DKFZP586D211), mRNA. /FEA=mRNA /GEN=DKFZP586D 211 /PROD=DKFZP586 D211 protein /DB_XREF=gi:1312 3773 /UG=Hs.31968 DKFZP586D211 protein /FL=gb:BC002923.1
204354 at	NM 01545	1 · · · · · · · · · · · · · · · · · · ·
208795_s_at	D55716	gb:D55716.1 //DEF=Human mRNA for P1cdc47, complete cds. /FEA=mRNA //GEN=P1cdc47 //PROD=P1cdc47 //DB_XREF=gi:1255 616 /UG=Hs.77152 minichromosome maintenance deficient (S. cerevisiae) 7 //FL=gb:D55716.1
200/30_5_at	D337 10	In r-30.0001 10.1

217835_x_at	NM 018840	gb:NM_018840.1 /DEF=Homo sapiens putative Rab5-interacting protein (LOC55969), mRNA. /FEA=mRNA /GEN=LOC55969 /PROD=putative Rab5-interacting protein /DB_XREF=gi:1004 7115 /UG=Hs.184062 putative Rab5- interacting protein /FL=gb:NM_018840 .1 gb:AF274936.1 gb:AF112213.1	
218593 at	NM 018077	gb:NM_018077.1 /DEF=Homo sapiens hypothetical protein FLJ10377 (FLJ10377), mRNA. /FEA=mRNA /GEN=FLJ10377 /PROD=hypothetica I protein FLJ10377 /DB_XREF=gi:8922 387 /UG=Hs.274263 hypothetical protein FLJ10377 /FL=gb:NM_018077 .1	

Figure 7a Co	-				
217808_s_at		NM_024117	gb:NM_024117.1 /DEF=Homo sapiens hypothetical protein MGC2745 (MGC2745), mRNA. /FEA=mRNA /GEN=MGC2745 /PROD=hypothetica I protein MGC2745 /DB_XREF=gi:1312 9137 /UG=Hs.324178 hypothetical protein MGC2745 /FL=gb:BC002326.1 gb:BC003044.1 gb:NM_024117.1 Homo sapiens,		
			Similar to N- terminal Asn amidase, clone MGC:29626 IMAGE:4872717, mRNA, complete		
213062_at		AA643304	cds		Hs.351573
		NM_012177	gb:NM_012177.1 /DEF=Homo sapiens F-box only protein 5 (FBXO5), mRNA. /FEA=mRNA /GEN=FBXO5 /PROD=F-box only protein 5 /DB_XREF=gi:6912 365 /UG=Hs.272027 F- box only protein 5 /FL=gb:AF129535.1 gb:NM_012177.1 zinc finger protein 3		
212684_at	ZNF3	AI752257	(A8-51)		Hs.155470
	1	1 0==0.	15	I	

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Tiguic 7a O]		gb:BC004815.1	
			/DEF=Homo	
			sapiens, clone	
		•	MGC:5139, mRNA,	
			complete cds.	
			/FEA=mRNA	
			/PROD=Unknown	
			(protein for	
			MGC:5139)	
			/DB XREF=gi:1343	
ļ			5956	:
			/UG=Hs.127610	
			acyl-Coenzyme A	
			dehydrogenase, C-	
			2 to C-3 short	
			chain	
			/FL=gb:BC004815.1	
			gb:M26393.1	
202365_at		BC004815	gb:NM_000017.1	
			heat shock 90kDa	
214328_s_at	HSPCA	R01140	protein 1, alpha	 Hs.289088
		1	gb:AF133207.1	
			/DEF=Homo	
			sapiens protein	
			kinase (H11)	
i i			mRNA, complete	
			cds. /FEA=mRNA	
			cds. /FEA=mRNA /GEN=H11	
			cds. /FEA=mRNA /GEN=H11 /PROD=protein	
			cds. /FEA=mRNA /GEN=H11 /PROD=protein kinase	
			cds. /FEA=mRNA /GEN=H11 /PROD=protein kinase /DB_XREF=gi:5901	
			cds. /FEA=mRNA /GEN=H11 /PROD=protein kinase /DB_XREF=gi:5901 654	
			cds. /FEA=mRNA /GEN=H11 /PROD=protein kinase /DB_XREF=gi:5901 654 /UG=Hs.111676	
			cds. /FEA=mRNA /GEN=H11 /PROD=protein kinase /DB_XREF=gi:5901 654 /UG=Hs.111676 protein kinase	
			cds. /FEA=mRNA /GEN=H11 /PROD=protein kinase /DB_XREF=gi:5901 654 /UG=Hs.111676 protein kinase H11; small stress	
			cds. /FEA=mRNA /GEN=H11 /PROD=protein kinase /DB_XREF=gi:5901 654 /UG=Hs.111676 protein kinase H11; small stress protein-like protein	
221667_s_at		AF133207	cds. /FEA=mRNA /GEN=H11 /PROD=protein kinase /DB_XREF=gi:5901 654 /UG=Hs.111676 protein kinase H11; small stress	

gb:BC000674.1 //DEF=Homo sapiens, dystonia 1, torsion (autosomal dominant; torsin A), clone MGC:1558, mRNA, complete cds. //EEA=mRNA //PROD=dystonia 1, torsion (autosomal dominant; torsinA) //DB_XREF=gi:1265 3776 //UG=Hs.19261 dystonia 1, torsion (autosomal dominant; torsin A) //FL=gb:BC000674.1 gb:AF007871.1 gb:NM_000113.1 hypothetical protein MGC3035 Rho-related BTB domain containing 3 Hs.10432 gb:NM_017896.1 //DEF=Homo sapiens hypothetical protein FLJ20602 (/FLJ20602), mRNA. //EEA=mRNA //GEN=FLJ20602 //PROD=hypothetica protein FLJ20602 //PROD=hypothetica	Figure /a Co	Jittu.		7		
hypothetical protein Hs.22412	202348 s at		BC000674	/DEF=Homo sapiens, dystonia 1, torsion (autosomal dominant; torsin A), clone MGC:1558, mRNA, complete cds. /FEA=mRNA /PROD=dystonia 1, torsion (autosomal dominant; torsinA) /DB_XREF=gi:1265 3776 /UG=Hs.19261 dystonia 1, torsion (autosomal dominant; torsin A) /FL=gb:BC000674.1 gb:AF007871.1		
Rho-related BTB domain containing 3 gb:NM_017896.1 /DEF=Homo sapiens hypothetical protein FLJ20602 (FLJ20602), mRNA. /FEA=mRNA /GEN=FLJ20602 /PROD=hypothetica I protein FLJ20602 /DB_XREF=gi:8923 556 /UG=Hs.103808 hypothetical protein FLJ20602 /FL=gb:NM_017896		MGC3035		hypothetical protein		Hs.22412
/DEF=Homo sapiens hypothetical protein FLJ20602 (FLJ20602), mRNA. /FEA=mRNA /GEN=FLJ20602 /PROD=hypothetica I protein FLJ20602 /DB_XREF=gi:8923 556 /UG=Hs.103808 hypothetical protein FLJ20602 /FL=gb:NM_017896				Rho-related BTB		
12 10440 at	218448_at		NM_017896	/DEF=Homo sapiens hypothetical protein FLJ20602 (FLJ20602), mRNA. /FEA=mRNA /GEN=FLJ20602 /PROD=hypothetica I protein FLJ20602 /DB_XREF=gi:8923 556 /UG=Hs.103808 hypothetical protein FLJ20602		

202168_at	NM_003187	gb:NM_003187.1 /DEF=Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, G, 32kD (TAF2G), mRNA. /FEA=mRNA /GEN=TAF2G /PROD=TATA box binding protein (TBP)- associatedfactor, RNA polymerase II, G, 32kD /DB_XREF=gi:4507 350 /UG=Hs.60679 TATA box binding protein (TBP)- associated factor, RNA polymerase II, G, 32kD /FL=gb:BC003400.1 gb:NM_003187.1 gb:U21858.1 gb:U25112.1 gb:U30504.1 Putative prostate	
209227_at N33	3 AU158251	cancer tumor suppressor	Hs.71119

Figure 7a Co	nit u.			-	
209212 s_at	A		gb:AB030824.1 /DEF=Homo sapiens mRNA for transcription factor BTEB2, complete cds. /FEA=mRNA /GEN=bteb2 /PROD=transcriptio n factor BTEB2 /DB_XREF=gi:8272 417 /UG=Hs.84728 Kruppel-like factor 5 (intestinal) /FL=gb:D14520.1 gb:AF132818.1 gb:AB030824.1 gb:AF287272.1		
218133_s_at	N		gb:NM_021824.1 /DEF=Homo sapiens NIF3 (Ngg1 interacting factor 3, S.pombe homolog)-like 1 (NIF3L1), mRNA. /FEA=mRNA /GEN=NIF3L1 /PROD=NIF3 (Ngg1 interacting factor 3, S.pombehomolog)-like 1 /DB_XREF=gi:1114 1898 /UG=Hs.21943 NIF3 (Ngg1 interacting factor 3, S.pombe homolog)-like 1 /FL=gb:AF182416.1 gb:NM_021824.1 gb:AF060513.1 gb:AB038949.1		
			Human putative zinc finger protein		
212689_s_at	Α	A524505	mRNA		Hs.383008

I iguie /a Co			r · · · · · · · · · · · · · · · · · ·	
202238_s_at		NM_006169	gb:NM_006169.1 /DEF=Homo sapiens nicotinamide N- methyltransferase (NNMT), mRNA. /FEA=mRNA /GEN=NNMT /PROD=nicotinamid e N- methyltransferase /DB_XREF=gi:5453 789 /UG=Hs.76669 nicotinamide N- methyltransferase /FL=gb:BC000234.1 gb:U08021.1 gb:NM_006169.1 gb:BC000436.1 /DEF=Homo sapiens,	
			endosulfine alpha, clone MGC:8394, mRNA, complete cds. /FEA=mRNA /PROD=endosulfine alpha /DB_XREF=gi:1265	
202596 at		BC000436	3334 /UG=Hs.111680 endosulfine alpha /FL=gb:BC000436.1 gb:BC004461.1 gb:NM_004436.1	
221806_s_at	FLJ10707	BF590997	hypothetical protein FLJ10707	Hs.7187

Application of: Liew, et. al. Our Docket #: 4231/2042 Figure 7a Cont'd.

		gb:NM_004592.1 /DEF=Homo sapiens splicing factor, arginineserine-rich 8 (suppressor-of- white-apricot, Drosophila homolog) (SFRS8), mRNA. /FEA=mRNA /GEN=SFRS8 /PROD=splicing factor, arginineserine-rich 8(suppressor-of- white-apricot, Drosophila homolog) /DB_XREF=gi:4759 101 /UG=Hs.84229 splicing factor,	
		white-apricot, Drosophila homolog) /DB_XREF=gi:4759 101 /UG=Hs.84229	
		arginineserine-rich 8 (suppressor-of- white-apricot, Drosophila	
202775_s_at	NM_004592	homolog) /FL=gb:NM_004592 .1 gb:U08377.1	

Figure 7a Co	Jit G.		,	
			gb:NM_014268.1 //DEF=Homo sapiens microtubule- associated protein, RPEB family, member 2 (MAPRE2), mRNA. //FEA=mRNA //GEN=MAPRE2 //PROD=microtubule- associated protein, RPEB family,member 2 //DB_XREF=gi:1034 6134 //UG=Hs.78335 microtubule- associated protein, RPEB family, member 2 //FL=gb:NM_014268	
202501_at		NM_014268	1.1	
			transmembrane 4 superfamily	
209386 at	TM4SF1	AI346835	member 1	Hs.351316
			gb:NM_003300.1 /DEF=Homo sapiens TNF receptor-associated factor 3 (TRAF3), mRNA. /FEA=mRNA /GEN=TRAF3 /PROD=TNF receptor-associated factor 3 /DB_XREF=gi:4507 678 /UG=Hs.297660 TNF receptor- associated factor 3 /FL=gb:NM_003300	
208315_x_at	<u></u>	NM_003300	.1 gb:U21092.1]

Figure /a Co	nicu.			
			gb:BC002431.1 /DEF=Homo sapiens, Similar to UDP- Gal:betaGlcNAc beta 1,4- galactosyltransferas e, polypeptide 2, clone MGC:2008, mRNA, complete cds. /FEA=mRNA /PROD=Similar to UDP- Gal:betaGlcNAc beta 1,4- galactosyltransferas e, polypeptide 2 /DB_XREF=gi:1280 3236 /UG=Hs.206713 UDP- Gal:betaGlcNAc beta 1,4- galactosyltransferas e, polypeptide 2 /DB_SREF=gi:1280 3236 /UG=Hs.206713 UDP- Gal:betaGlcNAc beta 1,4- galactosyltransferas e, polypeptide 2 /FL=gb:BC002431.1 gb:AF038660.1	
209413_at		BC002431	gb:NM_003780.1 gb:AB024434.1	
214700_x_at		AK000323	Consensus includes gb:AK000323.1 /DEF=Homo sapiens cDNA FLJ20316 fis, clone HEP07903, highly similar to U79263 Human clone 23760 mRNA. /FEA=mRNA /DB_XREF=gi:7020 332 /UG=Hs.225841 DKFZP434D193 protein	
213318_s_at	APOM	BG028844	apolipoprotein M	Hs.274348

Application of: Liew, et. al. Our Docket #: 4231/2042 Figure 7a Cont'd.

Tiguic ra oc					
202693_s_at		NM_004760	Consensus includes gb:AW194730 /FEA=EST /DB_XREF=gi:6473 630 /DB_XREF=est:xn4 3d11.x1 /CLONE=IMAGE:26 96469 /UG=Hs.9075 serinethreonine kinase 17a (apoptosis- inducing) /FL=gb:AB011420.1 gb:NM_004760.1		
214919 s at	FLJ20288	R39094	FLJ20288 protein		Hs.84045
221920_s_at	MSCP	BE677761	likely ortholog of mouse mitochondrial solute carrier protein		Hs.300496
219295		NIM 020420	gb:NM_020139.1 /DEF=Homo sapiens oxidoreductase UCPA (LOC56898), mRNA. /FEA=mRNA /GEN=LOC56898 /PROD=oxidoreductase UCPA /DB_XREF=gi:1004 7131 /UG=Hs.124696 oxidoreductase UCPA /FL=gb:NM_020139		
218285_s_at		NM_020139	.1 gb:AF164790.1	L	<u> </u>

Figure 7a CC	ntu.			
202886_s_at	M65254	gb:M65254.1 /DEF=Protein phosphatase 2A 65 kDa regulatory subunit-beta mRNA, complete cds. /FEA=mRNA /GEN=SNRPEP1 /PROD=protein phosphatase-2A regulatory subunit- beta /DB_XREF=gi:1894 29 /UG=Hs.108705 protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform /FL=gb:NM_002716 .1 gb:AF163473.1 gb:M65254.1 gb:AF087438.1		
218431_at	NM_02	gb:NM_022067.1 /DEF=Homo sapiens hypothetical protein FLJ12707 (FLJ12707), mRNA. /FEA=mRNA /GEN=FLJ12707 /PROD=hypothetica I protein FLJ12707 /DB_XREF=gi:1154 5778 /UG=Hs.16157 hypothetical protein FLJ12707 /FL=gb:NM_022067		

221669_s_at	BC001964	gb:BC001964.1 /DEF=Homo sapiens, acyl- Coenzyme A dehydrogenase family, member 8, clone MGC:4966, mRNA, complete cds. /FEA=mRNA /PROD=acyl- Coenzyme A dehydrogenase family, member 8 /DB_XREF=gi:1280 5020 /UG=Hs.14791 acyl Coenzyme A dehydrogenase family, member 8 /FL=gb:BC001964.1	
205523 at	U43328	gb:U43328.1 /DEF=Human link protein mRNA, complete cds. /FEA=mRNA /PROD=link protein /DB_XREF=gi:1151 008 /UG=Hs.2799 cartilage linking protein 1 /FL=gb:U43328.1 gb:NM_001884.1	

Figure /a Co	inta.	, 	
202439_s_at	NM 000202	gb:NM_000202.2 /DEF=Homo sapiens iduronate 2-sulfatase (Hunter syndrome) (IDS), transcript variant 1, mRNA. /FEA=mRNA /GEN=IDS /PROD=iduronate-2- sulfatase isoform a precursor /DB_XREF=gi:5360 215 /UG=Hs.172458 iduronate 2- sulfatase (Hunter syndrome) /FL=gb:M58342.1 gb:NM 000202.2	
221693_s_at	AB049952	gb:AB049952.1 /DEF=Homo sapiens MRPS18a mRNA for mitochondrial ribosomal protein S18a, complete cds. /FEA=mRNA /GEN=MRPS18a /PROD=mitochondri al ribosomal protein S18a /DB_XREF=gi:1362 0904 /FL=gb:AB049952.1	

Figure 7a Cont'd.	, 			
]		Consensus		
		includes		
		gb:AU144855		
		/FEA=EST		
		/DB XREF=gi:1100		
		6376		
		/DB XREF=est:AU		
		144855		
				i .
		/CLONE=HEMBA10		
		03161		
		/UG=Hs.154654		
		cytochrome P450,		
		subfamily I (dioxin-		
		inducible),		
		polypeptide 1		
		(glaucoma 3,		
		(gladcoma 3, primary infantile)		
<u> </u>				
		/FL=gb:NM_000104		
202436_s_at	NM_000104	.2 gb:U03688.1		
1				
<u> </u>		gb:NM_000104.2		
1		/DEF=Homo		
		sapiens		
	1	cytochrome P450,		
		subfamily I (dioxin-		
		inducible),		
1		polypeptide 1		
1		(glaucoma 3,		
		primary infantile)		
		(CYP1B1), mRNA.		
		/FEA=mRNA		
		/GEN=CYP1B1		
		/PROD=cytochrome	1	
		P450, subfamily I		
		(dioxin-		
		inducible),polypepti		
		de 1		
		/DB_XREF=gi:1332	{	
		5059		
		/UG=Hs.154654		
		cytochrome P450,		
		subfamily I (dioxin-		
	}	inducible),	ļ	ļ ļ
		polypeptide 1		
		(glaucoma 3,		
		primary infantile)		
		/FL=gb:NM_000104		
202427 0 =4	NIM COOACA			
202437_s_at	NM_000104	.2 gb:U03688.1	L	

Application of: Liew, et. al. Our Docket #: 4231/2042 Figure 7a Cont'd.

gb:NM_020189.1 /DEF=Homo sapiens DC6 protein (DC6), mRNA. /FEA=mRNA /GEN=DC6 /PROD=DC6 protein /DB_XREF=gi:9910 185 /UG=Hs.283740 DC6 protein /FL=gb:AF201940.1 gb:AF173296.1 gb:NM_020189.1 218482_at NM_020189 gb:D42063.1 /DEF=Human mRNA for RanBP2 (Ran-binding protein 2), complete cds. /FEA=mRNA /PROD=RanBP2 (Ran-binding protein 2) /DB_XREF=gi:9242 66 /UG=Hs.199179 RAN binding protein 2 /FL=gb:NM_006267 D42063 .2 gb:D42063.1 201713_s_at gb:AF041432.1 /DEF=Homo sapiens bet3 (BET3) mRNA, complete cds. /FEA=mRNA /GEN=BET3 /PROD=bet3 /DB_XREF=gi:2791 803 /UG=Hs.288013 similar to yeast BET3 (S. cerevisiae) /FL=gb:AF041432.1 203511_s_at AF041432 gb:NM_014408.1

I iguie 7a O	OTIL G.	T	T	
212793_at	DAAM2	BF513244	dishevelled associated activator of morphogenesis 2	Hs.387175
1			gb:NM_014242.1	
			/DEF=Homo	
		1	sapiens zinc finger	
		1	protein 237 (ZNF237), mRNA.	
			/FEA=mRNA	
			/GEN=ZNF237	
			/PROD=zinc finger	
			protein 237	·
			/DB_XREF=gi:7657	
			706	
			/UG=Hs.124386	
			zinc finger protein 237	
			/FL=gb:NM_014242	
206744_s_at		NM_014242	1.1	
212756 s at	KIAA0349	AI761518	KIAA0349 protein	Hs.15303
			transmembrane 9	
			superfamily	
209149_s_at	TM9SF1	BE899402	member 1	 Hs.91586
			gb:AF070558.1	
			/DEF=Homo	
			sapiens clone	}
			24450 RING zinc	
			finger protein RZF	
			mRNA, complete	
			cds. /FEA=mRNA	
1	-		/PROD=RING zinc finger protein RZF	
			/DB XREF=gi:3387	
			924 /UG=Hs.6900	
			ring finger protein]
1			13	
			/FL=gb:AF037204.1	
			gb:AF070558.1	
201779_s_at		AF070558	gb:NM_007282.1	L

Figure 7a CC	JIILU.			·	 1
			gb:NM_019903.1		İ
· ·			/DEF=Homo		
			sapiens adducin 3		
			(gamma) (ADD3),		
			transcript variant		
			2, mRNA.		
			/FEA=mRNA		
			/GEN=ADD3		
			/PROD=adducin 3,		
			isoform b		
			/DB_XREF=gi:9951		
			926		
			/UG=Hs.324470 adducin 3		
		·			
			(gamma) /FL=gb:D67031.1		
004750		NIM 010002	gb:NM_019903.1		
201753_s_at	KIAA1055	NM_019903 BF195608	KIAA1055 protein		Hs.126084
212796_s_at	KIAA 1055	BF 193000	NIAA 1000 protein	,	113.120004
			gb:AF248966.1		
			/DEF=Homo		
			sapiens HT028		
			mRNA, complete		
			cds. /FEA=mRNA		
			/PROD=HT028		
			/DB XREF=gi:1200		
			/UG=Hs.183434		
			ATPase, H+		
			transporting,		
			lysosomal	1	
			(vacuolar proton		
			pump) membrane		
			sector associated		
			protein M8-9		
			/FL=gb:AF248966.1		

Figure /a Co	 		
203620_s_at	NM_014824	gb:NM_014824.1 /DEF=Homo sapiens KIAA0769 gene product (KIAA0769), mRNA. /FEA=mRNA /GEN=KIAA0769 /PROD=KIAA0769 gene product /DB_XREF=gi:7662 295 /UG=Hs.19056 KIAA0769 gene product /FL=gb:AB018312.1 gb:NM_014824.1	
		gb:NM_007187.2 /DEF=Homo sapiens WW domain binding protein 4 (formin binding protein 21) (WBP4), mRNA. /FEA=mRNA /GEN=WBP4 /PROD=WW domain-containing binding protein 4 /DB_XREF=gi:9943 844 /UG=Hs.28307 WW domain binding protein 4 (formin binding protein 21) /FL=gb:AF071185.1	
203599_s_at	NM_007187	gb:NM_007187.2	

gb:AF104913.1 //DEF=Homo sapiens eukaryotic protein synthesis initiation factor mRNA, complete cds. //EA=mRNA //PROD=eukaryotic protein synthesis initiation factor //DB_XREF=gi:3941 723 //UG=Hs.211568 eukaryotic translation initiation factor 4 gamma, 1 //FL=gb:AF104913.1 gb:AF112345.1 //DEF=Homo sapiens integrin alpha 10 subunit (ITGA10) mRNA, complete cds. //FEA=mRNA //GEN=ITGA10 //PROD=integrin alpha 10 subunit //DB_XREF=gi:6650 627 //UG=Hs.158237 integrin, alpha 10 //FL=gb:AF074015.1 gb:NM_003637.2	/DEF=Homo sapiens eukaryotic protein synthesis initiation factor mRNA, complete cds. /FEA=mRNA /PROD=eukaryotic	
gb:AF112345.1 //DEF=Homo sapiens integrin alpha 10 subunit (ITGA10) mRNA, complete cds. //FEA=mRNA //GEN=ITGA10 //PROD=integrin alpha 10 subunit //DB_XREF=gi:6650 627 //UG=Hs.158237 integrin, alpha 10 //FL=gb:AF074015.1	initiation factor /DB_XREF=gi:3941 723 /UG=Hs.211568 eukaryotic translation initiation factor 4 gamma, 1	
206766_at AF112345 gb:AF112345.1	gb:AF112345.1 /DEF=Homo sapiens integrin alpha 10 subunit (ITGA10) mRNA, complete cds. /FEA=mRNA /GEN=ITGA10 /PROD=integrin alpha 10 subunit /DB_XREF=gi:6650 627 /UG=Hs.158237	

Application of: Liew, et. al. Our Docket #: 4231/2042 Figure 7a Cont'd.

Figure 7a C	One d.			
210962 s at		AB019691	gb:AB019691.1 /DEF=Homo sapiens mRNA for Centrosome- and Golgi-localized PKN-associated protein (CG-NAP), complete cds. /FEA=mRNA /GEN=cg-nap /PROD=Centrosom e- and Golgi- localized PKN- associatedprotein (CG-NAP) /DB_XREF=gi:5051 742 /UG=Hs.58103 A kinase (PRKA) anchor protein (yotiao) 9 /FL=gb:AB019691.1	
			calcium channel, voltage-dependent,	
34726_at	CACNB3	U07139	beta 3 subunit	Hs.250712
			ARP3 actin-related	
	A OTDO	770000	protein 3 homolog	11- 5224
213101_s_at	ACTR3	Z78330	(yeast)	 Hs.5321
213015_at		BF448315	ESTs	Hs.171553

Figure 7a Cont'd.		· · · · · · · · · · · · · · · · · · ·	
217995_at	NM_021199	gb:NM_021199.1 /DEF=Homo sapiens CGI-44 protein; sulfide dehydrogenase like (yeast) (CGI-44), mRNA. /FEA=mRNA /GEN=CGI-44 /PROD=CGI-44 protein; sulfide dehydrogenase like(yeast) /DB_XREF=gi:1086 4010 /UG=Hs.8185 CGI-44 protein; sulfide dehydrogenase like (yeast) /FL=gb:NM_021199 .1 gb:AF151802.1 gb:AF118085.1	
210119_at	U73191	gb:U73191.1 /DEF=Human inward rectifier potassium channel (Kir1.3), complete cds. /FEA=mRNA /GEN=Kir1.3 /PROD=inward rectifier potassium channel /DB_XREF=gi:1765 984 /UG=Hs.17287 potassium inwardly- rectifying channel, subfamily J, member 15 /FL=gb:U73191.1 gb:NM_002243.1	

Figure 7a Cont.d.			
219644 at	NM 016122	gb:NM_016122.1 /DEF=Homo sapiens NY-REN- 58 antigen (LOC51134), mRNA. /FEA=mRNA /GEN=LOC51134 /PROD=NY-REN- 58 antigen /DB_XREF=gi:7705 838 /UG=Hs.56148 NY-REN-58 antigen /FL=gb:AF155115.1 gb:NM 016122.1	
219032_x_at	NM_014322	gb:NM_014322.1 /DEF=Homo sapiens opsin 3 (encephalopsin) (OPN3), mRNA. /FEA=mRNA /GEN=OPN3 /PROD=opsin 3 (encephalopsin) /DB_XREF=gi:7657 070 /UG=Hs.279926 opsin 3 (encephalopsin) /FL=gb:AF140242.1 gb:NM_014322.1	

gb:NM_030569.1 //DEF=Homo sapiens hypothetical protein MGC10848 (MGC10848), mRNA. //ERA=mRNA //ERA=mRNA //ERA=gi:1338 6477 //UG=Hs.207443 hypothetical protein MGC10848 //FL=gb:BC004282.1 gb:NM_030569.1 gb:NM_030569.1 gb:NM_030569.1 gb:NM_030569.1 gb:NM_030569.1 gb:NM_030569.1	Figure 7a Co	nitu.			
/DEF=Homo sapiens uncharacterized hematopoietic stemprogenitor cells protein MDS031 (MDS031), mRNA. /FEA=mRNA /GEN=MDS031 /PROD=uncharacte rized hematopoietic stemprogenitorcells protein MDS031 /DB_XREF=gi:8923 933 /UG=Hs.110853 uncharacterized hematopoietic stemprogenitor cells protein MDS031 /FL=gb:BC005336.1			NM_030569	/DEF=Homo sapiens hypothetical protein MGC10848 (MGC10848), mRNA. /FEA=mRNA /GEN=MGC10848 /PROD=hypothetica I protein MGC10848 /DB_XREF=gi:1338 6477 /UG=Hs.207443 hypothetical protein MGC10848 /FL=gb:BC004282.1	
219015_s_at NM_018466 gb:NM_018466.1				/DEF=Homo sapiens uncharacterized hematopoietic stemprogenitor cells protein MDS031 (MDS031), mRNA. /FEA=mRNA /GEN=MDS031 /PROD=uncharacte rized hematopoietic stemprogenitorcells protein MDS031 /DB_XREF=gi:8923 933 /UG=Hs.110853 uncharacterized hematopoietic stemprogenitor cells protein MDS031 /FL=gb:BC005336.1 gb:AF220051.1	

Figure /a	Jonea.		CEDC protoin	
		1,1,4,4,0,0,4	SFRS protein	70050
203181_x_at	SRPK2	AW149364	kinase 2	Hs.78353
			gb:U69546.1	
			/DEF=Homo	
			sapiens RNA-	
			binding protein	
			BRUNOL3	
			(BRUNOL3)	
			mRNA, complete	
			cds. /FEA=mRNA	
			/GEN=BRUNOL3	
			/PROD=RNA-	
			1	
			binding protein	
			BRUNOL3	
			/DB_XREF=gi:1568	*
			642	
	1		/UG=Hs.211610	
			CUG triplet repeat,	
			RNA-binding	
			protein 2	
			/FL=gb:U69546.1	
			gb:AF036956.1	
	<u> </u>		gb:AF090694.1	
202157_s_at		U69546	gb:NM_006561.1	
202101_3_at		1009340	SMC2 structural	
	1		maintenance of	
	1		chromosomes 2-	l
213253_at	SMC2L1	AU154486	like 1 (yeast)	Hs.381940
			gb:NM_005165.1	
			/DEF=Homo	į.
			sapiens aldolase	
			C, fructose-	
			bisphosphate	
			(ALDOC), mRNA.	
			/FEA=mRNA	
			/GEN=ALDOC	
			/PROD=aldolase	
			C, fructose-	
			bisphosphate	
			/DB_XREF=gi:4885	
			062	
			/UG=Hs.155247	
	1		aldolase C,	
ļ	1		fructose-	
			bisphosphate	
			/FL=gb:BC003613.1	
	I	1	1 -	
			gb:AF054987.1	1

Figure /a Co	 	r	
206015_s_at	NM_014947	gb:NM_014947.1 /DEF=Homo sapiens KIAA1041 protein (KIAA1041), mRNA. /FEA=mRNA /GEN=KIAA1041 /PROD=KIAA1041 protein /DB_XREF=gi:7662 455 /UG=Hs.26023 KIAA1041 protein /FL=gb:AB028964.1 gb:NM_014947.1	
203211_s_at	AK027038	Consensus includes gb:AK027038.1 /DEF=Homo sapiens cDNA: FLJ23385 fis, clone HEP16802. /FEA=mRNA /DB_XREF=gi:1044 0053 /UG=Hs.181326 KIAA1073 protein /FL=gb:AB028996.1 gb:NM_016156.1	
221509_at	AB014731	gb:AB014731.1 /DEF=Homo sapiens mRNA for SMAP-3, complete cds. /FEA=mRNA /GEN=smap-3 /PROD=SMAP-3 /DB_XREF=gi:1224 8760 /UG=Hs.22393 density-regulated protein /FL=gb:AB014731.1	

	,			
203375_s_at		NM 003291	gb:NM_003291.1 /DEF=Homo sapiens tripeptidyl peptidase II (TPP2), mRNA. /FEA=mRNA /GEN=TPP2 /PROD=tripeptidyl peptidase II /DB_XREF=gi:4507 656 /UG=Hs.1117 tripeptidyl peptidase II /FL=gb:M73047.1 gb:NM_003291.1	
201859_at		NM_002727	gb:NM_002727.1 /DEF=Homo sapiens proteoglycan 1, secretory granule (PRG1), mRNA. /FEA=mRNA /GEN=PRG1 /PROD=proteoglyca n 1, secretory granule /DB_XREF=gi:4506 044 /UG=Hs.1908 proteoglycan 1, secretory granule /FL=gb:J03223.1 gb:NM_002727.1	
	01404		GM2 ganglioside	
212737_at	GM2A	AL513583	activator protein	Hs.289082

Figure 7a Co	Jill G.	,			·
206414_s_at		NM_003887	gb:NM_003887.1 /DEF=Homo sapiens development and differentiation enhancing factor 2 (DDEF2), mRNA. /FEA=mRNA /GEN=DDEF2 /PROD=ADP- ribosylation factorarf-directed GTPaseactivating protein /DB_XREF=gi:4502 248 /UG=Hs.12802 development and differentiation enhancing factor 2 /FL=gb:AB007860.1 gb:NM_003887.1		
212388_at		AB028980	Consensus includes gb:AB028980.1 /DEF=Homo sapiens mRNA for KIAA1057 protein, partial cds. /FEA=mRNA /GEN=KIAA1057 /PROD=KIAA1057 protein /DB_XREF=gi:5689 450 /UG=Hs.7243 ubiquitin specific protease 24		

Tigure ra co				
219080_s_at	NM_019857	gb:NM_019857.1 /DEF=Homo sapiens CTP synthase II (CTPS2), mRNA. /FEA=mRNA /GEN=CTPS2 /PROD=CTP synthase II /DB_XREF=gi:9789 918 /UG=Hs.58553 CTP synthase II /FL=gb:AF226667.1 gb:NM_019857.1	•	
		<u> </u>		
218515_at	NM_016631	gb:NM_016631.1 /DEF=Homo sapiens hypothetical protein (LOC51325), mRNA. /FEA=mRNA /GEN=LOC51325 /PROD=hypothetica I protein /DB_XREF=gi:7706 175 /UG=Hs.26461 hypothetical protein /FL=gb:AF208862.1 gb:NM_016631.1		

I iguie 7a Co	int G.	,		y · · · · ·	
218324_s_at		NM_023071	gb:NM_023071.1 /DEF=Homo sapiens hypothetical protein FLJ13117 (FLJ13117), mRNA. /FEA=mRNA /GEN=FLJ13117 /PROD=hypothetica I protein FLJ13117 /DB_XREF=gi:1275 1480 /UG=Hs.152982 hypothetical protein FLJ13117 /FL=gb:NM_023071 .1		
			Consensus		
			includes gb:Z14077.1		
			/DEF=H.sapiens		
			mRNA for YY1NF-		
			E1 protein.		
			/FEA=mRNA		
			/PROD=YY1 NF- E1		
Ì			E1 /DB_XREF=gi:3801		
			0 /UG=Hs.97496		
			YY1 transcription		
			factor		
			/FL=gb:M77698.1		
			gb:M76541.1		
201901_s_at		NM_003403	gb:NM_003403.2		

Figure 7a Co	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,			
206342_x_at		NM_006123	gb:NM_006123.1 /DEF=Homo sapiens iduronate 2-sulfatase (Hunter syndrome) (IDS), transcript variant 2, mRNA. /FEA=mRNA /GEN=IDS /PROD=iduronate-2- sulfatase isoform b precursor /DB_XREF=gi:5360 207 /UG=Hs.172458 iduronate 2- sulfatase (Hunter syndrome) /FL=gb:L40586.1 gb:NM_006123.1 ATPase, H+	
214150_x_at	ATP6V0E	BE043477	transporting, lysosomal 9kDa, V0 subunit e	Hs.24322
			gb:BC002842.1 /DEF=Homo sapiens, H2B histone family, member B, clone MGC:3802, mRNA, complete cds. /FEA=mRNA /PROD=H2B histone family, member B /DB_XREF=gi:1280 3984 /UG=Hs.180779 H2B histone family, member B /FL=gb:NM_021063	
209911_x_at		BC002842	.1 gb:BC002842.1	

Application of: Liew, et. al. Our Docket #: 4231/2042 Figure 7a Cont'd.

Tigure 7a Oc	iii G.			
205401_at	in C.	NM_003659	gb:NM_003659.1 /DEF=Homo sapiens alkylglycerone phosphate synthase (AGPS), mRNA. /FEA=mRNA /GEN=AGPS /PROD=alkylglycero ne phosphate synthase precursor /DB_XREF=gi:4501 992 /UG=Hs.22580 alkylglycerone phosphate synthase /FL=gb:NM_003659 .1	
206571_s_at		NM_004834	gb:NM_004834.1 /DEF=Homo sapiens mitogen- activated protein kinase kinase kinase kinase 4 (MAP4K4), mRNA. /FEA=mRNA /GEN=MAP4K4 /PROD=mitogen- activated protein kinase kinase kinasekinase 4 /DB_XREF=gi:4758 523 /UG=Hs.3628 mitogen-activated protein kinase kinase kinase kinase kinase kinase kinase kinase 4 /FL=gb:AF096300.1 gb:NM_004834.1	

Figure	7a	Co	nť	d.
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Figure 7a Col	ntu.				
			Consensus		
1			includes		
			gb:AF229253.1		
			/DEF=Homo		
			sapiens clone FIF		
			N1 fibroblast		
1			growth factor 2-		
			interacting factor		
1					
			(API5) mRNA,		
			partial cds.;		
			alternatively		,
			spliced.		
	•		/FEA=mRNA		
1			/GEN=API5		
			/PROD=fibroblast		
]			growth factor 2-		
			interacting factor		
			/DB_XREF=gi:1265		
			6082		
	ŀ		/UG=Hs.227913		
	1.				
214959_s_at		AF229253	API5-like 1		
	ŀ		gb:NM_004887.1		
			/DEF=Homo		į į
			sapiens small		
"			inducible cytokine		
	ŀ		subfamily B (Cys-		
	l		X-Cys), member		
			14 (BRAK)		
			(SCYB14), mRNA.		
1			/FEA=mRNA		
	ļ		/GEN=SCYB14		
	1		/PROD=small		
			inducible cytokine		
1	1		subfamily B(Cys-X-		
	1		Cys), member 14		
			(BRAK)		
			/DB_XREF=gi:4757		
			869 /UG=Hs.24395		
			small inducible		
			cytokine subfamily		
			B (Cys-X-Cys),		l l
				ŀ	
1			member 14		
			(BRAK)		[
			/FL=gb:BC003513.1		
			gb:AF073957.1		
			gb:NM_004887.1		
			gb:AF144103.1]
040000	1.	NIN# 004007	gb:AF106911.1		
218002_s_at	<u> </u>	NM_004887	Ign.AF 1009 I I. I	<u> </u>	

I igule 7a Co	, , , , , , , , , , , , , , , , , , , ,	T	
220575 at	NM 024974	gb:NM_024974.1 /DEF=Homo sapiens hypothetical protein FLJ11800 (FLJ11800), mRNA. /FEA=mRNA /GEN=FLJ11800 /PROD=hypothetica I protein FLJ11800 /DB_XREF=gi:1337 6473 /UG=Hs.287456 hypothetical protein FLJ11800 /FL=gb:NM_024974 .1	
220575_at	Z25429	gb:Z25429.1 /DEF=H.sapiens protein- serinethreonine kinase gene, complete CDS. /FEA=mRNA /PROD=protein- serinethreonine kinase /DB_XREF=gi:4057 36 /FL=gb:Z25429.1	
209339_at	U76248	gb:U76248.1 /DEF=Human hSIAH2 mRNA, complete cds. /FEA=mRNA /PROD=hSIAH2 /DB_XREF=gi:2673 967 /UG=Hs.20191 seven in absentia (Drosophila) homolog 2 /FL=gb:U76248.1 gb:NM_005067.1	

Application of: Liew, et. al. Our Docket #: 4231/2042 Figure 7a Cont'd.

Tigule 7a Ot				
210973_s_at		M63889	gb:M63889.1 //DEF=Human heparin-binding growth factor receptor (HBGF-R- alpha-a3) mRNA, complete cds. //FEA=mRNA //GEN=HBGF-R //PROD=heparin- binding growth factor receptor //DB_XREF=gi:1838 82 //UG=Hs.748 fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome) //FL=gb:M63889.1 ROD1 regulator of	
,		AVA/400070	differentiation 1 (S.	Un 445070
214697_s_at	ROD1	AW190873	pombe)	 Hs.145078
209229_s_at		BC002799	gb:BC002799.1 /DEF=Homo sapiens, KIAA1115 protein, clone MGC:3534, mRNA, complete cds. /FEA=mRNA /PROD=KIAA1115 protein /DB_XREF=gi:1280 3904 /UG=Hs.72172 KIAA1115 protein /FL=gb:BC002799.1 insulin-degrading	
217496_s_at	IDE	AA918442	enzyme	 Hs.1508

I iguic /a oc	111.01			
		Consensus		
	1	includes		
		gb:X60188.1		
		/DEF=Human		
		ERK1 mRNA for		
		protein		
		serinethreonine		
,		kinase.		
		/FEA=mRNA		
		/GEN=ERK1		
		/PROD=protein		
		serinethreonine		
		kinase		
		/DB_XREF=gi:3122		
1		0 /UG=Hs.861		
		mitogen-activated		
212046 x at	X60188	protein kinase 3		
212010_X_dt	,,,,,,,			· ·
İ				
		gb:U70370.1		
1		/DEF=Human		
		hindlimb expressed		
		homeobox protein		
		backfoot (Bft)		
		mRNA, complete		
		cds. /FEA=mRNA		
		/GEN=Bft		
		/PROD=hindlimb	1	
		expressed	[
		homeobox protein		
		backfoot		
		/DB_XREF=gi:1870		
		670 /UG=Hs.84136	1	
		paired-like	Į	•
		homeodomain		
		transcription factor]	
		1		
		/FL=gb:BC003685.1		
200597 04	1170270			
209587_at	U70370	gb:U70370.1		

i iguie 7a Oo			
205431_s_at	NM_021073	gb:NM_021073.1 /DEF=Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA. /FEA=mRNA /GEN=BMP5 /PROD=bone morphogenetic protein 5 /DB_XREF=gi:1083 5090 /UG=Hs.1104 bone morphogenetic protein 5 /FL=gb:NM_021073 .1 gb:M60314.1	
202075_s_at	NM_006227	gb:NM_006227.1 /DEF=Homo sapiens phospholipid transfer protein (PLTP), mRNA. /FEA=mRNA /GEN=PLTP /PROD=phospholipi d transfer protein /DB_XREF=gi:5453 913 /UG=Hs.283007 phospholipid transfer protein /FL=gb:L26232.1 gb:NM_006227.1	
202010_5_at	14141_000221	ESTs, Weakly similar to hypothetical protein FLJ20378 [Homo sapiens]	
215203_at	 AW438464	[H.sapiens]	 Hs.288760

Figure 7a Co	nitu.		
206685_at	NM_0189	gb:NM_018985.1 /DEF=Homo sapiens hypothetical protein (HCGIV.9), mRNA. /FEA=mRNA /GEN=HCGIV.9 /PROD=hypothetica I protein /DB_XREF=gi:9506 770 /UG=Hs.60856 hypothetical protein /FL=gb:NM_018985 .1	
210493_s_at	BC001279	gb:BC001279.1 //DEF=Homo sapiens, Similar to KIAA0626 gene product, clone MGC:5129, mRNA, complete cds. //FEA=mRNA //PROD=Similar to KIAA0626 gene product //DB_XREF=gi:1265 4870 //UG=Hs.285318 Homo sapiens, Similar to KIAA0626 gene product, clone MGC:5129, mRNA, complete cds //FL=gb:BC001279.1 AU148154 MAMMA1 Homo sapiens cDNA clone MAMMA1002744 3', mRNA	
215392_at	AU148154	sequence.	<u> </u>

Figure 7a C	ont a.			
210378_s_at		BC004118	gb:BC004118.1 /DEF=Homo sapiens, clone MGC:11170, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:11170) /DB_XREF=gi:1327 8674 /UG=Hs.18528 Sjogrens syndrome nuclear autoantigen 1 /FL=gb:BC004118.1 ESTs, Moderately similar to	
217608_at		AW408767	hypothetical protein FLJ20489 [Homo sapiens] [H.sapiens]	Hs.383211
205211_s_at		NM_004292	gb:NM_004292.1 /DEF=Homo sapiens ras inhibitor (RIN1), mRNA. /FEA=mRNA /GEN=RIN1 /PROD=ras inhibitor /DB_XREF=gi:4759 039 /UG=Hs.1030 ras inhibitor /FL=gb:L36463.1 gb:NM_004292.1	
	LITATIO		HIV-1 Tat interactive protein,	 U- 000 t
214258_x_at	HTATIP	AA886971	60kDa	Hs.6364

Figure 7a CC	7			
204488_at		NM_014908	gb:NM_014908.1 /DEF=Homo sapiens KIAA1094 protein (KIAA1094), mRNA. /FEA=mRNA /GEN=KIAA1094 /PROD=KIAA1094 protein /DB_XREF=gi:7662 481 /UG=Hs.161166 KIAA1094 protein /FL=gb:AB029017.1 gb:NM_014908.1	
218578_at		NM_024529	gb:NM_024529.1 /DEF=Homo sapiens hypothetical protein FLJ23316 (FLJ23316), mRNA. /FEA=mRNA /GEN=FLJ23316 /PROD=hypothetica I protein FLJ23316 /DB_XREF=gi:1337 5677 /UG=Hs.5722 hypothetical protein FLJ23316 /FL=gb:AF312865.1 gb:NM_024529.1	

Figure /a Cont'd.	T	L-L-AE405000 4		
		gb:AF105230.1		
		/DEF=Homo		
		sapiens neutral		
		amino acid		
1		transporter		
1		(SLC1A5) mRNA,		
1		complete cds.		
		/FEA=mRNA		
		/GEN=SLC1A5		
		/PROD=neutral		
		amino acid		
		transporter		
		/DB_XREF=gi:4191		
		561		
		/UG=Hs.183556		
		solute carrier		
		family 1 (neutral		
		amino acid		
		transporter),		
		member 5		
		/FL=gb:BC000062.1		
		gb:U53347.1		
1	1	gb:AF102826.1		
		gb:AF105230.1		
		gb:AF105230.1 gb:AF105423.1		
208016 34	AE40E020	1 ~		
208916_at	AF105230	gb:NM_005628.1		
		abil 157050 4		
		gb:U57059.1		
		/DEF=Homo		
		sapiens Apo-2		
		ligand mRNA,		
		complete cds.		
	1	/FEA=mRNA		
		/PROD=Apo-2		
		ligand		
		/DB_XREF=gi:1336		
		207 /UG=Hs.83429		
		tumor necrosis		
		factor (ligand)		
		superfamily,		
	[member 10		
	ļ	/FL=gb:U37518.1		
		- Januari	· ·	
į į		gb:U57059.1		

Figure /a Cont'd.				
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		sapiens cDNA		
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1		clone		
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		moderately similar		
		to MOB1		
		PROTEIN.		
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	İ	/DB_XREF=gi:1043		
		5206		
	İ	/UG=Hs.196437		
		hypothetical protein		
		FLJ10788	!	
		/FL=gb:AB016839.1		
		gb:BC003398.1		
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		gb:NM_001531.1		
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		histocompatibility		
		complex, class I-		
		like sequence		,
		(HLALS), mRNA.		
		/FEA=mRNA		
		/GEN=HLALS		
		/PROD=major		
		histocompatibility		
		complex, class I-		
		likesequence		
		/DB_XREF=gi:4504		
		416		
		/UG=Hs.101840		
		major	1	
		histocompatibility		
		complex, class I-		
		like sequence		
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207565_s_at	NM_001531	.1 gb:U22963.1		

Figure 7a Co	mu.			
220761_s_at		NM 016281	gb:NM_016281.1 /DEF=Homo sapiens STE20-like kinase (JIK), mRNA. /FEA=mRNA /GEN=JIK /PROD=STE20-like kinase /DB_XREF=gi:7705 559 /UG=Hs.12040 STE20-like kinase /FL=gb:AF179867.1 gb:NM_016281.1	
u		11.0010201	<u> </u>	
221978_at	HLA-F	BE138825	major histocompatibility complex, class I, F	 Hs.377850
221490_at		AL136733	gb:AL136733.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434N1010 (from clone DKFZp434N1010); complete cds. /FEA=mRNA /GEN=DKFZp434N 1010 /PROD=hypothetica I protein /DB_XREF=gi:1205 2984 /UG=Hs.75425 ubiquitin associated protein /FL=gb:AL136733.1 gb:AF222043.2 gb:NM_016525.2	
			cyclin-dependent	
213182_x_at	CDKN1C	R78668	kinase inhibitor 1C (p57, Kip2)	Hs.106070
217704_x_at		AI820796	ESTs, Weakly similar to hypothetical protein FLJ20489 [Homo sapiens] [H.sapiens]	Hs.310806

Figure /a Co	Jile G.	T	T	
209398_at		BC002649	gb:BC002649.1 /DEF=Homo sapiens, H1 histone family, member 2, clone MGC:3992, mRNA, complete cds. /FEA=mRNA /PROD=H1 histone family, member 2 /DB_XREF=gi:1280 3628 /UG=Hs.7644 H1 histone family, member 2 /FL=gb:BC002649.1 gb:NM_005319.1	
202254_at		AB007900	Consensus includes gb:AB007900.1 /DEF=Homo sapiens KIAA0440 mRNA, partial cds. /FEA=mRNA /GEN=KIAA0440 /DB_XREF=gi:2662 160 /UG=Hs.172180 KIAA0440 protein /FL=gb:AF090990.1 gb:NM_015556.1	
203836_s_at		D84476	gb:D84476.1 /DEF=Homo sapiens mRNA for ASK1, complete cds. /FEA=mRNA /PROD=ASK1 /DB_XREF=gi:1805 499 /UG=Hs.151988 mitogen-activated protein kinase kinase kinase 5 /FL=gb:U67156.1 gb:D84476.1 gb:NM_005923.2	

Figure 7a Co	ont'd.				
			gb:AF012074.1		
ŀ			/DEF=Homo		
			sapiens cAMP-	·	
			specific		,
[phosphodiesterase		
			PDE4D2 (PDE4D)		
			mRNA, complete		
			cds. /FEA=mRNA		
			/GEN=PDE4D		
1			I/PROD=cAMP-		
			specific		
			phosphodiesterase		
			PDE4D2		
1			/DB_XREF=gi:2735		
1			858		
			/UG=Hs.172081		
			phosphodiesterase		
	1	1	4D, cAMP-specific		
1			(dunce		
	•		(Drosophila)-		
			homolog	,	
			phosphodiesterase		
			E3)		
	İ		/FL=gb:U50158.1		
210027 0 01		AF012074	gb:AF012074.1		
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[sapiens Down		
			syndrome critical		
					l I
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			1 (DSCR1L1), mRNA. /FEA=mRNA		
			1 (DSCR1L1), mRNA. /FEA=mRNA /GEN=DSCR1L1		
			1 (DSCR1L1), mRNA. /FEA=mRNA /GEN=DSCR1L1 /PROD=Down		
			1 (DSCR1L1), mRNA. /FEA=mRNA /GEN=DSCR1L1 /PROD=Down syndrome critical		
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			1 (DSCR1L1), mRNA. /FEA=mRNA /GEN=DSCR1L1 /PROD=Down syndrome critical region gene 1-like 1protein		
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			1 (DSCR1L1), mRNA. /FEA=mRNA /GEN=DSCR1L1 /PROD=Down syndrome critical region gene 1-like 1protein		
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			1 (DSCR1L1), mRNA. /FEA=mRNA /GEN=DSCR1L1 /PROD=Down syndrome critical region gene 1-like 1protein /DB_XREF=gi:5032 234 /UG=Hs.156007 Down syndrome		
			1 (DSCR1L1), mRNA. /FEA=mRNA /GEN=DSCR1L1 /PROD=Down syndrome critical region gene 1-like 1protein /DB_XREF=gi:5032 234 /UG=Hs.156007 Down syndrome critical region gene		
			1 (DSCR1L1), mRNA. /FEA=mRNA /GEN=DSCR1L1 /PROD=Down syndrome critical region gene 1-like 1protein /DB_XREF=gi:5032 234 /UG=Hs.156007 Down syndrome critical region gene 1-like 1		
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I iguic ra o	 		
220751_s_at	NM_016348	gb:NM_016348.1 /DEF=Homo sapiens chromosome 5 open reading frame 4 (C5ORF4), mRNA. /FEA=mRNA /GEN=C5ORF4 /PROD=putative tumor suppressor /DB_XREF=gi:7705 942 /UG=Hs.10235 chromosome 5 open reading frame 4 /FL=gb:AF159165.1 gb:NM_016348.1	
219255 x at	NM_018725	gb:NM_018725.1 /DEF=Homo sapiens IL-17B receptor (IL17BR), mRNA. /FEA=mRNA /GEN=IL17BR /PROD=IL-17B receptor /DB_XREF=gi:8923 816 /UG=Hs.5470 IL-17B receptor /FL=gb:BC000980.1 gb:AF212365.1 gb:NM_018725.1 gb:AF208110.1	

I iguie 7a Co	one a.			-	
221073_s_at		NM_006092	gb:NM_006092.1 /DEF=Homo sapiens caspase recruitment domain 4 (NOD1), mRNA. /FEA=mRNA /GEN=NOD1 /PROD=caspase recruitment domain 4 /DB_XREF=gi:5174 616 /UG=Hs.19405 caspase recruitment domain 4 /FL=gb:AF113925.1 gb:NM_006092.1 gb:NM_006092.1 gb:NM_000206.1 /DEF=Homo sapiens interleukin 2 receptor, gamma (severe combined immunodeficiency) (IL2RG), mRNA. /FEA=mRNA /GEN=IL2RG /PROD=interleukin 2 receptor, gamma chain, precursor /DB_XREF=gi:4557 881 /UG=Hs.84 interleukin 2 receptor, gamma (severe combined		
204116_at		NM_000206	receptor, gamma		

rigure /a CC	int d.			
218953_s_at			gb:NM_024028.1 /DEF=Homo sapiens hypothetical protein MGC3265 (MGC3265), mRNA. /FEA=mRNA /GEN=MGC3265 /PROD=hypothetical protein MGC3265 /DB_XREF=gi:1312 8973 /UG=Hs.257111 hypothetical protein MGC3265 /FL=gb:BC000014.1 gb:NM_024028.1	
218953_s_at		NIM_U24U28	Consensus includes gb:NM_024028.1 //DEF=Homo sapiens hypothetical protein DKFZp586E1923 (DKFZP586E1923), mRNA. /FEA=CDS //GEN=DKFZP586E	
213312_at		NM_020425	1923 /PROD=hypothetica I protein DKFZp586E1923 /DB_XREF=gi:1009 2684 /UG=Hs.70769 hypothetical protein DKFZp586E1923 /FL=gb:NM_020425 .1	

rigure 7a Contu.		1		
		gb:NM_003431.1 /DEF=Homo		
		sapiens zinc finger		:
		protein 124 (HZF-		
		16) (ZNF124),		
		mRNA.	•	
1		/FEA=mRNA		
		/GEN=ZNF124		
		/PROD=zinc finger		
		protein 124 (HZF-		
		16)		
1		/DB_XREF=gi:4507		
		976		ļ
}		/UG=Hs.180248		
		zinc finger protein		
		124 (HZF-16) /FL=gb:NM 003431		
206928 at	NM 003431	1.1		
200920_at	14101_003431	. 1		
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		6469		
		/UG=Hs.287448		
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	ont a.			
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			(CCAAT	
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:			(CCAAT	
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			7	
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	*			
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			/UG=Hs.147049	
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			like 1 (CCAAT	
	٠		displacement	
			protein)	
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202367_at		NM_001913	.1 gb:L12579.1	
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				l l
			lincludes	l
1			includes	
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			gb:AK023368.1 /DEF=Homo	
			gb:AK023368.1 /DEF=Homo sapiens cDNA	
			gb:AK023368.1 /DEF=Homo	
			gb:AK023368.1 /DEF=Homo sapiens cDNA FLJ13306 fis,	
			gb:AK023368.1 /DEF=Homo sapiens cDNA FLJ13306 fis, clone	
			gb:AK023368.1 /DEF=Homo sapiens cDNA FLJ13306 fis, clone OVARC1001417,	
·			gb:AK023368.1 /DEF=Homo sapiens cDNA FLJ13306 fis, clone OVARC1001417, highly similar to	
			gb:AK023368.1 /DEF=Homo sapiens cDNA FLJ13306 fis, clone OVARC1001417, highly similar to Homo sapiens	
	·		gb:AK023368.1 /DEF=Homo sapiens cDNA FLJ13306 fis, clone OVARC1001417, highly similar to	
			gb:AK023368.1 /DEF=Homo sapiens cDNA FLJ13306 fis, clone OVARC1001417, highly similar to Homo sapiens	
	·		gb:AK023368.1 /DEF=Homo sapiens cDNA FLJ13306 fis, clone OVARC1001417, highly similar to Homo sapiens thyroid hormone receptor-associated	
	·		gb:AK023368.1 /DEF=Homo sapiens cDNA FLJ13306 fis, clone OVARC1001417, highly similar to Homo sapiens thyroid hormone receptor-associated protein complex	
	·		gb:AK023368.1 /DEF=Homo sapiens cDNA FLJ13306 fis, clone OVARC1001417, highly similar to Homo sapiens thyroid hormone receptor-associated protein complex component	
	·		gb:AK023368.1 /DEF=Homo sapiens cDNA FLJ13306 fis, clone OVARC1001417, highly similar to Homo sapiens thyroid hormone receptor-associated protein complex component TRAP170 mRNA.	
	·		gb:AK023368.1 /DEF=Homo sapiens cDNA FLJ13306 fis, clone OVARC1001417, highly similar to Homo sapiens thyroid hormone receptor-associated protein complex component TRAP170 mRNA. /FEA=mRNA	
	·		gb:AK023368.1 /DEF=Homo sapiens cDNA FLJ13306 fis, clone OVARC1001417, highly similar to Homo sapiens thyroid hormone receptor-associated protein complex component TRAP170 mRNA.	
	·		gb:AK023368.1 /DEF=Homo sapiens cDNA FLJ13306 fis, clone OVARC1001417, highly similar to Homo sapiens thyroid hormone receptor-associated protein complex component TRAP170 mRNA. /FEA=mRNA	
	·		gb:AK023368.1 /DEF=Homo sapiens cDNA FLJ13306 fis, clone OVARC1001417, highly similar to Homo sapiens thyroid hormone receptor-associated protein complex component TRAP170 mRNA. /FEA=mRNA /DB_XREF=gi:1043 5273	
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	·		gb:AK023368.1 /DEF=Homo sapiens cDNA FLJ13306 fis, clone OVARC1001417, highly similar to Homo sapiens thyroid hormone receptor-associated protein complex component TRAP170 mRNA. /FEA=mRNA /DB_XREF=gi:1043 5273 /UG=Hs.21586 cofactor required	
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217120_s_at		AK023368	gb:AK023368.1 /DEF=Homo sapiens cDNA FLJ13306 fis, clone OVARC1001417, highly similar to Homo sapiens thyroid hormone receptor-associated protein complex component TRAP170 mRNA. /FEA=mRNA /DB_XREF=gi:1043 5273 /UG=Hs.21586 cofactor required for Sp1 transcriptional	

rigule 1a CC	in a.	r	gb:NM_004333.1		
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			murine sarcoma		
			viral oncogene		
			homolog B1		
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1			/GEN=BRAF		
			/PROD=v-raf		
			murine sarcoma		
			viral oncogene		
			homolog B1		
			/DB_XREF=gi:4757		
			867 /UG=Hs.622 v-		
			raf murine	•	
			sarcoma viral		
			oncogene homolog		
			B1		
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			gb:NM_017765.1		
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			sapiens		
			hypothetical protein		
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			mRNA.		
1	·		/FEA=mRNA		
			/GEN=FLJ20320		
			/PROD=hypothetica I protein FLJ20320		
			/DB_XREF=gi:8923		
			300		
			/UG=Hs.263081		
			hypothetical protein		
			FLJ20320		
			/FL=ab:NM 017765		
220453_at		NM_017765	/FL=gb:NM_017765 .1		

- i iguro ra oc			
201714_at	NM_001070	gb:NM_001070.1 /DEF=Homo sapiens tubulin, gamma 1 (TUBG1), mRNA. /FEA=mRNA /GEN=TUBG1 /PROD=tubulin, gamma 1 /DB_XREF=gi:4507 730 /UG=Hs.21635 tubulin, gamma 1 /FL=gb:BC000619.1 gb:M61764.1 gb:NM_001070.1	
		<u> </u>	
		gb:NM_018214.1 /DEF=Homo sapiens hypothetical protein FLJ10775 (FLJ10775), mRNA. /FEA=mRNA /GEN=FLJ10775 /PROD=hypothetica I protein FLJ10775 /DB_XREF=gi:8922 660 /UG=Hs.35091 hypothetical protein FLJ10775 /FL=gb:BC003193.1	
218816_at	NM_01821		
213839_at	AW028110	ESTs	Hs.301478

Figure 7a CC	int G.			· · · · · · · · · · · · · · · · · · ·	
203205_at		NM 014663	gb:NM_014663.1 /DEF=Homo sapiens KIAA0677 gene product (KIAA0677), mRNA. /FEA=mRNA /GEN=KIAA0677 /PROD=KIAA0677 gene product /DB_XREF=gi:7662 245 /UG=Hs.155983 KIAA0677 gene product /FL=gb:BC002558.1 gb:AB014577.1 gb:NM_014663.1		
203203_at		- VIVI_U 14003	gb:U58331.1 /DEF=Human placental delta sarcoglycan		
		,	mRNA, complete cds. /FEA=mRNA /PROD=delta	,	
			sarcoglycan /DB_XREF=gi:1695 856 /UG=Hs.151899		
			sarcoglycan, delta (35kD dystrophin- associated		
210330_at	Į	J58331	glycoprotein) /FL=gb:U58331.1		

rigule /a CC		,	
215506_s_at	AK021882	Consensus includes gb:AK021882.1 /DEF=Homo sapiens cDNA FLJ11820 fis, clone HEMBA1006445, highly similar to Homo sapiens putative tumor supressor NOEY2 mRNA. /FEA=mRNA /DB_XREF=gi:1043 3168 /UG=Hs.194695 ras homolog gene family, member I	·
		Consensus	
		includes	
		gb:X07868	
		/DEF=Human DNA for insulin-like	
		growth factor II	
		(IGF-2); exon 7	
		and additional	
		ORF /FEA=mRNA_1	
		/DB_XREF=gi:3299	
		8 /UG=Hs.251664	
		insulin-like growth	
		factor 2 (somatomedin A)	
		/FL=gb:BC000531.1	
		gb:J03242.1	
		gb:M17426.1	
202409_at	X07868	gb:NM_000612.2	

1 1guro 7 u oc			
216347_s_at	AK023188	Consensus includes gb:AK023188.1 //DEF=Homo sapiens cDNA FLJ13126 fis, clone NT2RP3002909, weakly similar to P53-BINDING PROTEIN 2. //FEA=mRNA //DB_XREF=gi:1043 5002 //UG=Hs.6162 KIAA0771 protein gb:NM_015487.1 //DEF=Homo	
		sapiens DKFZP434D174 protein (DKFZP434D174), mRNA. /FEA=mRNA /GEN=DKFZP434D 174 /PROD=DKFZP434 D174 protein /DB_XREF=gi:1109 4402 /UG=Hs.302421 DKFZP434D174 protein	·
205527_s_at	NM_015487	/FL=gb:NM_015487 .1	

Figure 7a Co	nita.	 	 -	····
221430_s_at		gb:NM_030963.1 /DEF=Homo sapiens hypothetical protein DKFZp434O1427 (DKFZP434O1427), mRNA. /FEA=CDS /GEN=DKFZP434O 1427 /PROD=hypothetica I protein DKFZp434O1427 /DB_XREF=gi:1362 4336 /FL=gb:NM_030963 .1		
204724_s_at		gb:NM_001853.1 /DEF=Homo sapiens collagen, type IX, alpha 3 (COL9A3), mRNA. /FEA=mRNA /GEN=COL9A3 /PROD=collagen, type IX, alpha 3 /DB_XREF=gi:4502 966 /UG=Hs.53563 collagen, type IX, alpha 3 /FL=gb:L41162.1 gb:NM_001853.1		

Figure 7a Cor	it d.		 ·
204602_at	NM_012242	gb:NM_012242.1 /DEF=Homo sapiens dickkopf (Xenopus laevis) homolog 1 (DKK1), mRNA. /FEA=mRNA /GEN=DKK1 /PROD=dickkopf (Xenopus laevis) homolog 1 /DB_XREF=gi:7110 718 /UG=Hs.40499 dickkopf (Xenopus laevis) homolog 1 /FL=gb:AF127563.1 gb:AF177394.1 gb:NM_012242.1	
	11111_012212	<u> </u>	
204010_s_at	NM 004985	gb:NM_004985.1 /DEF=Homo sapiens v-Ki-ras2 Kirsten rat sarcoma 2 viral oncogene homolog (KRAS2), mRNA. /FEA=mRNA /GEN=KRAS2 /PROD=v-Ki-ras2 Kirsten rat sarcoma 2 viral oncogenehomolog /DB_XREF=gi:4826 811 /UG=Hs.184050 v- Ki-ras2 Kirsten rat sarcoma 2 viral oncogene homolog /FL=gb:M54968.1 gb:NM_004985.1	

gb:NM_002760.1 /DEF=Homo sapiens protein kinase, Y-linked (PRKY), mRNA. /FEA=mRNA /GEN=PRKY /PROD=protein kinase, Y-linked /DB_XREF=gi:1083 5064 /UG=Hs.56336 protein kinase, Ylinked /FL=gb:NM_002760 NM_002760 206279_at .1 gb:NM_020386.1 /DEF=Homo sapiens H-REV107 protein-related protein (LOC57110), mRNA. /FEA=mRNA /GEN=LOC57110 /PROD=H-REV107 protein-related protein /DB_XREF=gi:9966 858 /UG=Hs.36761 H-REV107 proteinrelated protein /FL=gb:AB030816.1 219983_at NM_020386 gb:NM_020386.1

rigule /a CC	ine d.				
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			sapiens cytosolic		
			beta-glucosidase		
			(GLUC), mRNA.		
			/FEA=mRNA		
			/GEN=GLUC		
			/PROD=cytosolic		
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			3312		
			/UG=Hs.146182		
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			glucosidase		
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			gb:AF317840.1		
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	-		gb:NM_017849.1		
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		ļ	/GEN=FLJ20507		
			-	·	
			/PROD=hypothetica		
			I protein FLJ20507		
			/DB_XREF=gi:8923		
			465		
			/UG=Hs.202955		
			hypothetical protein		
			FLJ20507		
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		gb:NM_001274.1 /DEF=Homo sapiens CHK1 (checkpoint, S.pombe) homolog (CHEK1), mRNA. /FEA=mRNA /GEN=CHEK1	
205394 at	NM 001274	/PROD=CHK1 (checkpoint, S.pombe) homolog /DB_XREF=gi:4502 802 /UG=Hs.20295 CHK1 (checkpoint, S.pombe) homolog /FL=gb:AF016582.1 gb:NM 001274.1	
200004_ut	1441_001274		
214140_at SLC25	5A16 AI827990	solute carrier family 25 (mitochondrial carrier; Graves disease autoantigen), member 16	Hs.180408
209008_x_at	U76549	gb:U76549.1 /DEF=Human cytokeratin 8 mRNA, complete cds. /FEA=mRNA /PROD=cytokeratin 8 /DB_XREF=gi:1673 574 /UG=Hs.242463 keratin 8 /FL=gb:BC000654.1 gb:U76549.1 gb:M34225.1 gb:M26324.1 gb:NM_002273.1	

I iguic 7 a o					
			Consensus		
			includes		
			gb:AB020716.1		
İ			/DEF=Homo		:
			sapiens mRNA for		
1			KIAA0909 protein,		
			partial cds.		
			/FEA=mRNA		
			/GEN=KIAA0909		
			/PROD=KIAA0909		
			protein		
			/DB_XREF=gi:4240		
			306		
			/UG=Hs.107362		
040040 =4		A DO20746	KIAA0909 protein		
212948_at		AB020716	NAA0909 protein		
			L D00004074		
	•		gb:BC000487.1		
*			/DEF=Homo		
			sapiens, Similar to		
			POM (POM121 rat		
			homolog) and ZP3		
			fusion protein,		
			clone MGC:8359,		
			mRNA, complete		
			cds. /FEA=mRNA		
			/PROD=Similar to]
			POM (POM121 rat		
			homolog) and		
			ZP3fusion protein		
1			/DB_XREF=gi:1265		
			3432		
			/UG=Hs.296380		
			POM (POM121 rat		
			homolog) and ZP3		
			fusion protein		
210910_s_at		BC000487	/FL=gb:BC000487.1		
2 100 10 3 at	L	15000401	1 35.50000401.1	L	

Figure 7a Cont.		_		
210715 s at	AF027205	gb:AF027205.1 /DEF=Homo sapiens Kunitz-type protease inhibitor (kop) mRNA, complete cds. /FEA=mRNA /GEN=kop /PROD=Kunitz-type protease inhibitor /DB_XREF=gi:2598 967 /UG=Hs.31439 serine protease inhibitor, Kunitz type, 2 /FL=gb:AF027205.1		
209006_s_at	AF247168	gb:AF247168.1 /DEF=Homo sapiens NPD014 (NPD014) mRNA, complete cds. /FEA=mRNA /GEN=NPD014 /PROD=NPD014 /DB_XREF=gi:1200 5626 /UG=Hs.8084 hypothetical protein dJ465N24.2.1 /FL=gb:AF247168.1 gb:AF267856.1	:	

rigule la Ci	ont a.		
219292 at	NM_018105	gb:NM_018105.1 /DEF=Homo sapiens hypothetical protein FLJ10477 (FLJ10477), mRNA. /FEA=mRNA /GEN=FLJ10477 /PROD=hypothetica I protein FLJ10477 /DB_XREF=gi:8922 445 /UG=Hs.7432 hypothetical protein FLJ10477 /FL=gb:NM_018105	
212232_at	AB023231	Consensus includes gb:AB023231.1 /DEF=Homo sapiens mRNA for KIAA1014 protein, partial cds. /FEA=mRNA /GEN=KIAA1014 /PROD=KIAA1014 protein /DB_XREF=gi:4589 677 /UG=Hs.6834 KIAA1014 protein	

Figure	7a	Cont'	d.

I igure /a Oc		- -			
				:	
			Consensus includes gb:Z97056 /DEF=Human DNA sequence from clone RP3-434P1 on chromosome 22 Contains the KCNJ4 gene for inwardly rectifying potassium channel J4 (hippocampal inward rectifier, HIR, HRK1, HIRK2, KIR2.3), the KDELR3 gene for KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulu /FEA=mRNA_5 /DB_XREF=gi:2832 593 /UG=Hs.6179		
			DEADH (Asp-Glu-		:
			Ala-AspHis) box polypeptide 17 (72kD)	•	
000740 -4		707050	/FL=gb:BC000595.1 gb:NM_006386.2		
208718_at		Z97056	gb:U59321.1 Consensus		
			includes gb:D87453.1 /DEF=Human mRNA for		
			KIAA0264 gene, partial cds. /FEA=mRNA /GEN=KIAA0264 /DB_XREF=gi:1665		
			794		
212145_at		D87453	/UG=Hs.122669 KIAA0264 protein		
			nucleosome assembly protein 1-		
208752_x_at	NAP1L1	AI888672	like 1 Homo sapiens		Hs.302649
			OK/SW-cl.14 mRNA, complete		
212077_at		AL583520	cds		Hs.374993

Figure 7a C 212919_at	KIAA1096	AV715578	KIAA1096 protein	Hs.69559
211406_at		AF119875	gb:AF119875.1 /DEF=Homo sapiens PRO2309 mRNA, complete cds. /FEA=mRNA /PROD=PRO2309 /DB_XREF=gi:7770 186 /UG=Hs.283037 HSPC039 protein /FL=gb:AF119875.1	
			gb:BC003375.1 /DEF=Homo sapiens, mitochondrial ribosomal protein L3, clone MGC:5219, mRNA, complete cds. /FEA=mRNA /PROD=mitochondri al ribosomal protein L3 /DB_XREF=gi:1309 7224 /UG=Hs.79086 mitochondrial ribosomal protein L3 /FL=gb:BC003375.1	
208787_at		BC003375	gb:NM_007208.1 gb:NM_014953.1 /DEF=Homo sapiens KIAA1008 protein (KIAA1008), mRNA. /FEA=mRNA /GEN=KIAA1008 /PROD=KIAA1008 protein /DB_XREF=gi:7662 443 /UG=Hs.323346 KIAA1008 protein /FL=gb:AB023225.1 gb:NM_014953.1	

I iguie 7a Oc		1		
219377_at		NM_022751	gb:NM_022751.1 /DEF=Homo sapiens hypothetical protein FLJ21610 (FLJ21610), mRNA. /FEA=mRNA /GEN=FLJ21610 /PROD=hypothetica I protein FLJ21610 /DB_XREF=gi:1223 2414 /UG=Hs.12727 hypothetical protein FLJ21610 /FL=gb:NM_022751 .1	
208093_s_at		NM_030808	gb:NM_030808.1 /DEF=Homo sapiens LIS1- interacting protein NUDEL; endooligopeptidase A (NUDEL), mRNA. /FEA=mRNA /GEN=NUDEL /PROD=LIS1- interacting protein NUDEL;endooligop eptidase A /DB_XREF=gi:1354 0599 /FL=gb:NM_030808	·
212491_s_at	DNAJC8	AA843895	DnaJ (Hsp40) homolog, subfamily C, member 8	Hs.74711

Figure 7a Co	illu.		
213005_s_at	D79994	Consensus includes gb:D79994.1 /DEF=Human mRNA for KIAA0172 gene, partial cds. /FEA=mRNA /GEN=KIAA0172 /DB_XREF=gi:1136 403 /UG=Hs.77546 KIAA0172 protein	
209632_at	L07590	Consensus includes gb:Al760130 /FEA=EST /DB_XREF=gi:5175 797 /DB_XREF=est:wg5 8b07.x1 /CLONE=IMAGE:23 69269 /UG=Hs.28219 protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 72), alpha isoform and (PR 130), beta isoform /FL=gb:L07590.1	
218356_at	NM_013393	gb:NM_013393.1 /DEF=Homo sapiens cell division protein FtsJ (FJH1), mRNA. /FEA=mRNA /GEN=FJH1 /PROD=cell division protein FtsJ /DB_XREF=gi:7019 376 /UG=Hs.279877 cell division protein FtsJ /FL=gb:AF093415.1 gb:NM_013393.1	

Figure /a C	one a.		,	
212560_at	СОХ6В	AV728268	cytochrome c oxidase subunit VIb Consensus	Hs.174031
			includes	
			gb:BG292065 /FEA=EST	
			/DB_XREF=gi:1305	
			0507 /DB_XREF=est:602	
			386350F1	
			/CLONE=IMAGE:45	
			15036 /UG=Hs.69171	
			protein kinase C-	
212628_at		AK023692	like 2	
			gb:AF151867.1	
			/DEF=Homo	
			sapiens CGI-109 protein mRNA,	
			complete cds.	
			/FEA=mRNA	
			/PROD=CGI-109 protein	
			/DB_XREF=gi:4929	
			686	
			/UG=Hs.278391 CGI-109 protein	
209404_s_at		AF151867	/FL=gb:AF151867.1	

Figure /a Co	ontu.				
209444_at		BC001851	gb:BC001851.1 /DEF=Homo sapiens, Similar to RAP1, GTP-GDP dissociation stimulator 1, clone MGC:4525, mRNA, complete cds. /FEA=mRNA /PROD=Similar to RAP1, GTP-GDP dissociation stimulator1 /DB_XREF=gi:1280 4812 /UG=Hs.7940 RAP1, GTP-GDP dissociation stimulator 1 /FL=gb:NM_021159 .1 gb:BC001851.1 gb:BC001816.1 gb:AF237413.1		
209534_x_at	AKAP13	BF222823	A kinase (PRKA) anchor protein 13	-,	Hs.301946
212499_s_at		AK025580	Consensus includes gb:AK025580.1 //DEF=Homo sapiens cDNA: FLJ21927 fis, clone HEP04178, highly similar to HSU90909 Human clone 23722 mRNA sequence. /FEA=mRNA //DB_XREF=gi:1043 8139 //UG=Hs.81360 Homo sapiens cDNA: FLJ21927 fis, clone HEP04178, highly similar to HSU90909 Human clone 23722 mRNA sequence		

209392_at	L35594	gb:L35594.1 /DEF=Human autotaxin mRNA, complete cds. /FEA=mRNA /PROD=autotaxin /DB_XREF=gi:5379 05 /UG=Hs.174185 ectonucleotide pyrophosphataseph osphodiesterase 2 (autotaxin) /FL=gb:L35594.1	
218379 at	NM 016090	gb:NM_016090.1 /DEF=Homo sapiens RNA binding motif protein 7 (RBM7), mRNA. /FEA=mRNA /GEN=RBM7 /PROD=RNA binding motif protein 7 /DB_XREF=gi:9994 184 /UG=Hs.5887 RNA binding motif protein 7 /FL=gb:AF156098.1 gb:NM 016090.1	

Figure 7a C	 	r	r	
210367_s_at	AF010316	gb:AF010316.1 /DEF=Homo sapiens Pig12 (PIG12) mRNA, complete cds. /FEA=mRNA /GEN=PIG12 /PROD=Pig12 /DB_XREF=gi:2415 307 /UG=Hs.146688 prostaglandin E synthase /FL=gb:AF010316.1	·	
209814_at	BC004421	gb:BC004421.1 //DEF=Homo sapiens, nucleolar cysteine-rich protein, clone MGC:1452, mRNA, complete cds. //FEA=mRNA //PROD=nucleolar cysteine-rich protein //DB_XREF=gi:1332 5205 //UG=Hs.120766 nucleolar cysteine- rich protein //FL=gb:BC004421.1 gb:NM_014487.2		
218461_at	NM_016301	gb:NM_016301.1 /DEF=Homo sapiens protein x 0004 (LOC51184), mRNA. /FEA=mRNA /GEN=LOC51184 /PROD=protein x 0004 /DB_XREF=gi:9994 188 /UG=Hs.284164 protein x 0004 /FL=gb:AF117229.1 gb:NM_016301.1		

MISS Al671747 mouse MAPK-interacting and spindle-stabilizing protein Hs.388281	mouse MAPK- interacting and spindle-stabilizing protein	Figure 7a Co	onta.			
gb:NM_017866.1 //DEF=Homo sapiens hypothetical protein FLJ20533 (FLJ20533), mRNA. //FA=mRNA //GEN=FLJ20533 //PROD=hypothetica l protein FLJ20533 //PROD=hypothetica l protein FLJ20533 //BRSPE=gi:8923 499 //JG=Hs.106650 hypothetical protein FLJ20533 //FL=gb:BC002748.1 gb:NM_017866.1 calcium/calmodulin- dependent protein kinase (CaM kinase) II gamma Hs.153406 gb:NM_022755.1 //DEF=Homo sapiens hypothetical protein FLJ13163 ((FLJ13163), mRNA. //FA=mRNA //GEN=FLJ13163 //PROD=hypothetica l protein FLJ13163 //PROD=hypothetica l protein FLJ13163 //PROD=hypothetica l protein FLJ13163 //PROD=hypothetica l protein FLJ13163 //PROD=hypothetica l protein FLJ13163 //PROD=hypothetica l protein FLJ13163 //PROD=hypothetica l protein FLJ13163 //PROD=hypothetica l protein FLJ13163 //PROD=hypothetica l protein FLJ13163 //PROD=hypothetica l protein FLJ13163 //PROD=hypothetica l protein FLJ13163 //PROD=hypothetica l protein FLJ13163 //PROD=hypothetical protein FLJ13163	gb:NM_017866.1 //DEF=Homo sapiens hypothetical protein FI_J20533 (FLJ20533), mRNA. //EEA=mRNA //GEN=FLJ20533 //PROD=hypothetica I protein FLJ20533 //PROD=hypothetica I protein FLJ20533 //PROD=hypothetica I protein FLJ20533 //PROD=hypothetical protein FLJ20533 //FL=gb:BC002748.1 gb:NM_017866.1 219449_s_at NM_017866 SF111268	040040	MICC	A1674747	interacting and spindle-stabilizing	Llo 200204
/DEF=Homo sapiens hypothetical protein FLJ20533 (FLJ20533), mRNA. /FEA=mRNA /GEN=FLJ20533 /PROD=hypothetica protein FLJ20533 /PROD=hypothetica protein FLJ20533 /PROD=hypothetica protein FLJ20533 /PROD=hypothetica protein FLJ20533 /PROD=hypothetical protein FLJ20533 /PL=gb:BC002748.1 gb:NM_017866.1 gb:NM_017866.1 calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma	DEF=Homo sapiens hypothetical protein FLJ20533 (FLJ20533), mRNA. /FEA=mRNA /GEN=FLJ20533 /PROD=hypothetica l protein FLJ20533 /PROD=hypothetica l protein FLJ20533 /PSOD=hypothetica l protein FLJ20533 /PSOD=hypothetica l protein FLJ20533 /PSOD=hypothetica protein FLJ20533 /PSOD=hypothetical protein FLJ20533 /FL=gb:BC002748.1 gb:NM_017866.1 calcium/calmodulin-dependent protein kinase (CaM kinase) l gamma Hs.153406 gb:NM_022755.1 /DEF=Homo sapiens hypothetical protein FLJ13163 (FLJ13163), mRNA /FEA=mRNA /GEN=FLJ13163 /PROD=hypothetica l protein FLJ13163 /PROD=hypothetica l protein FLJ13163 /PROD=hypothetica l protein FLJ13163 /PS_XREF=gi:1223 2422 /UG=Hs.16603 hypothetical protein FLJ13163 /FL-gb:NM_022755 /FL-	212643_at	MISS	Al6/1/4/	protein	 HS.388281
calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma BF111268	calcium/calmodulin-dependent protein kinase (CaM 212757_s_at CAMK2G BF111268 kinase) II gamma Hs.153406 gb:NM_022755.1 //DEF=Homo sapiens hypothetical protein FLJ13163 (FLJ13163), mRNA. //FEA=mRNA //GEN=FLJ13163 //PROD=hypothetica I protein FLJ13163 //DB_XREF=gi:1223 2422 //UG=Hs.16603 hypothetical protein FLJ13163 //FL=gb:NM_022755				/DEF=Homo sapiens hypothetical protein FLJ20533 (FLJ20533), mRNA. /FEA=mRNA /GEN=FLJ20533 /PROD=hypothetica I protein FLJ20533 /DB_XREF=gi:8923 499 /UG=Hs.106650 hypothetical protein FLJ20533 /FL=gb:BC002748.1	
dependent protein kinase (CaM kinase) II gamma Hs.153406 gb:NM_022755.1 //DEF=Homo sapiens hypothetical protein FLJ13163 (FLJ13163), mRNA. //FEA=mRNA //GEN=FLJ13163 //PROD=hypothetica I protein FLJ13163 //DB_XREF=gi:1223 2422 //UG=Hs.16603 hypothetical protein FLJ13163	dependent protein kinase (CaM kinase) gamma Hs.153406	219449_s_at		NM_017866	gb:NM_017866.1	
/DEF=Homo sapiens hypothetical protein FLJ13163 (FLJ13163), mRNA. /FEA=mRNA /GEN=FLJ13163 /PROD=hypothetica I protein FLJ13163 /DB_XREF=gi:1223 2422 /UG=Hs.16603 hypothetical protein FLJ13163	/DEF=Homo sapiens hypothetical protein FLJ13163 (FLJ13163), mRNA. /FEA=mRNA /GEN=FLJ13163 /PROD=hypothetica I protein FLJ13163 /DB_XREF=gi:1223 2422 /UG=Hs.16603 hypothetical protein FLJ13163 /FL=gb:NM_022755	212757_s_at	CAMK2G	BF111268	dependent protein kinase (CaM	Hs.153406
		219092_s_at		NM_022755	/DEF=Homo sapiens hypothetical protein FLJ13163 (FLJ13163), mRNA. /FEA=mRNA /GEN=FLJ13163 /PROD=hypothetica I protein FLJ13163 /DB_XREF=gi:1223 2422 /UG=Hs.16603 hypothetical protein FLJ13163 /FL=gb:NM_022755	

Figure /a Co	incu.				
			gb:U50748.1		
			/DEF=Homo		
			sapiens leptin		
			receptor short		
			form (db) mRNA,		
			complete cds.		
:			/FEA=mRNA		
	:		/GEN=db		
			/PROD=leptin		
			receptor		
			/DB_XREF=gi:3236	-	
			285		
			/UG=Hs.226627		
			leptin receptor		
209894_at		U50748	/FL=gb:U50748.1		
			ribosomal protein		
210034_s_at	RPL5	AA582460	L5		Hs.180946
			gb:NM_005415.2		
			/DEF=Homo		
			sapiens solute		
			carrier family 20		
			(phosphate		
			transporter),		
			member 1		
			(SLC20A1),		
			mRNA.		
			/FEA=mRNA		
			/GEN=SLC20A1		
			/PROD=solute		
			carrier family 20		
			(phosphatetransport		
			er), member 1		ŀ
			/DB_XREF=gi:7382		
			462 /UG=Hs.78452		
			solute carrier		
			family 20		
			(phosphate		
			transporter),		
			member 1		
			/FL=gb:L20859.1		
201920_at		NM_005415	gb:NM_005415.2		

ont a.	· · · · · · · · · · · · · · · · · · ·	r		
	NM 014914	gb:NM_014914.1 /DEF=Homo sapiens KIAA1099 protein (KIAA1099), mRNA. /FEA=mRNA /GEN=KIAA1099 /PROD=KIAA1099 protein /DB_XREF=gi:7662 483 /UG=Hs.159377 KIAA1099 protein /FL=gb:AB029022.1 gb:NM_014914.1		
				Hs.389296
		gb:NM_004596.1 /DEF=Homo sapiens small nuclear ribonucleoprotein polypeptide A (SNRPA), mRNA. /FEA=mRNA /GEN=SNRPA /PROD=small nuclear ribonucleoprotein polypeptide A /DB_XREF=gi:4759 155 /UG=Hs.173255 small nuclear ribonucleoprotein polypeptide A /FL=gb:BC000405.1		
	NM_004596			<u> </u>
PHF3	Al949220	3		Hs.78893
U2AF1RS2	AW089584	U2 small nuclear ribonucleoprotein auxiliary factor, small subunit 2		Hs.171909
	PHF3	NM_014914 AW974823 NM_004596 PHF3 AI949220	gb:NM_014914.1 //DEF=Homo sapiens KIAA1099 protein (KIAA1099), mRNA. //FEA=mRNA //GEN=KIAA1099 //PROD=KIAA1099 protein //DB_XREF=gi:7662 483 //UG=Hs.159377 KIAA1099 protein //FL=gb:AB029022.1 NM_014914 gb:NM_014914.1 AW974823 ESTs gb:NM_004596.1 //DEF=Homo sapiens small nuclear ribonucleoprotein polypeptide A (SNRPA), mRNA. //FEA=mRNA //GEN=SNRPA //PROD=small nuclear ribonucleoprotein polypeptide A //DB_XREF=gi:4759 155 //UG=Hs.173255 small nuclear ribonucleoprotein polypeptide A //DB_XREF=gi:4759 155 //UG=Hs.173255 small nuclear ribonucleoprotein polypeptide A //DB_XREF=gi:4759 155 //UG=Hs.173255 small nuclear ribonucleoprotein polypeptide A //DB_SREF=gi:4759 155 //UG=Hs.173255 small nuclear ribonucleoprotein polypeptide A //DB_SREF=gi:4759 155 //UG=Hs.173255 small nuclear ribonucleoprotein polypeptide A //DB_SREF=gi:4759 155 //UG=Hs.173255 small nuclear ribonucleoprotein polypeptide A //DB_SREF=gi:4759 155 //UG=Hs.173255 small nuclear ribonucleoprotein polypeptide A //DB_SREF=gi:4759 155 //UG=Hs.173255 small nuclear ribonucleoprotein polypeptide A //DB_SREF=gi:4759 155 //UG=Hs.173255 small nuclear ribonucleoprotein polypeptide A //DB_SREF=gi:4759 155 //UG=Hs.173255 small nuclear ribonucleoprotein polypeptide A //DB_SREF=gi:4759 155 //UG=Hs.173255 small nuclear ribonucleoprotein polypeptide A //DB_SREF=gi:4759 155 //UG=Hs.173255 small nuclear ribonucleoprotein polypeptide A //DB_SREF=gi:4759 155 //UG=Hs.173255 small nuclear ribonucleoprotein polypeptide A //DB_SREF=gi:4759 155 //UG=Hs.173255	gb:NM_014914.1 //DEF=Homo sapiens KIAA1099 protein (KIAA1099), mRNA. //FEA=mRNA //GEN=KIAA1099 //PROD=KIAA1099 protein //DB_XREF=gi:7662 483 //UG=Hs.159377 KIAA1099 protein //FL=gb:AB029022.1 ym_014914 gb:NM_014914.1 AW974823 ESTs gb:NM_04596.1 //DEF=Homo sapiens small nuclear ribonucleoprotein polypeptide A (SNRPA), mRNA. //FEA=mRNA //GEN=SNRPA //PROD=small nuclear ribonucleoprotein polypeptide A //DB_XREF=gi:4759 155 //UG=Hs.173255 small nuclear ribonucleoprotein polypeptide A //DB_XREF=gi:4759 155 //UG=Hs.173255 small nuclear ribonucleoprotein polypeptide A //DB_XBEF=gi:4759 155 //UG=Hs.173255 small nuclear ribonucleoprotein polypeptide A //DB_XBEF=gi:4759 155 //UG=Hs.173255 small nuclear ribonucleoprotein polypeptide A //DB_XBEF=gi:4759 155 //UG=Hs.173255 small nuclear ribonucleoprotein polypeptide A //DB_XBEF=gi:4759 155 //UG=Hs.173255 small nuclear ribonucleoprotein polypeptide A //L=gb:BC000405.1 ym_004596.1 PHD finger protein 3 U2 small nuclear ribonucleoprotein auxiliary factor,

F	iau	re	7a	$C \cap$	nt'd.	
г	uu		ı a	-	ntu.	

i iguic 7a oc	771t W.				
			includes		
			gb:AL031133		
			/DEF=Human DNA		
			sequence from		
			clone 281H8 on		
			chromosome		
			6q25.1-25.3.		
			Contains up to		
			four novel genes,		
			one with similarity		
			to KIAA0323 and		
			worm C30F12.1		
			and another with		
			Ubiquitin-Like		
			protein gene		
			SMT3 (the latter		
			in an intron of a		
			novel gene).		
			Contains		
			/FEA=mRNA_2		
			/DB_XREF=gi:3676		
			189		
	•		/UG=Hs.113293		-
		1	Human DNA		
			sequence from		
			clone 281H8 on		
	1		chromosome		
		1	6q25.1-25.3.		
			Contains up to		
			four novel genes,		
			one with similarity	ł	
215452_x_at		AL031133	to KIAA0323 and		
			trans-golgi network		
203833_s_at	TGOLN2	BF061845	protein 2		Hs.14894
		I	1'		·

Figure 7a CC			
203851 at	NM 002178	gb:NM_002178.1 /DEF=Homo sapiens insulin-like growth factor binding protein 6 (IGFBP6), mRNA. /FEA=mRNA /GEN=IGFBP6 /PROD=insulin-like growth factor binding protein 6 /DB_XREF=gi:1132 1592 /UG=Hs.274313 insulin-like growth factor binding protein 6 /FL=gb:NM_002178 .1 gb:BC003507.1 gb:BC005007.1 gb:M62402.1	y
	, , , , , , , , , , , , , , , , , , ,	gb:NM_002768.1	
		/DEF=Homo sapiens procollagen (type	
		III) N- endopeptidase (PCOLN3), mRNA.	
		/FEA=mRNA /GEN=PCOLN3	
		/PROD=procollagen (type III) N- endopeptidase	
		/DB_XREF=gi:4506	
		/UG=Hs.183138 procollagen (type	
		III) N- endopeptidase /FL=gb:U58048.1	
201933_at	NM_002768	gb:NM_002768.1 gb:AF281063.1	

1 iguic 7a oc	 		
201976_s_at	NM_012334	gb:NM_012334.1 /DEF=Homo sapiens myosin X (MYO10), mRNA. /FEA=mRNA /GEN=MYO10 /PROD=myosin X /DB_XREF=gi:1103 7056 /UG=Hs.61638 myosin X /FL=gb:NM_012334 .1 gb:AF234532.1 gb:AF247457.2	
		gb:NM_017871.1 /DEF=Homo sapiens hypothetical protein FLJ20542 (FLJ20542), mRNA. /FEA=mRNA /GEN=FLJ20542 /PROD=hypothetica I protein FLJ20542 /DB_XREF=gi:8923 511 /UG=Hs.6449 hypothetical protein FLJ20542 /FL=gb:AL136813.1	
217994_x_at	NM_017871	gb:NM_017871.1	

Figure 7a Co	ont u.		,		
			gb:NM_017567.1		
			/DEF=Homo		
			sapiens N-		
			Acetylglucosamine		
			kinase		
			(HSA242910),		
			mRNA.		
			/FEA=mRNA		
			/GEN=HSA242910		
			/PROD=N-	•	
			Acetylglucosamine		
ļ			kinase		
		,	/DB_XREF=gi:8923		
			736 /UG=Hs.7036		
	1		N-		
			Acetylglucosamine		
			kinase		
			/FL=gb:BC001029.1		
ŀ			gb:BC005371.1		
218231_at		NM_017567	gb:NM_017567.1		
-			RAN binding protein		
201711_x_at	RANBP2	AI681120	2		Hs.179825
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	PIN4		gb:NM_024090.1 /DEF=Homo sapiens hypothetical protein MGC5487 (MGC5487), mRNA. /FEA=mRNA /GEN=MGC5487 /PROD=hypothetica I protein MGC5487 /DB_XREF=gi:1312 9087 /UG=Hs.211556 hypothetical protein MGC5487 /FL=gb:NM_024090 .1 protein (peptidyl-prolyl cis/trans		Hs.11774

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Sapiens protein Kinase, interferon-inducible double stranded RNA dependent (PRKR), mRNA. /FEA=mRNA /GEN=PRKR /PROD=protein kinase, interferon-inducible doublestranded RNA dependent /DB_XREF=gi-4506 102 /UG=Hs.274382 protein kinase, interferon-inducible double stranded RNA dependent //DB_XREF=gi-4506 102 /UG=Hs.274382 protein kinase, interferon-inducible double stranded RNA dependent /FI=gb.M35663.1 gb.M85294.1				gb:NM_002759.1		
kinase, interferon- inducible double stranded RNA dependent (PRKR), mRNA, /FEA=mRNA /GEN=PRKR /PROD=protein kinase, interferon- inducible doublestranded RNA dependent /DB_XREF=gi-4506 102 //UG=Hs.274382 protein kinase, interferon-inducible double stranded RNA dependent /FL=gb:M35663.1 gb:M85294.1 gb:NM_002759.1 heat shock 90kDa protein (peptidyl- protein (peptidyl- prolei			ľ			
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dependent (PRKR), mRNA. /FEA=mRNA /F						
(PRKR), mRNA. /FEA=mRNA /GEN=PRKR /PROD=protein kinase, interferon-inducible doublestranded RNA dependent /DB_XREF=gi;4506 102 /UG=Hs.274382 protein kinase, interferon-inducible double stranded RNA dependent /FL=gb:M35663.1 gb:M35663.1 gb:M35294.1 gb:M35663.1 gb:M35294.1						
/FEA=mRNA //GEN=PRKR //PROD=protein kinase, interferon- inducible doublestranded RNA dependent //DB_XREF=gi:4506 102 //UG=Hs.274382 protein kinase, interferon-inducible double stranded RNA dependent //FL=gb:M35663.1 gb:M85294.1 gb:M85				i '		
//GEN-PRKR //PROD=protein kinase, interferon- inducible doublestranded RNA dependent //DB_XREF=gi:4506 102 //UG=Hs.274382 protein kinase, interferon-inducible double stranded RNA dependent //FL=gb:M3568.1 gb:M85294.1 gb:M85294.1 gb:M85294.1 gb:M85294.1 gb:M85294.1 gb:M85294.1 gb:M85294.1 gb:M85294.1 gb:M85294.1 gb:M87294.1 gb:M8				1,		
/PROD=protein kinase, interferon-inducible doublestranded RNA dependent /DB_XREF=gi:4506 102 /UG=Hs.274382 protein kinase, interferon-inducible double stranded RNA dependent /FL=gb:Mis5663.1 gb:Mis5294.1 gb:Mis5294.1 gb:Mis5294.1 lbeat shock 90kDa protein f. beta protein f. beta protein f. petidyl-protyl cis/trans isomerase) NIMA-interacting, 4 (parvulin) Hs.11774 214224_s_at PIN4 BE674061 (parvulin) Hs.11774 BE674061 (parvulin) Hs.11774 gb:NM_014753.1 /DEF=Homo sapiens KIAA0187 gene product (KIAA0187), mRNA. /FEA=mRNA /GEN=KIAA0187 gene product (PRRODE) (PRROD						
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inducible doublestranded RNA dependent //DB_XREF=gi:4506 102 //UG=Hs.274382 protein kinase, interferon-inducible double stranded RNA dependent //FL=gb:M35663.1 gb:M85294.1 gb				·		
doublestranded RNA dependent //DB_XREF=gi:4506 102 //UG=Hs.274382 protein kinase, interferon-inducible double stranded RNA dependent //EL-gb:M35663.1 gb:M35693.1 gb:M35094.1 gb:MM_002759.1 heat shock 90kDa protein 1, beta Hs.74335 protein 1, beta Hs.74335 protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting, 4 (parvulin) Hs.11774 db:NM_014753.1 //DEF=Homo sapiens KIAA0187 gene product (KIAA0187), mRNA, //FEA=mRNA //GEN=KIAA0187 gene product //DB_XREF=gi:7661 979 //UG=Hs.10848 KIAA0187 gene product //DB_XREF=gi:7661 979 //UG=Hs.10848 KIAA0187 gene product //DB_XREF=gi:7661 979 //UG=Hs.10848 KIAA0187 gene product //DB_XREF=gi:7661 979 //UG=Hs.10848 KIAA0187 gene product //DB_XREF=gi:7661 979 //UG=Hs.10848 KIAA0187 gene product //DB_XREF=gi:7661 979 //UG=Hs.10848 KIAA0187 gene product ///UG=DB:D80009.1 ///UG=DB:D80009.1 ////UG=DB:D80009.1 ///////////////////////////////////				kinase, interferon-		
RNA dependent //DB_XREF=gi.4506 102 //UG=Hs.274382 protein kinase, interferon-inducible double stranded RNA dependent //FL=gb:M35663.1 gb:M85294.1 gb:NM_002759.1 heat shock 90kDa protein (peptidyl- protyl cis/trans isomerase) NIMA- interacting, 4 (parvulin) BE674061 (parvulin) Hs.11774 gb:NM_014753.1 //DEF=Homo sapiens KIAA0187 gene product (KIAA0187), mRNA. //EA=mRNA //GEN=KIAA0187 gene product //DB_XREF=gi:7661 979 /UG=Hs.10848 KIAA0187 gene product //DB_XREF=gi:7661 979 /UG=Hs.10848 KIAA0187 gene product //DB_XREF=gi:7661 979 /UG=Hs.10848 KIAA0187 gene product //DB_XREF=gi:7661 979 /UG=Hs.10848 KIAA0187 gene product //DB_XREF=gi:7661 979 /UG=Hs.10848 KIAA0187 gene product //DB_XREF=gi:7661 979 /UG=Hs.10848 KIAA0187 gene product //DB_XREF=gi:7661 979 /UG=Hs.10848 KIAA0187 gene product //DB_XREF=gi:7661 979 /UG=Hs.10848 KIAA0187 gene product //DB_XREF=gi:7661 979 /UG=Hs.10848 KIAA0187 gene product //DB_XREF=gi:7661 979 /UG=Hs.10848 KIAA0187 gene product //DB_XREF=gi:7661 979 /UG=Hs.10848 KIAA0187 gene product //DB_XREF=gi:7661 979 /UG=Hs.10848 KIAA0187 gene product //DB_XREF=gi:7661 979 /UG=Hs.10848 KIAA0187 gene product //DB_XREF=gi:7661 979 /UG=Hs.10848 KIAA0187 gene product //DB_XREF=gi:7661 979 /UG=Hs.10848 KIAA0187 gene product //DB_XREF=gi:7661				inducible		
IDB_KREF=gi:4506 102						
102 //UG=Hs.274382 protein kinase, interferon-inducible double stranded RNA dependent //FL=gb:M35663.1 gb:M85294.1 204211_x_at NM_002759 gb:NM_002759.1 heat shock 90kDa protein 1, beta protein (peptidyl- prolyl cis/frans isomerase) NIMA- interacting, 4 (parvulin) Hs.11774 gb:NM_014753.1 //DEF=Homo sapiens KIAA0187 gene product (KIAA0187), mRNA. //FEA=mRNA //GEN=KIAA0187 gene product //DB_XREF=gi:7661 979 //UG=Hs.10848 KIAA0187 gene product //DB_XREF=gi:7661 979 //UG=Hs.10848 KIAA0187 gene product //FL=gb:D80009.1 //FL=gb:D80009.1 //FL=gb:D80009.1 //FL=gb:D80009.1 //FYK receptor-like				RNA dependent		
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protein kinase, interferon-inducible double stranded RNA dependent /FL=gb:M35663.1 gb:M85294.1 gb:M85294.1 gb:M85294.1 gb:M85294.1 gb:M85294.1 gb:M85294.1 gb:M8_002759.1 heat shock 90kDa protein 1, beta protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting, 4 lbs.74335 protein (pertidyl-prolyl cis/trans isomerase) NIMA-interacting, 4 lbs.11774 gb:NM_014753.1 //DEF=Homo sapiens KIAA0187 gene product (KIAA0187), mRNA. /FEA=mRNA /GEN=KIAA0187 gene product //DB_XREF=gi:7661 grg //DB_XREF=gi:7661						
interferon-inducible double stranded RNA dependent /FL=gb:M35663.1 gb:M85294.61 gb:M85294.61 gb:M85294.1 gb:M85294.1 gb:M8529.1 heat shock 90kDa protein 1, beta protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting, 4 (parvulin) Hs.11774 214224_s_at PIN4 BE674061 (parvulin) Hs.11774 gb:NM_014753.1 /DEF=Homo sapiens KIAA0187 gene product (KIAA0187), mRNA. /FEA=mRNA /GEN=KIAA0187 gene product /DB_XREF=gi:7661 979 /UG=Hs.10848 KIAA0187 gene product /DB_XREF=gi:7661 979 /UG=Hs.10848 KIAA0187 gene product /FL=gb:D80009.1 gb:NM_014753.1 RYK receptor-like				/UG=Hs.274382		
double stranded RNA dependent				protein kinase,		
RNA dependent /FL=gb:M35663.1 gb:M85294.1 gb:NM_002759.1 214359_s_at				interferon-inducible		
/FL=gb:M35663.1 gb:M85294.1 gb:M85294.1 gb:M85294.1 gb:M85294.1 gb:M85294.1 gb:M85294.1 gb:M8_002759.1 heat shock 90kDa protein 1, beta protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting, 4 lbs.11774 214224_s_at PIN4 BE674061 (parvulin) Hs.11774 gb:NM_014753.1 //DEF=Homo sapiens KIAA0187 gene product (KIAA0187), mRNA. //FEA=mRNA //GEN=KIAA0187 gene product (KIAA0187) gene product (VBLAA0187) gene product (VBLAA0187) gene product (VBLAA0187) gene product (VBLAA0187) gene product (VBLAA0187) gene product (VBLAA0187) gene product (VBLAA0187) gene product (VBLAA0187) gene product (VBL-gb:D80009.1 gb:NM_014753.1 RYK receptor-like				double stranded		
gb:M85294.1 gb:NM_002759.1 heat shock 90kDa protein 1, beta protein (peptidyl- prolyl cis/trans isomerase) NIMA- interacting, 4 (parvulin) BE674061 gb:NM_014753.1 //DEF=Homo sapiens KIAA0187 gene product (KIAA0187), mRNA. //FEA=mRNA //GEN=KIAA0187 gene product //DB_XREF=gi:7661 979 /UG=Hs.10848 KIAA0187 gene product //FL=gb:D80009.1 gb:NM_014753.1 RYK receptor-like				RNA dependent		
204211_x_at	1			/FL=gb:M35663.1		
Al218219 heat shock 90kDa protein 1, beta hs.74335				gb:M85294.1		
Al218219 heat shock 90kDa protein 1, beta hs.74335	204211 x at		NM 002759	gb:NM_002759.1		
protein (peptidyl- prolyl cis/trans isomerase) NIMA- interacting, 4 (parvulin) BE674061 Gb:NM_014753.1 //DEF=Homo sapiens KIAA0187 gene product (KIAA0187), mRNA. //FEA=mRNA //GEN=KIAA0187 //PROD=KIAA0187 gene product //DB_XREF=gi:7661 979 /UG=Hs.10848 KIAA0187 gene product //DB_XREF=gi:7661 979 /UG=Hs.10848 KIAA0187 gene product //FL=gb:D80009.1 gb:NM_014753.1 RYK receptor-like				heat shock 90kDa		
prolyl cis/trans isomerase) NIMA-interacting, 4 214224_s_at PIN4 BE674061 (parvulin) Hs.11774 gb:NM_014753.1 //DEF=Homo sapiens KIAA0187 gene product (KIAA0187), mRNA. //FEA=mRNA //GEN=KIAA0187 //PROD=KIAA0187 gene product //DB_XREF=gi:7661 979 /UG=Hs.10848 KIAA0187 gene product //DB_XREF=gi:7661 979 /UG=Hs.10848 KIAA0187 gene product //FL=gb:D80009.1 RYK receptor-like	214359_s_at	HSPCB	Al218219	protein 1, beta		Hs.74335
isomerase) NIMA- interacting, 4 (parvulin) BE674061 gb:NM_014753.1 /DEF=Homo sapiens KIAA0187 gene product (KIAA0187), mRNA. /FEA=mRNA /GEN=KIAA0187 gene product /DB_XREF=gi:7661 979 /UG=Hs.10848 KIAA0187 gene product /DB_XREF=gi:7661 979 /UG=Hs.10848 KIAA0187 gene product /FL=gb:D80009.1 RYK receptor-like				protein (peptidyl-		
interacting, 4 (parvulin) gb:NM_014753.1 /DEF=Homo sapiens KIAA0187 gene product (KIAA0187), mRNA. /FEA=mRNA /GEN=KIAA0187 /PROD=KIAA0187 gene product /DB_XREF=gi:7661 979 /UG=Hs.10848 KIAA0187 gene product /FL=gb:D80009.1 RYK receptor-like				prolyl cis/trans	·	
214224_s_at PIN4 BE674061 (parvulin) Hs.11774 gb:NM_014753.1 //DEF=Homo sapiens KIAA0187 gene product (KIAA0187), mRNA. //FEA=mRNA //GEN=KIAA0187 //PROD=KIAA0187 gene product //DB_XREF=gi:7661 979 /UG=Hs.10848 KIAA0187 gene product //FL=gb:D80009.1 RYK receptor-like	İ			isomerase) NIMA-		
gb:NM_014753.1 //DEF=Homo sapiens KIAA0187 gene product (KIAA0187), mRNA. //FEA=mRNA //GEN=KIAA0187 //PROD=KIAA0187 gene product //DB_XREF=gi:7661 979 /UG=Hs.10848 KIAA0187 gene product //FL=gb:D80009.1 RYK receptor-like				interacting, 4		
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sapiens KIAA0187 gene product (KIAA0187), mRNA. /FEA=mRNA /GEN=KIAA0187 /PROD=KIAA0187 gene product /DB_XREF=gi:7661 979 /UG=Hs.10848 KIAA0187 gene product /FL=gb:D80009.1 RYK receptor-like				-		
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/DB_XREF=gi:7661 979 /UG=Hs.10848 KIAA0187 gene product /FL=gb:D80009.1 203082_at NM_014753 gb:NM_014753.1 RYK receptor-like				· ·		
979 /UG=Hs.10848 KIAA0187 gene product /FL=gb:D80009.1 203082_at NM_014753 gb:NM_014753.1 RYK receptor-like				, ·		ļ
KIAA0187 gene product /FL=gb:D80009.1 203082_at NM_014753 gb:NM_014753.1 RYK receptor-like			1			
product /FL=gb:D80009.1 203082_at NM_014753 gb:NM_014753.1 RYK receptor-like						
/FL=gb:D80009.1 203082_at NM_014753 gb:NM_014753.1 RYK receptor-like				KIAA0187 gene		
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RYK receptor-like				/FL=gb:D80009.1		
	203082_at		NM_014753			
214172_x_at				1		
<u> </u>	214172_x_at	RYK	BG032035	tyrosine kinase		Hs.79350

I igule /a C				
221599 at		BC002752	gb:BC002752.1 /DEF=Homo sapiens, Similar to PTD015 protein, clone MGC:3367, mRNA, complete cds. /FEA=mRNA /PROD=Similar to PTD015 protein /DB_XREF=gi:1280 3822 /UG=Hs.95870 PTD015 protein /FL=gb:BC002752.1	
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			Consensus		
			includes		
			gb:AL049437.1		
	İ		/DEF=Homo		
			sapiens mRNA;		
			cDNA		
			DKFZp586E1120		
			(from clone		
			DKFZp586E1120).		
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			220		
			/UG=Hs.100292		
			Homo sapiens		
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			(from clone	:	
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			:		
			gb:NM_015176.1		
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	,		protein		
			(KIAA0483),		
			mRNA.		
			/FEA=mRNA		
			/GEN=KIAA0483		
	}		/PROD=KIAA0483		
			protein		
			/DB_XREF=gi:7662		
			157 /UG=Hs.64691		ļ
		1	KIAA0483 protein		
			•		
0000704		NINA 04547C	/FL=gb:NM_015176		
202272_s_at		NM_015176	.1		
			sema domain,		
			immunoglobulin	1	
	}		domain (Ig), short		
		1	basic domain,		
			secreted,		
203788_s_at	SEMA3C	AI962897	(semaphorin) 3C		Hs.171921

Figure 7a Co	TTC G.		
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214801_at	W88821	[H.sapiens]	 Hs.408958
217792_at	NM_014426	gb:NM_014426.1 /DEF=Homo sapiens sorting nexin 5 (SNX5), mRNA. /FEA=mRNA /GEN=SNX5 /PROD=sorting nexin 5 /DB_XREF=gi:7657 598 /UG=Hs.13794 sorting nexin 5 /FL=gb:BC000100.1 gb:AF121855.1 gb:NM_014426.1	

Figure 7a Co	onta.		 		
			Consensus		
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İ			KIAA0741 protein,		
			complete cds.		
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			/GEN=KIAA0741		
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			protein		
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			202		:
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			product		
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201025_at		NM_015904	gb:NM 015904.1		
217717 s at	GW128	BF246499	GW128 protein		Hs.182238
			gb:NM_000621.1		
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			sapiens 5-		
			hydroxytryptamine		
			(serotonin)		
			receptor 2A		
			(HTR2A), mRNA.		
			/FEA=mRNA		
			/GEN=HTR2A		
			/PROD=5-		
			hydroxytryptamine		
			(serotonin)		
			receptor 2A		,
			/DB_XREF=gi:1083		
			5174		
			/UG=Hs.298623 5-		
			hydroxytryptamine		
			(serotonin)		
			receptor 2A		
			/FL=gb:NM_000621		
207135_at		NM_000621	.1		
			ESTs, Weakly		
			similar to		
			hypothetical protein		
			FLJ20378 [Homo		
			sapiens]		
217645_at		AW088547	[H.sapiens]		Hs.390733
∠17045_at	<u> </u>	MVVU6854/	[[rī.sapiens]	L	[⊓8.ა ყ ∪/აპ

Figure /a Co	one d.			
206818_s_at		NM_017649	gb:NM_017649.1 /DEF=Homo sapiens hypothetical protein FLJ20064 (FLJ20064), mRNA. /FEA=mRNA /GEN=FLJ20064 /PROD=hypothetica I protein FLJ20064 /DB_XREF=gi:8923 070 /UG=Hs.271221 hypothetical protein FLJ20064 /FL=gb:NM_017649 .1	
200010_3_at		14101_017045	capillary	
61732 r at	CMG1	AI610355	morphogenesis protein 1	Hs.288617
			<u>, </u>	
205839_s_at		NM_004758	gb:NM_004758.1 /DEF=Homo sapiens peripheral benzodiazepine receptor-associated protein 1 (PRAX- 1), mRNA. /FEA=mRNA /GEN=PRAX-1 /PROD=peripheral benzodiazepine receptor- associatedprotein 1 /DB_XREF=gi:4758 955 /UG=Hs.112499 peripheral benzodiazepine receptor-associated protein 1 /FL=gb:AF039571.1 gb:NM_004758.1	

Figure 7a Co	Jiita.		
213164_at	Al867198	ESTs, Weakly similar to A43932 mucin 2 precursor, intestinal - human (fragments) [H.sapiens]	Hs.389698
200803_s_at	AF033095	gb:AF033095.1 /DEF=Homo sapiens testis enhanced gene transcript protein (TEGT) mRNA, complete cds. /FEA=mRNA /GEN=TEGT /PROD=testis enhanced gene transcript protein /DB_XREF=gi:2645 728 /UG=Hs.74637 testis enhanced gene transcript (BAX inhibitor 1) /FL=gb:BC000916.1 gb:AF033095.1 gb:NM_003217.1	

Figure 7a Co	ont a.				
217790_s_at 213503_x_at	ANXA2	NM_007107 BE908217	gb:NM_007107.1 /DEF=Homo sapiens signal sequence receptor, gamma (translocon- associated protein gamma) (SSR3), mRNA. /FEA=mRNA /GEN=SSR3 /PROD=signal sequence receptor, gamma(translocon- associated protein gamma) /DB_XREF=gi:6005 883 /UG=Hs.28707 signal sequence receptor, gamma (translocon- associated protein gamma) /FL=gb:AF110647.1 gb:NM_007107.1 annexin A2 PTH-responsive		Hs.217493
37549_g_at	B1	U87408	osteosarcoma B1 protein	NM_014451	Hs.79340
			Consensus includes gb:AL096716.1 /DEF=Homo sapiens mRNA; cDNA DKFZp564M1462 (from clone DKFZp564M1462); partial cds. /FEA=mRNA /GEN=DKFZp564M 1462 /PROD=hypothetica I protein /DB_XREF=gi:5419 850 /UG=Hs.226007 DKFZP564M1462		113.7 JAU
217042_at	<u></u>	AL096716	protein	l	<u> </u>

201348_at		NM_002084	gb:NM_002084.2 /DEF=Homo sapiens glutathione peroxidase 3 (plasma) (GPX3), mRNA. /FEA=mRNA /GEN=GPX3 /PROD=plasma glutathione peroxidase 3 precursor /DB_XREF=gi:6006 000 /UG=Hs.172153 glutathione peroxidase 3 (plasma) /FL=gb:D00632.1 gb:NM_002084.2 gb:AF217787.1		
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gb:NM_001047.1 /DEF=Homo sapiens steroid-5alpha-reductase, alpha polypeptide 1 (3-oxo-5 alphasteroid delta 4dehydrogenase alpha 1) (SRD5A1), mRNA. /FEA=mRNA /GEN=SRD5A1 /PROD=steroid-5alpha-reductase, alpha polypeptide 1(3-oxo-5 alphasteroid delta 4dehydrogenase alpha 1) /DB_XREF=gi:4507 200 /UG=Hs.552 steroid-5-alphareductase, alpha polypeptide 1 (3oxo-5 alpha-steroid delta 4dehydrogenase alpha 1) /FL=gb:M32313.1 gb:AF052126.1 gb:NM_001047.1 NM_001047 204675_at gb:NM_014946.2 /DEF=Homo sapiens spastic paraplegia 4 (autosomal dominant; spastin) (SPG4), mRNA. /FEA=mRNA /GEN=SPG4 /PROD=spastin /DB_XREF=gi:1187 5210 /UG=Hs.26334 spastic paraplegia 4 (autosomal dominant; spastin) /FL=gb:NM_014946 207724_s_at NM_014946

gb:NM_003801.2 //DEF=Homo sapiens anchor attachment protein 1 (Gaa1p, yeast) homolog (GPAA1), mRNA. //EEA=mRNA //GEN=GPAA1 //PROD=anchor attachment protein 1 //DB_XREF=gi:6031 166 /UG=Hs.4742 anchor attachment protein 1 (Gaa1p, yeast) homolog //FL=gb:BC003171.1 gb:BC004129.1 gb:AB006969.1 gb:NB_003801.2 201618_x_at NM_003801 gb:NM_003801.2 transcription termination factor, RNA polymerase I gb:NM_003641.1 //DEF=Homo sapiens interferon induced transmembrane protein 1 (9-27) (IFITM1), mRNA. //EEA=mRNA	1 igule /a Ci	J. 1. G.	···		
International Processing					
sapiens anchor attachment protein 1 (Gaa1p, yeast) homolog (GPAA1), mRNA. /FEA=mRNA //SEN=GPAA1 //PROD=anchor attachment protein 1 //DB_XREF=gi:6031 166 //JG=Hs.4742 anchor attachment protein 1 (Gaa1p, yeast) homolog /FL=gb:BC003171.1 gb:BC004129.1 gb:AB006969.1 gb:AB006969.1 gb:AB002135.1 gb:NM_003801.2 transcription termination factor, RNA polymerase I gb:NM_003641.1 //DEF=Homo sapiens interferon induced transmembrane protein 1 (9-27) ((IFITM1), mRNA.				gb:NM_003801.2	
attachment protein 1 (Gaa1p, yeast) homolog (GPAA1), mRNA. //FEA=mRNA //GEN=GPAA1 //PROD=anchor attachment protein 1 //DB_XREF=gi:6031 166 /UG=Hs.4742 anchor attachment protein 1 (Gaa1p, yeast) homolog //FL=gb:BC003171.1 gb:BC004129.1 gb:AB006969.1 gb:AB006969.1 gb:AB002135.1 gb:NM_003801.2 transcription termination factor, RNA polymerase I gb:NM_003641.1 //DEF=Homo sapiens interferon induced transmembrane protein 1 (9-27) ((IFITM1), mRNA.					
1 (Gaa1p, yeast) homolog (GPAA1), mRNA. //FEA=mRNA //GEN=GPAA1 //PROD=anchor attachment protein 1 //DB_XREF=gi:6031 166 //UG=Hs.4742 anchor attachment protein 1 (Gaa1p, yeast) homolog //FL=gb:BC003171.1 gb:BC004129.1 gb:A8006969.1 gb:A8002135.1 gb:A8002135.1 gb:NM_003801.2 transcription termination factor, RNA polymerase I gb:NM_003641.1 //DEF=Homo sapiens interferon induced transmembrane protein 1 (9-27) (IFITM1), mRNA.					
homolog (GPAA1), mRNA. //EA=mRNA //GEN=GPAA1 //PROD=anchor attachment protein 1 //DB_XREF=gi:6031 166 /UG=Hs.4742 anchor attachment protein 1 (Gaa1p, yeast) homolog //FL=gb:BC003171.1 gb:BC004129.1 gb:AB006969.1 gb:AB006969.1 gb:AB002135.1 yb:AB002135.1 yb:M_003801.2 transcription termination factor, RNA polymerase I gb:NM_003641.1 //DEF=Homo sapiens interferon induced transmembrane protein 1 (9-27) (IFITM1), mRNA.					
mRNA. //FEA=mRNA //GEN=GPAA1 //PROD=anchor attachment protein 1 //DB_XREF=gi:6031 166 /UG=Hs.4742 anchor attachment protein 1 (Gaa1p, yeast) homolog //FL=gb:BC003171.1 gb:BC004129.1 gb:AB006969.1 gb:AB006969.1 gb:AB002135.1 201618_x_at NM_003801 gb:NM_003801.2 transcription termination factor, RNA polymerase I gb:NM_003641.1 //DEF=Homo sapiens interferon induced transmembrane protein 1 (9-27) (IFITM1), mRNA.					İ
/FEA=mRNA //GEN=GPAA1 //PROD=anchor attachment protein 1 //DB_XREF=gi:6031 166 /UG=Hs.4742 anchor attachment protein 1 (Gaa1p, yeast) homolog //FL=gb:BC003171.1 gb:BC004129.1 gb:AB006969.1 gb:AB006969.1 gb:AB002135.1 201618_x_at NM_003801 gb:NM_003801.2 transcription termination factor, RNA polymerase I gb:NM_003641.1 //DEF=Homo sapiens interferon induced transmembrane protein 1 (9-27) (IFITM1), mRNA.					
/GEN=GPAA1 //PROD=anchor attachment protein 1 //DB_XREF=gi:6031 166 /UG=Hs.4742 anchor attachment protein 1 (Gaa1p, yeast) homolog //FL=gb:BC003171.1 gb:BC004129.1 gb:AB006969.1 gb:AB006969.1 gb:AB002135.1 ltranscription termination factor, RNA polymerase I gb:NM_003641.1 //DEF=Homo sapiens interferon induced transmembrane protein 1 (9-27) (IFITM1), mRNA.					
/PROD=anchor attachment protein 1 //DB_XREF=gi:6031 166 /UG=Hs.4742 anchor attachment protein 1 (Gaa1p, yeast) homolog /FL=gb:BC003171.1 gb:BC004129.1 gb:AB006969.1 gb:AB002135.1 gb:NM_003801.2 transcription termination factor, RNA polymerase I gb:NM_003641.1 //DEF=Homo sapiens interferon induced transmembrane protein 1 (9-27) (IFITM1), mRNA.					
attachment protein 1 //DB_XREF=gi:6031 166 /UG=Hs.4742 anchor attachment protein 1 (Gaa1p, yeast) homolog //FL=gb:BC003171.1 gb:BC004129.1 gb:AB006969.1 gb:AB002135.1 gb:NM_003801.2 transcription termination factor, RNA polymerase I 204771_s_at TTF1 Al632304 RNA polymerase I gb:NM_003641.1 //DEF=Homo sapiens interferon induced transmembrane protein 1 (9-27) (IFITM1), mRNA.					
1 //DB_XREF=gi:6031 166 /UG=Hs.4742 anchor attachment protein 1 (Gaa1p, yeast) homolog //FL=gb:BC003171.1 gb:BC004129.1 gb:AB006969.1 gb:AB002135.1 201618_x_at NM_003801			:		
166 /UG=Hs.4742 anchor attachment protein 1 (Gaa1p, yeast) homolog /FL=gb:BC003171.1 gb:BC004129.1 gb:AB006969.1 gb:AB002135.1 gb:NM_003801.2 transcription termination factor, RNA polymerase I gb:NM_003641.1 /DEF=Homo sapiens interferon induced transmembrane protein 1 (9-27) (IFITM1), mRNA.					
anchor attachment protein 1 (Gaa1p, yeast) homolog /FL=gb:BC003171.1 gb:BC004129.1 gb:AB006969.1 gb:AB002135.1 gb:NM_003801 gb:NM_003801.2 transcription termination factor, RNA polymerase I gb:NM_003641.1 //DEF=Homo sapiens interferon induced transmembrane protein 1 (9-27) (IFITM1), mRNA.					
protein 1 (Gaa1p, yeast) homolog /FL=gb:BC003171.1 gb:BC004129.1 gb:AB006969.1 gb:AB002135.1 gb:NM_003801.2 transcription termination factor, RNA polymerase I gb:NM_003641.1 //DEF=Homo sapiens interferon induced transmembrane protein 1 (9-27) (IFITM1), mRNA.				1	
yeast) homolog /FL=gb:BC003171.1 gb:BC004129.1 gb:AB006969.1 gb:AB002135.1 201618_x_at NM_003801 gb:NM_003801.2 transcription termination factor, RNA polymerase I gb:NM_003641.1 //DEF=Homo sapiens interferon induced transmembrane protein 1 (9-27) (IFITM1), mRNA.					
/FL=gb:BC003171.1 gb:BC004129.1 gb:AB006969.1 gb:AB002135.1 201618_x_at					
gb:BC004129.1 gb:AB006969.1 gb:AB002135.1 201618_x_at				, ,	
gb:AB006969.1 gb:AB002135.1 201618_x_at NM_003801 gb:NM_003801.2 transcription termination factor, RNA polymerase I gb:NM_003641.1 //DEF=Homo sapiens interferon induced transmembrane protein 1 (9-27) (IFITM1), mRNA.		`			
gb:AB002135.1 gb:NM_003801.2 transcription termination factor, RNA polymerase I gb:NM_003641.1 //DEF=Homo sapiens interferon induced transmembrane protein 1 (9-27) (IFITM1), mRNA.				1~	
transcription termination factor, 204771_s_at TTF1 Al632304 RNA polymerase I gb:NM_003641.1 //DEF=Homo sapiens interferon induced transmembrane protein 1 (9-27) (IFITM1), mRNA.		,		1-	
termination factor, RNA polymerase I gb:NM_003641.1 //DEF=Homo sapiens interferon induced transmembrane protein 1 (9-27) (IFITM1), mRNA.	201618_x_at		NM_003801		
204771_s_at TTF1 Al632304 RNA polymerase I Hs.54780 gb:NM_003641.1 //DEF=Homo sapiens interferon induced transmembrane protein 1 (9-27) (IFITM1), mRNA.					
gb:NM_003641.1 /DEF=Homo sapiens interferon induced transmembrane protein 1 (9-27) (IFITM1), mRNA.				•	11. 54700
/DEF=Homo sapiens interferon induced transmembrane protein 1 (9-27) (IFITM1), mRNA.	204//1_s_at		Al632304		 HS.54/80
sapiens interferon induced transmembrane protein 1 (9-27) (IFITM1), mRNA.					
induced transmembrane protein 1 (9-27) (IFITM1), mRNA.					
protein 1 (9-27) (IFITM1), mRNA.					:
(IFITM1), mRNA.				1	
				, ,	
				1 ·	
/GEN=IFITM1					
//OEN-IFTIMI					
induced					
transmembrane				t .	
protein 1(9-27)					
/DB_XREF=gi:4504			ŀ		
580				E .	
/UG=Hs.146360					
interferon induced transmembrane					
protein 1 (9-27)					
/FL=gb:BC000897.1	1	1	Ī		
gb:J04164.1				1/FL=qb:BC000897.1	1
201601_x_at NM_003641 gb:NM_003641.1					

Figure 7a Co	med.			
216870_x_at	nica.	AF264787	Consensus includes gb:AF264787.1 //DEF=Homo sapiens BCMS-upstream neighbor (BCMSUN) mRNA, partial sequence. //FEA=mRNA //DB_XREF=gi:1114 1510 //UG=Hs.43628 deleted in lymphocytic leukemia, 2 gb:NM_014183.1 //DEF=Homo sapiens HSPC162	
			protein (HSPC162), mRNA. /FEA=mRNA /GEN=HSPC162 /PROD=HSPC162 protein /DB_XREF=gi:7661 821 /UG=Hs.100002 HSPC162 protein /FL=gb:BC002481.1 gb:AY026513.1 gb:AF161511.1 gb:NM_014183.1	
217918_at		NM_014183	gb:AF165516.1	

Figure 7a CC	iii G.		
201189_s_at	NM 002224	gb:NM_002224.1 /DEF=Homo sapiens inositol 1,4,5-triphosphate receptor, type 3 (ITPR3), mRNA. /FEA=mRNA /GEN=ITPR3 /PROD=inositol 1,4,5-triphosphate receptor, type 3 /DB_XREF=gi:4504 794 /UG=Hs.77515 inositol 1,4,5- triphosphate receptor, type 3 /FL=gb:D26351.1 gb:NM_002224.1 gb:U01062.1	
201109_s_at	NW_002224	gb:NM_003102.1 /DEF=Homo sapiens superoxide dismutase 3, extracellular (SOD3), mRNA. /FEA=mRNA /GEN=SOD3 /PROD=superoxide	
205236_x_at	NM_003102	dismutase 3, extracellular /DB_XREF=gi:4507 150 /UG=Hs.2420 superoxide dismutase 3, extracellular /FL=gb:J02947.1 gb:NM_003102.1	

I igule /a CC	me d.	· · · · · · · · · · · · · · · · · · ·			
rigule ru oc	an d		gb:NM_001553.1 /DEF=Homo sapiens insulin-like growth factor binding protein 7 (IGFBP7), mRNA. /FEA=mRNA /GEN=IGFBP7 /PROD=insulin-like growth factor binding protein 7 /DB_XREF=gi:4504 618 /UG=Hs.119206 insulin-like growth factor binding		
201162_at		NM 001553	protein 7 /FL=gb:L19182.1 gb:NM_001553.1		
			gb:NM_006148.1 /DEF=Homo sapiens LIM and SH3 protein 1 (LASP1), mRNA. /FEA=mRNA /GEN=LASP1 /PROD=LIM and SH3 protein 1 /DB_XREF=gi:5453 709 /UG=Hs.75080 LIM and SH3 protein 1 /FL=gb:NM_006148		
200618_at		NM_006148	.1	l	

Figure /a Col	it u.				
			gb:NM_019071.1		
			/DEF=Homo		
			sapiens inhibitor of		i
ļ		ļ	growth family,		
			member 3 (ING3),		
İ	i		mRNA.		
			/FEA=mRNA		
			/GEN=ING3		
			/PROD=inhibitor of		
			growth family,		
			member 3		
			/DB_XREF=gi:9506		
			658		
			/UG=Hs.143198		
			inhibitor of growth		
	İ		family, member 3	ļ	
			/FL=gb:AF074968.1		
			gb:AY007790.1]	
205070_at	INM		gb:NM_019071.1		
			İ		
			gb:J02783.1		
			/DEF=Human		
			thyroid hormone		
1			binding protein		
			(p55) mRNA,		
			complete cds.		
			/FEA=mRNA		
	ļ		/GEN=P4HB		
			/DB_XREF=gi:3396		
			46 /UG=Hs.75655		
	1		procollagen-proline,		
			2-oxoglutarate 4-		
			dioxygenase	[
			(proline 4-		
			hydroxylase), beta		
1	1		polypeptide		
		ļ	(protein disulfide		
			isomerase; thyroid	}	
			hormone binding	1	
			protein p55)		
			/FL=gb:J02783.1		
200654_at		2783	gb:NM_000918.1		

Tigule 7a CC			·	
217832_at		NM 006372	Consensus includes gb:BE672181 /FEA=EST /DB_XREF=gi:1003 2712 /DB_XREF=est:7b5 1c08.x1 /CLONE=IMAGE:32 31758 /UG=Hs.155489 NS1-associated protein 1 /FL=gb:AF155568.1 gb:NM_006372.1	
			splicing factor 3b,	
214305_s_at	SF3B1	AW003030	subunit 1, 155kDa	 Hs.334826
200617 ot		NIM 014720	gb:NM_014730.1 /DEF=Homo sapiens KIAA0152 gene product (KIAA0152), mRNA. /FEA=mRNA /GEN=KIAA0152 /PROD=KIAA0152 gene product /DB_XREF=gi:7661 947 /UG=Hs.181418 KIAA0152 gene product /FL=gb:BC000371.1 gb:D63486.1	
200617_at		NM_014730	gb:NM_014730.1	

Figure 7a Co	iitu.	 	
212268 at	N	Consensus includes gb:NM_030666.1 /DEF=Homo sapiens serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 1 (SERPINB1), mRNA. /FEA=CDS /GEN=SERPINB1 /PROD=serine (or cysteine) proteinase inhibitor, cladeB (ovalbumin), member 1 /DB_XREF=gi:1348 9086 /UG=Hs.183583 serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 1 /FB_SERPINB1 /PROD=serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 1 /FL=gb:NM_030666 .1	
211779_x_at	В	gb:BC006155.1 /DEF=Homo sapiens, clone MGC:13188, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:13188) /DB_XREF=gi:1354 4040 /FL=gb:BC006155.1	

Figure 7a Co	inta.	12	
212264_s_at_	D87450	Consensus includes gb:BE645850 /FEA=EST /DB_XREF=gi:9970 161 /DB_XREF=est:7e7 7c03.x1 /CLONE=IMAGE:32 88484 /UG=Hs.154978 KIAA0261 protein	
209869 at	AF284095	gb:AF284095.1 /DEF=Homo sapiens alpha-2A adrenergic receptor mRNA, complete cds. /FEA=mRNA /PROD=alpha-2A adrenergic receptor /DB_XREF=gi:1344 7750 /UG=Hs.249159 adrenergic, alpha- 2A-, receptor /FL=gb:AF284095.1 gb:NM_000681.1	
		Homo sapiens BX1	
211929_at	NM_006570	mRNA, partial cds gb:NM_006570.1 /DEF=Homo sapiens Ras- related GTP- binding protein (RAGA), mRNA. /FEA=mRNA /GEN=RAGA /PROD=Ras-related GTP-binding protein /DB_XREF=gi:5729 998 /UG=Hs.57304 Ras-related GTP- binding protein /FL=gb:U41654.1 gb:NM_006570.1	Hs.249247

Consensus includes gb:AB011126.1 //DEF=Homo sapiens mRNA for KIAA0554 protein, partial cds. //FEA=mRNA //GEN=KIAA0554 //PROD=KIAA0554 //PROD=KIAA0554 //PROD=KIAA0554 //DB_XREF=gi:3043 631 //UG=Hs.301763 XIAA0554 protein gb:M21154.1 //DEF=Human S-adenosylmethionine decarboxylase mRNA, complete cds. //FEA=mRNA //GEN=AMD2 //DB_XREF=gi:1785 17 //UG=Hs.262476 S-adenosylmethionine decarboxylase 1 //FL=gb:BC000171.2 gb:M21154.1 gb:NM_01634.3	Figure 7a Co	nta.				
/DEF=Homo sapiens mRNA for KIAA0554 protein, partial cds. //FEA=mRNA //GEN=KIAA0554 protein //DB_KREF=gi:3043 631 //UG=Hs.301763 KIAA0554 protein //DB_KREF=gi:3043 631 //UG=Hs.301763 KIAA0554 protein //DEF=Human S-adenosylmethionine decarboxylase mRNA, complete cds. //FEA=mRNA //GEN=AMD2 //DB_KREF=gi:1785 17 //UG=Hs.262476 S-adenosylmethionine decarboxylase 1 //FL=gb:BC000171.2 gb:M21154.1				Consensus includes		
sapiens mRNA for KIAA0554 protein, partial cds. //FEA=mRNA //GEN=KIAA0554 //PROD=KIAA0554 protein //DB_XREF=gi:3043 631 //UG=Hs.301763 KIAA0554 protein gb:M21154.1 //DEF=Human S-adenosylmethionine decarboxylase mRNA, complete cds. //FEA=mRNA //GEN=AMD2 //DB_XREF=gi:1785 17 /UG=Hs.262476 S-adenosylmethionine decarboxylase 1 //FL=gb:BC000171.2 gb:M21154.1				gb:AB011126.1		
KIAA0554 protein, partial cds. //EA=mRNA //GEN=KIAA0554 //PROD=KIAA0554 protein //DB_XREF=gi:3043 631 //UG=Hs.301763 KIAA0554 protein gb:M21154.1 //DEF=Human S-adenosylmethionine decarboxylase mRNA, complete cds. //FEA=mRNA //GEN=AMD2 //DB_XREF=gi:1785 17 //UG=Hs.262476 S-adenosylmethionine decarboxylase 1 //FL=gb:BC000171.2 gb:M21154.1						
partial cds. //FEA=mRNA //GEN=KIAA0554 //PROD=KIAA0554 protein //DB_XREF=gi:3043 631 //UG=Hs.301763 KIAA0554 protein gb:M21154.1 //DEF=Human S- adenosylmethionine decarboxylase mRNA, complete cds. //FEA=mRNA //GEN=AMD2 //DB_XREF=gi:1785 17 //UG=Hs.262476 S- adenosylmethionine decarboxylase 1 //FL=gb:BC000171.2 gb:M21154.1						
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/GEN=KIAA0554 /PROD=KIAA0554 protein /DB_XREF=gi:3043 631 /UG=Hs.301763 AB011126 KIAA0554 protein gb:M21154.1 //DEF=Human S- adenosylmethionine decarboxylase mRNA, complete cds. /FEA=mRNA //GEN=AMD2 //DB_XREF=gi:1785 17 /UG=Hs.262476 S- adenosylmethionine decarboxylase 1 //FL=gb:BC000171.2 gb:M21154.1				B •		
/PROD=KIAA0554 protein /DB_XREF=gi:3043 631 /UG=Hs.301763 212288_at AB011126 KIAA0554 protein gb:M21154.1 //DEF=Human S- adenosylmethionine decarboxylase mRNA, complete cds. /FEA=mRNA /GEN=AMD2 //DB_XREF=gi:1785 17 /UG=Hs.262476 S- adenosylmethionine decarboxylase 1 /FL=gb:BC000171.2 gb:M21154.1				1	; :	
protein //DB_XREF=gi:3043 631 //UG=Hs.301763 KIAA0554 protein gb:M21154.1 //DEF=Human S- adenosylmethionine decarboxylase mRNA, complete cds. /FEA=mRNA //GEN=AMD2 //DB_XREF=gi:1785 17 /UG=Hs.262476 S- adenosylmethionine decarboxylase 1 //FL=gb:BC000171.2 gb:M21154.1						
/DB_XREF=gi:3043 631 //UG=Hs.301763 KIAA0554 protein gb:M21154.1 //DEF=Human S- adenosylmethionine decarboxylase mRNA, complete cds. /FEA=mRNA //GEN=AMD2 //DB_XREF=gi:1785 17 /UG=Hs.262476 S- adenosylmethionine decarboxylase 1 //FL=gb:BC000171.2 gb:M21154.1						
212288_at AB011126 AB011126 KIAA0554 protein gb:M21154.1 //DEF=Human S- adenosylmethionine decarboxylase mRNA, complete cds. /FEA=mRNA //GEN=AMD2 //DB_XREF=gi:1785 17 /UG=Hs.262476 S- adenosylmethionine decarboxylase 1 //FL=gb:BC000171.2 gb:M21154.1				1 •		
/UG=Hs.301763 Z12288_at AB011126 KIAA0554 protein gb:M21154.1 //DEF=Human S- adenosylmethionine decarboxylase mRNA, complete cds. /FEA=mRNA //GEN=AMD2 //DB_XREF=gi:1785 17 /UG=Hs.262476 S- adenosylmethionine decarboxylase 1 //FL=gb:BC000171.2 gb:M21154.1		!				
gb:M21154.1 //DEF=Human S- adenosylmethionine decarboxylase mRNA, complete cds. /FEA=mRNA //GEN=AMD2 //DB_XREF=gi:1785 17 //UG=Hs.262476 S- adenosylmethionine decarboxylase 1 //FL=gb:BC000171.2 gb:M21154.1						
/DEF=Human S- adenosylmethionine decarboxylase mRNA, complete cds. /FEA=mRNA /GEN=AMD2 /DB_XREF=gi:1785 17 /UG=Hs.262476 S- adenosylmethionine decarboxylase 1 /FL=gb:BC000171.2 gb:M21154.1	212288_at		AB011126	KIAA0554 protein		
/DEF=Human S- adenosylmethionine decarboxylase mRNA, complete cds. /FEA=mRNA /GEN=AMD2 /DB_XREF=gi:1785 17 /UG=Hs.262476 S- adenosylmethionine decarboxylase 1 /FL=gb:BC000171.2 gb:M21154.1				ab:M21154 1		
adenosylmethionine decarboxylase mRNA, complete cds. /FEA=mRNA /GEN=AMD2 /DB_XREF=gi:1785 17 /UG=Hs.262476 S- adenosylmethionine decarboxylase 1 /FL=gb:BC000171.2 gb:M21154.1						
decarboxylase mRNA, complete cds. /FEA=mRNA /GEN=AMD2 /DB_XREF=gi:1785 17 /UG=Hs.262476 S- adenosylmethionine decarboxylase 1 /FL=gb:BC000171.2 gb:M21154.1						
cds. /FEA=mRNA /GEN=AMD2 /DB_XREF=gi:1785 17 /UG=Hs.262476 S- adenosylmethionine decarboxylase 1 /FL=gb:BC000171.2 gb:M21154.1				•		
/GEN=AMD2 /DB_XREF=gi:1785 17 /UG=Hs.262476 S- adenosylmethionine decarboxylase 1 /FL=gb:BC000171.2 gb:M21154.1				mRNA, complete		
/DB_XREF=gi:1785 17 /UG=Hs.262476 S- adenosylmethionine decarboxylase 1 /FL=gb:BC000171.2 gb:M21154.1						
17 /UG=Hs.262476 S- adenosylmethionine decarboxylase 1 /FL=gb:BC000171.2 gb:M21154.1						
S- adenosylmethionine decarboxylase 1 /FL=gb:BC000171.2 gb:M21154.1				. – -		
adenosylmethionine decarboxylase 1 /FL=gb:BC000171.2 gb:M21154.1						
decarboxylase 1 /FL=gb:BC000171.2 gb:M21154.1						
/FL=gb:BC000171.2 gb:M21154.1						
gb:M21154.1						
				, -		
	201196_s_at		M21154	1 ~		
Consensus				Consensus		
includes						
gb:D25304.1						
/DEF=Human				_		
mRNA for				mRNA for		
KIAA0006 gene,						
partial cds.				1.		
/FEA=mRNA						
/GEN=KIAA0006						
/DB_XREF=gi:4354 45 /UG=Hs.79307						
RacCdc42 guanine						
exchange factor					·	
(GEF) 6						
209539_at D25304 /FL=gb:D13631.1	209539 at		D25304	, ,		

Figure 7a Cont d.		TO	·	
		Consensus		
	1	includes		
	ì	gb:AL080232.1		
		/DEF=Homo		
		sapiens mRNA;		
		cDNA		
		DKFZp586A061		
]		(from clone		
		DKFZp586A061).		
		/FEA=mRNA		
		1		
	1	/DB_XREF=gi:5262		
		725		
1		/UG=Hs.220696		
		Homo sapiens		
		mRNA; cDNA		
	,	DKFZp586A061		
		(from clone		
214902_x_at	AL080232	DKFZp586A061)		
		gb:NM_015607.1		
1		/DEF=Homo		
		sapiens		
		DKFZP547E1010	ļ	
1		protein		
		(DKFZP547E1010),	İ	
<u> </u>		mRNA.		
		/FEA=mRNA		
		/GEN=DKFZP547E		
		1010		
		/PROD=DKFZP547		
İ				
		E1010 protein		
		/DB_XREF=gi:7661		
]		589		
		/UG=Hs.323817		
		DKFZP547E1010	1	
		protein		
1		/FL=gb:NM_015607		
202560_s_at	NM_015607	.1		
		eukaryotic		
]		translation initiation		
201018_at EIF1A	BE542684	factor 1A		Hs.4310

Figure 7a Co	onta.			
203991_s_at		NM 021140	gb:NM_021140.1 /DEF=Homo sapiens ubiquitously transcribed tetratricopeptide repeat gene, X chromosome (UTX), mRNA. /FEA=mRNA /GEN=UTX /PROD=ubiquitousl y transcribed tetratricopeptiderep eat gene, X chromosome /DB_XREF=gi:1086 3942 /UG=Hs.13980 ubiquitously transcribed tetratricopeptide repeat gene, X chromosome /FB_SREF=gi:1086 3942 /UG=Hs.13980 ubiquitously transcribed tetratricopeptide repeat gene, X chromosome /FL=gb:NM_021140 .1 gb:AF000992.1 gb:AF000993.1	
205191_at		NM_006915	gb:NM_006915.1 /DEF=Homo sapiens retinitis pigmentosa 2 (X- linked recessive) (RP2), mRNA. /FEA=mRNA /GEN=RP2 /PROD=XRP2 protein /DB_XREF=gi:5902 059 /UG=Hs.44766 retinitis pigmentosa 2 (X-linked recessive) /FL=gb:NM_006915 .1	
205191_at		NM_006915	ESTs, Weakly similar to	
			hypothetical protein FLJ20378 [Homo sapiens]	
221498_at		BF939727	[H.sapiens]	Hs.409278

1 iguio ru o					
208706_s_at		AL080102	Consensus includes gb:AK026933.1 /DEF=Homo sapiens cDNA: FLJ23280 fis, clone HEP07194. /FEA=mRNA /DB_XREF=gi:1043 9907 /UG=Hs.286236 eukaryotic translation initiation factor 5 /FL=gb:AL080102.1		
220173_at		NM_025057	gb:NM_025057.1 /DEF=Homo sapiens hypothetical protein FLJ23189 (FLJ23189), mRNA. /FEA=mRNA /GEN=FLJ23189 /PROD=hypothetica I protein FLJ23189 /DB_XREF=gi:1337 6590 /UG=Hs.287733 hypothetical protein FLJ23189 /FL=gb:NM_025057 .1		
208677_s_at	BSG	AL550657	basigin (OK blood group)		Hs.74631
		100000	13. 4461	I	1

Figure 7a Cont'd.			
220044_x_at	NM_016424	gb:NM_016424.1 /DEF=Homo sapiens cisplatin resistance- associated overexpressed protein (LUC7A), mRNA. /FEA=mRNA /GEN=LUC7A /PROD=cisplatin resistance- associated overexpressedprote in /DB_XREF=gi:7706 534 /UG=Hs.3688 cisplatin resistance- associated overexpressed protein /FL=gb:NM_016424 .1	
203694_s_at	NM_003587	gb:NM_003587.2 //DEF=Homo sapiens DEADH (Asp-Glu-Ala-AspHis) box polypeptide 16 (DDX16), mRNA. //FEA=mRNA //GEN=DDX16 //PROD=DEADH (Asp-Glu-Ala-AspHis) box polypeptide 16 //DB_XREF=gi:1378 7201 //UG=Hs.12797 DEADH (Asp-Glu-Ala-AspHis) box polypeptide 16 //FL=gb:NM_003587 .2 gb:AB011149.1 gb:AB001601.1	

Figure 7a Cont'd.		
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		/DEF=Homo
		sapiens, NCK
		adaptor protein 2,
		clone MGC:1698,
		mRNA, complete
		cds. /FEA=mRNA
		/PROD=NCK
l :		adaptor protein 2
	1	, , , , , , , , , , , , , , , , , , ,
		/DB_XREF=gi:1265
		2708
		/UG=Hs.101695
]		NCK adaptor
		protein 2
		/FL=gb:BC000103.1
		gb:AF043119.1
		gb:AF047487.1
203315_at	BC000103	gb:NM_003581.1
		/DEF=Homo
'		sapiens aldo-keto
1		reductase family 1,
		member C1
		(dihydrodiol
		dehydrogenase 1;
		20-alpha (3-alpha)-
1		hydroxysteroid
1 ·		dehydrogenase)
1		(AKR1C1), mRNA.
		/FEA=mRNA
		/GEN=AKR1C1
		/PROD=aldo-keto
	r	reductase family 1,
1		member
		C1(dihydrodiol
		dehydrogenase 1;
		20-alpha(3-alpha)-
	1	hydroxysteroid
 		dehydrogenase)
		/DB_XREF=gi:5453
		542
		/UG=Hs.306098
1		aldo-keto
]		reductase family 1,
		member C1
		(dihydrodiol
		dehydrogenase 1;
1		20-alpha (3-alpha)-
		hydroxysteroid
		dehydrogenase)
204151_x_at	NM_001353	/FL=gb:U05684.1

F	ia	ure	7:	a C)Or	٦ť'	d.
-	•		- 1				

Figure 7a Cont	<u>u. </u>			
	[Consensus		
	[includes		
	ì	gb:BG033593		
	1	/FEA=EST		
		/DB_XREF=gi:1242		
		6042		
	.	/DB_XREF=est:602		
		301717F1		
]	ŀ	/CLONE=IMAGE:44		
	!	03212		
		/UG=Hs.183648		
		protein tyrosine		
		phosphatase,	-	
		receptor type, f		
		polypeptide		
	İ	(PTPRF),		
	[interacting protein		
		(liprin), alpha 1		
	j	/FL=gb:NM_003626		
202065 2 24	NM_003626	.1 gb:U22816.1		ļ
202065_s_at		gb:NM_004406.1		
		/DEF=Homo		
		sapiens deleted in		
		malignant brain	·	
		tumors 1		
	, ((DMBT1),		
		transcript variant		
		1, mRNA.		
		/FEA=mRNA		
		/GEN=DMBT1		
		/PROD=deleted in		
	<u> </u>	malignant brain		
		tumors 1 isoform		
		aprecursor		
		/DB_XREF=gi:4758		
		169		
		/UG=Hs.279611		
		deleted in		
		malignant brain		
1		tumors 1		
		/FL=gb:NM_004406		
208250_s_at	NM_004406	.1	ļ	

Figure 7a Ci	3776 47.				
			Consensus		
			includes		
			gb:Al348094		
			/FEA=EST		
			/DB_XREF=gi:4085		
			300		
			/DB_XREF=est:qp6		
			1g12.x1		
			/CLONE=IMAGE:19		
			27558	:	
			/UG=Hs.90419	•	
212956_at		AB020689	KIAA0882 protein		
<u> </u>		7.502000	protein kinase,		
39313_at	PRKWNK1	AB002342	lysine deficient 1	NM_018979	Hs.184592
00010ut		7.15002012	lyonio donoione i		
			gb:AF176699.1		
			/DEF=Homo		
į			sapiens F-box		
			protein FBL4		
			mRNA, complete		
			cds. /FEA=mRNA		
			/PROD=F-box		
			protein FBL4		
			/DB XREF=gi:6103		
			636 /UG=Hs.49526		
			f-box and leucine-		
			rich repeat protein		1
			14		
			/FL=gb:AF176699.1		
			gb:AF199355.1		
209943 at		AF176699	gb:NM_012160.1		
209943_at		VE 110099	hepatic leukemia		
204754 at	HLF	Al810712	factor		Hs.250692
204/04_at	Inc	[AIO 107 12	Taciol	l	113.200032

Figure	7a	Col	nť	d.

Figure /a Co	JIILU.		,		
206467_x_at	CX3CL1	NM_003823 U84487	gb:NM_003823.1 /DEF=Homo sapiens tumor necrosis factor receptor superfamily, member 6b, decoy (TNFRSF6B), mRNA. /FEA=mRNA /GEN=TNFRSF6B /PROD=decoy receptor 3 /DB_XREF=gi:4507 584 /UG=Hs.278556 tumor necrosis factor receptor superfamily, member 6b, decoy /FL=gb:AF104419.1 gb:NM_003823.1 gb:AF134240.1 gb:AF217794.1 chemokine (C-X3-C motif) ligand 1	NM_002996	Hs.80420
823_at	CASCLI	NM_013262	gb:NM_013262.2 /DEF=Homo sapiens myosin regulatory light chain interacting protein (MIR), mRNA. /FEA=mRNA /GEN=MIR /PROD=myosin regulatory light chain interactingprotein /DB_XREF=gi:1088 0121 /UG=Hs.20072 myosin regulatory light chain interacting protein /FL=gb:AF187016.2 gb:NM_013262.2 gb:BC002860.1		HS.00420

215854_at	AU146050	ESTs	Hs.287459
210004_at	AU 140000	gb:NM_017637.1 /DEF=Homo sapiens hypothetical protein FLJ20043 (FLJ20043), mRNA. /FEA=mRNA /GEN=FLJ20043 /PROD=hypothetica I protein FLJ20043 /DB_XREF=gi:8923 050 /UG=Hs.103853 hypothetical protein FLJ20043	115.201408
	NIA 047007	/FL=gb:NM_017637	
220272_at	NM_017637	.1	
		Consensus includes gb:AL049983.1 //DEF=Homo sapiens mRNA; cDNA DKFZp564D042 (from clone DKFZp564D042). //FEA=mRNA //DB_XREF=gi:4884 234 //UG=Hs.240136 Homo sapiens mRNA; cDNA	
216595_at	AL049983	DKFZp564D042 (from clone DKFZp564D042)	

I iguie ra C	Ont G.				r
207554_x_at		NM_001060	gb:NM_001060.1 /DEF=Homo sapiens thromboxane A2 receptor (TBXA2R), mRNA. /FEA=mRNA /GEN=TBXA2R /PROD=thromboxa ne A2 receptor /DB_XREF=gi:4507 380 /UG=Hs.89887 thromboxane A2 receptor /FL=gb:NM_001060 .1 gb:D38081.1 gb:U27325.1		
47560_at	FLJ11939	Al525402	hypothetical protein FLJ11939		Hs.94229
203797_at		AF039555	gb:AF039555.1 /DEF=Homo sapiens visinin-like protein 1 (VSNL1) mRNA, complete cds. /FEA=mRNA /GEN=VSNL1 /PROD=visinin-like protein 1 /DB_XREF=gi:4104 813 /UG=Hs.2288 visinin-like 1 /FL=gb:AF039555.1 gb:NM_003385.1 gb:AB001104.1 gb:U14747.1		

Figure 7a Co	ntu.		
219263 at	NM_024539	gb:NM_024539.1 /DEF=Homo sapiens hypothetical protein FLJ23516 (FLJ23516), mRNA. /FEA=mRNA /GEN=FLJ23516 /PROD=hypothetica I protein FLJ23516 /DB_XREF=gi:1337 5696 /UG=Hs.9238 hypothetical protein FLJ23516 /FL=gb:NM_024539 .1	
2 13203_at	TAINI_024338	Consensus	
213393_at	U79290	includes gb:Al767210 /FEA=EST /DB_XREF=gi:5233 719 /DB_XREF=est:wi9 4d05.x1 /CLONE=IMAGE:24 00969 /UG=Hs.90449 Human clone 23908 mRNA sequence	
202756_s_at	NM_002081	gb:NM_002081.1 /DEF=Homo sapiens glypican 1 (GPC1), mRNA. /FEA=mRNA /GEN=GPC1 /PROD=glypican 1 precursor /DB_XREF=gi:4504 080 /UG=Hs.2699 glypican 1 /FL=gb:NM_002081	

Figure 7a Co	Jill U.		T	
203337_x_at		NM_004763	gb:NM_004763.1 /DEF=Homo sapiens integrin cytoplasmic domain-associated protein 1 (ICAP- 1A), transcript variant 1, mRNA. /FEA=mRNA /GEN=ICAP-1A /PROD=integrin cytoplasmic domain-associated protein1, isoform 1 /DB_XREF=gi:4758 577 /UG=Hs.173274 integrin cytoplasmic domain-associated protein 1 /FL=gb:AF012023.1 gb:NM_004763.1	
214277_at	COX11	Al376724	COX11 homolog, cytochrome c oxidase assembly protein (yeast)	Hs.241515
215695_s_at		U94357	Consensus includes gb:U94357.1 /DEF=Homo sapiens glycogenin-2 delta (glycogenin-2) mRNA, partial cds. /FEA=mRNA /GEN=glycogenin-2 /PROD=glycogenin-2 delta /DB_XREF=gi:2618 756 /UG=Hs.58589 glycogenin 2	

Figure 7	′a C	ont'o	J.
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Figure 7a C	ont a.				
		l '	gb:NM_004583.1		
			/DEF=Homo		
			sapiens RAB5C,		
			member RAS		
			oncogene family		
			(RAB5C), mRNA.		
			/FEA=mRNA		
			/GEN=RAB5C		
			/PROD=RAB5C,		
	1		member RAS		
			oncogene family		
			/DB_XREF=gi:4759		
			019 /UG=Hs.479		
			RAB5C, member		
			RAS oncogene		
			family		
			/FL=gb:NM_004583	-	ļ
			.1 gb:U11293.1		
			gb:U18420.1		
201140_s_at		NM 004583	gb:AF141304.1		
201170_0_00	 		heterogeneous		
			nuclear		,
			ribonucleoprotein D		
			(AU-rich element		
			RNA binding protein		
213359_at	HNRPD	W74620	1, 37kDa)		Hs.303627
210009_at	THAIR D	1000	i, orkbaj		110.000021
			gb:NM_022662.1		
			/DEF=Homo		
			sapiens meiotic		
			checkpoint		
			regulator (MCPR),		
			mRNA.		
			/FEA=mRNA		
		ļ	/GEN=MCPR		
			/PROD=meiotic		
			checkpoint		
			regulator	1	
			/DB_XREF=gi:1205		
			6970		
		1	/UG=Hs.40137		
			anaphase-		
	1			1	
1			promoting complex		
1			1; meiotic		
			1; meiotic checkpoint		
:			1; meiotic checkpoint regulator		
218575_at		NM_022662	1; meiotic checkpoint		

— ·	_	A
Licuito	· / つ	CODEA
- FRIIIF	. 10	Cont'd.
	,	

I Iguio 7 a oc	 		
	NIM 024706	gb:NM_024796.1 /DEF=Homo sapiens hypothetical protein FLJ22639 (FLJ22639), mRNA. /FEA=mRNA /GEN=FLJ22639 /PROD=hypothetica I protein FLJ22639 /DB_XREF=gi:1337 6167 /UG=Hs.157184 hypothetical protein FLJ22639 /FL=gb:NM_024796	
220399_at	NM_024796	gb:NM_004902.1 /DEF=Homo sapiens splicing factor (CC1.3) (CC1.3), mRNA. /FEA=mRNA /GEN=CC1.3 /PROD=splicing factor (CC1.3) /DB_XREF=gi:4757 925 /UG=Hs.145696 splicing factor (CC1.3) /FL=gb:L10910.1	
207941_s_at	NM_004902	gb:NM_004902.1	

Figure 7a Co	onta.			
207969_x_at	nt a.	NM_020109	gb:NM_020109.1 /DEF=Homo sapiens acrosomal vesicle protein 1 (ACRV1), transcript variant 5, mRNA. /FEA=mRNA /GEN=ACRV1 /PROD=acrosomal vesicle protein 1, isoform eprecursor /DB_XREF=gi:9955 932 /UG=Hs.169222 acrosomal vesicle protein 1 /FL=gb:NM_020109 .1 dJ781L3.1 (similar to IFITM3 (interferon induced	
			transmembrane protein 3 (1-8U))) match: proteins: Sw:Q01628 Sw:Q01629 Tr:Q9R175 Tr:Q9R176 Sw:Q91499 Sw:P26376 Tr:O88728 Sw:P13164; Human DNA sequence from clone RP4- 781L3 on chromosome 1p34.3-36.11 Contains a pseudogene similar	
216565_x_at	dJ781L3.1	AL121994	to IFITM3 (interferon inducedntransmem brane protein 3 (1- 8U)), STSs and GSSs, complete sequence.	

Figure 7a Co	one a.			
213083_at		AJ005866	Consensus includes gb:AJ005866.1 //DEF=Homo sapiens mRNA for putative Sqv-7-like protein, partial. //FEA=mRNA //PROD=Sqv-7-like protein //DB_XREF=gi:4008 516 //UG=Hs.90078 nucleotide-sugar transporter similar to C. elegans sqv-7	
207332_s_at		NM_003234	gb:NM_003234.1 /DEF=Homo sapiens transferrin receptor (p90, CD71) (TFRC), mRNA. /FEA=mRNA /GEN=TFRC /PROD=transferrin receptor (p90, CD71) /DB_XREF=gi:4507 456 /UG=Hs.77356 transferrin receptor (p90, CD71) /FL=gb:NM_003234 .1	
207332_s_at		NM_003234	vingless-type	
			MMTV integration site family, member	
71933_at	WNT6	Al218134	6	 Hs.29764

Figure /a Co	AILU.		I-I-NIA 004500 4		
			gb:NM_001500.1		
			/DEF=Homo		
			sapiens GDP-		
			mannose 4,6-		
			dehydratase		
			(GMDS), mRNA.		
			/FEA=mRNA		
			/GEN=GMDS		
			/PROD=GDP-		•
			1		
			mannose 4,6-		
			dehydratase		
	•		/DB_XREF=gi:4504	•	
			030		
			/UG=Hs.105435		
			GDP-mannose 4,6-		
			dehydratase		
			/FL=gb:BC000117.1		
			gb:AF042377.1		
204875 s at		NM 001500	gb:NM_001500.1		
204073_s_at		14101_00 1000	gb.14141_00 1000.1		
			Consensus		
Ì			includes		
			i		
			gb:AB014511.1		
			/DEF=Homo		
			sapiens mRNA for		
			KIAA0611 protein,		
			partial cds.		
			/FEA=mRNA		
			/GEN=KIAA0611		
			/PROD=KIAA0611		
	1		protein		
			/DB_XREF=gi:3327		
			035 /UG=Hs.70604		
			ATPase, Class II,		
212062 04		AB014511	type 9A		
212062_at	FLJ20288	AU160676	FLJ20288 protein		Hs.84045
208772_at	FLJZUZ00	100076	Consensus		113.04043
			includes		
			gb:AK025663.1		
			/DEF=Homo		
1			sapiens cDNA:		
			FLJ22010 fis,		
			clone HEP07134.		
			/FEA=mRNA		
			/DB_XREF=gi:1043		
			8253		
			/UG=Hs.285848		
216399_s_at		AK025663	KIAA1454 protein		
2 10099_3_at	L	1, 11020000	Transcrator biotom	l <u></u>	11

Application of: Liew, et. al. Our Docket #: 4231/2042 Figure 7a Cont'd.

Figure 7a Co	nit u.				
212168_at		AB018308	Consensus includes gb:AL514547 /FEA=EST /DB_XREF=gi:1277 8041 /DB_XREF=est:AL5 14547 /CLONE=CL0BB00 4ZC07 (3 prime) /UG=Hs.180895 putative brain nuclearly-targeted protein		
216268_s_at		U77914	Consensus includes gb:U77914.1 /DEF=Human soluble protein Jagged mRNA, partial cds. /FEA=mRNA /PROD=soluble protein Jagged /DB_XREF=gi:1684 889 /UG=Hs.91143 jagged 1 (Alagille syndrome)		
			gb:NM_001494.2 /DEF=Homo sapiens GDP dissociation inhibitor 2 (GDI2), mRNA. /FEA=mRNA /GEN=GDI2 /PROD=GDP dissociation inhibitor 2 /DB_XREF=gi:6598 322 /UG=Hs.56845 GDP dissociation inhibitor 2 /FL=gb:BC005145.1 gb:D13988.1		
200009_at		NM_001494	gb:NM_001494.2	<u> </u>	

Figure /a Co	Jit G.				
218351_at		NM_017845	gb:NM_017845.1 /DEF=Homo sapiens hypothetical protein FLJ20502 (FLJ20502), mRNA. /FEA=mRNA /GEN=FLJ20502 /PROD=hypothetica I protein FLJ20502 /DB_XREF=gi:8923 457 /UG=Hs.23956 hypothetical protein FLJ20502 /FL=gb:AF182421.1 gb:NM_017845.1		
			gb:NM_024561.1 /DEF=Homo sapiens hypothetical protein FLJ22054 (FLJ22054), mRNA. /FEA=mRNA /GEN=FLJ22054 /PROD=hypothetica I protein FLJ22054 /DB_XREF=gi:1337 5728 /UG=Hs.13277 hypothetical protein FLJ22054 /FL=gb:NM_024561	•	
219378_at		NM_024561	.1 insulin induced		
201626_at	INSIG1	BE300521	gene 1		Hs.56205
213300_at	KIAA0404	AW168132	KIAA0404 protein		Hs.105850
201160_s_at	CSDA	AL556190	cold shock domain protein A		Hs.198726

Figure 7a Co	ont a.			
208328_s_at		NM_005587	gb:NM_005587.1 /DEF=Homo sapiens MADS box transcription enhancer factor 2, polypeptide A (myocyte enhancer factor 2A) (MEF2A), mRNA. /FEA=mRNA /GEN=MEF2A /PROD=MADS box transcription enhancer factor 2,polypeptide A (myocyte enhancer factor 2A) /DB_XREF=gi:5031 906 /UG=Hs.182280 MADS box transcription enhancer factor 2, polypeptide A (myocyte enhancer factor 2A) /FL=gb:NM_005587 .1	
219467_at		NM_017676	gb:NM_017676.1 /DEF=Homo sapiens hypothetical protein FLJ20125 (FLJ20125), mRNA. /FEA=mRNA /GEN=FLJ20125 /PROD=hypothetica I protein FLJ20125 /DB_XREF=gi:8923 123 /UG=Hs.24088 hypothetical protein FLJ20125 /FL=gb:NM_017676 .1	

			B-cell translocation	i
	1		1	l l
	i		gene 1, anti-	1
200920_s_at	BTG1	AL535380	proliferative	Hs.77054
200920 <u>s</u> at	БІСІ	ALSSSSOO	gb:NM_021732.1 /DEF=Homo sapiens hypothetical protein PP5395 (PP5395), mRNA. /FEA=mRNA /GEN=PP5395 /PROD=hypothetica I protein PP5395 /DB_XREF=gi:1111 9427 /UG=Hs.23918 hypothetical protein PP5395	113.7700-4
			/FL=gb:NM_021732	ŀ
			.1 gb:AF241786.1	
210621 -		NM_021732	gb:BC000877.1	
218631_at 208655 at	CCNI	BG530368	cyclin I	Hs.79933
200000_at	CCIVI	DG330300	protein tyrosine	113.73333
			phosphatase type	
000045+	DTD4AO	DE705404	1' ' ' ' ' '	Hs.82911
208615_s_at	PTP4A2	BF795101	IVA, member 2	ПS.02911
			ATP synthase, H+	1
			transporting,	
			mitochondrial F1	
l			complex, gamma	11- 455400
213366_x_at	ATP5C1	AV711183	polypeptide 1	Hs.155433
208611_s_at		U83867	gb:U83867.1 /DEF=Human alpha II spectrin mRNA, complete cds. /FEA=mRNA /PROD=alpha II spectrin /DB_XREF=gi:1805 279 /UG=Hs.77196 spectrin, alpha, non-erythrocytic 1 (alpha-fodrin) /FL=gb:J05243.1 gb:U83867.1 gb:NM_003127.1	

Figure 7a Co	nt'd.		
219443 at	NM 017	gb:NM_017714.1 /DEF=Homo sapiens hypothetical protein FLJ20212 (FLJ20212), mRNA. /FEA=mRNA /GEN=FLJ20212 /PROD=hypothetica I protein FLJ20212 /DB_XREF=gi:8923 201 /UG=Hs.88367 hypothetical protein FLJ20212 /FL=gb:NM_017714	
219443_at	NM_0177	includes gb:AL031778 /DEF=Human DNA sequence from clone 34B21 on chromosome 6p12.1-21.1. Contains part of a gene for a novel protein with ZU5 domain similar to part of Tight Junction Protein ZO1 (TJP1) and UNC5 Homologs, the gene for a novel BZRP (peripheral benzodiazapine	-
213322_at	AL03177	/FEA=mRNA_2 /DB_XREF=gi:4153 958 /UG=Hs.183056 Human DNA sequence from clone 34B21 on chromosome 6p12.1-21.1. Contains part of a gene for a novel protein with ZU5 domain similar to	

Figure /a Co	ntu.			
		gb:NM_022152.	1	
		/DEF=Homo		
		sapiens PP120	ļ 	
		protein (PP1201	l),	
İ		mRNA.	"	
		/FEA=mRNA		
		/GEN=PP1201		
		/PROD=PP1201		
		protein		
		/DB_XREF=gi:1	154	
		5897	İ	
		/UG=Hs.184052	•	
		PP1201 protein		
		/FL=gb:NM_022	152	
217730_at	NM_C	22152 .1	ŀ	
=				
		Consensus		
· ·		includes		
		gb:X76061.1		
		/DEF=H.sapiens		
		p130 mRNA fo		
		130K protein.	'	
		/FEA=mRNA		
		/GEN=p130		
		/PROD=130K		
		protein		
		/DB_XREF=gi:4		
		30 /UG=Hs.793	62	
		retinoblastoma-l	ike	
		2 (p130)		
		/FL=gb:NM_005	611	
212331_at	l NM (05611 .1		
		Consensus		
}		includes		
		gb:AB014593.1		
		/DEF=Homo		
		sapiens mRNA	for	
		KIAA0693 prote		
		partial cds.	·"',	
		/FEA=mRNA		
		•	,	
		/GEN=KIAA069	1	
		/PROD=KIAA06	93	
		protein		1
		/DB_XREF=gi:3	327	
		199		
		/UG=Hs.154429	+ 1	
213140_s_at	AB01	4593 KIAA0693 prote	ein	
		1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	<u>4</u>	

Figure /a Co	m. u.		,	
213133_s_at		BE908931	ESTs, Highly similar to GCHUH glycine cleavage system protein H precursor human [H.sapiens]	Hs.356054
200789_at		NM_001398	gb:NM_001398.1 /DEF=Homo sapiens enoyl Coenzyme A hydratase 1, peroxisomal (ECH1), mRNA. /FEA=mRNA /GEN=ECH1 /PROD=peroxisoma I enoyl-coenzyme A hydratase- likeprotein /DB_XREF=gi:4503 446 /UG=Hs.196176 enoyl Coenzyme A hydratase 1, peroxisomal /FL=gb:NM_001398 .1 gb:U16660.1	
217168_s_at		AF217990	Consensus includes gb:AF217990.1 /DEF=Homo sapiens clone PP1722 unknown mRNA. /FEA=mRNA /PROD=unknown /DB_XREF=gi:1044 1910 /UG=Hs.146393 homocysteine- inducible, endoplasmic reticulum stress- inducible, ubiquitin- like domain member 1	

Figure	7a	Cont'd.

Figure /a Co	iii G.			
211168_s_at		D86988	gb:D86988.1 /DEF=Human mRNA for KIAA0221 gene, complete cds. /FEA=mRNA /GEN=KIAA0221 /PROD=KIAA0221 /DB_XREF=gi:1944 406 /UG=Hs.12719 regulator of nonsense transcripts 1 /FL=gb:D86988.1	
201200_at		NM_003851	gb:NM_003851.1 /DEF=Homo sapiens cellular repressor of E1A- stimulated genes (CREG), mRNA. /FEA=mRNA /GEN=CREG /PROD=cellular repressor of E1A- stimulated genes /DB_XREF=gi:4503 036 /UG=Hs.5710 cellular repressor of E1A-stimulated genes /FL=gb:AF084523.1 gb:NM_003851.1	
211378_x_at		BC001224	gb:BC001224.1 /DEF=Homo sapiens, clone MGC:982, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:982) /DB_XREF=gi:1265 4762 /UG=Hs.267690 KIAA1228 protein /FL=gb:BC001224.1	

Application of: Liew, et. al. Our Docket #: 4231/2042 Figure 7a Cont'd.

Tigare 74 Co	 			
205911 at	NM_000316	gb:NM_000316.1 /DEF=Homo sapiens parathyroid hormone receptor 1 (PTHR1), mRNA. /FEA=mRNA /GEN=PTHR1 /PROD=parathyroid hormone receptor 1 /DB_XREF=gi:4506 270 /UG=Hs.1019 parathyroid hormone receptor 1 /FL=gb:L04308.1 gb:NM_000316.1 gb:U17418.1		
204908_s_at	NM_005178	gb:NM_005178.1 /DEF=Homo sapiens B-cell CLLlymphoma 3 (BCL3), mRNA. /FEA=mRNA /GEN=BCL3 /PROD=B-cell CLLlymphoma 3 /DB_XREF=gi:4885 086 /UG=Hs.31210 B-cell CLLlymphoma 3 /FL=gb:M31732.1 gb:NM_005178.1		

Т.	abiNIM 000000 4		
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1.			
	•		
B.			
	•		
	-		
;	352 /UG=Hs.771		
l,	phosphorylase,		
[9	glycogen; liver		
]((Hers disease,		
L'	•		
L'	-		
1_002863	gb:NM_002863.1		
	~h.NIM 000206 4		<u> </u>
	•		
l'			
1			
	•		
			·
	.1 gb:U13665.1		
	1_002863	gb:NM_000396.1 /DEF=Homo sapiens cathepsin K (pycnodysostosis) (CTSK), mRNA. /FEA=mRNA /GEN=CTSK /PROD=cathepsin K (pycnodysostosis) /DB_XREF=gi:4503 150 /UG=Hs.83942 cathepsin K (pycnodysostosis) /FL=gb:NM_000396	/DEF=Homo sapiens phosphorylase, glycogen; liver (Hers disease, glycogen storage disease type VI) (PYGL), mRNA. /FEA=mRNA /GEN=PYGL /PROD=phosphoryl ase, glycogen; liver (Hers disease, glycogen storage disease type VI) /DB_XREF=gi:4506 352 /UG=Hs.771 phosphorylase, glycogen; liver (Hers disease, glycogen; liver (Hers disease, glycogen; liver (Hers disease, glycogen; liver (Hers disease, glycogen; liver (Hers disease, glycogen; liver (Hers disease) disease type VI) /FL=gb:M14636.1 gb:AF066858.1 gb:AF046785.1 gb:AF046785.1 gb:NM_002863.1 gb:NM_000396.1 /DEF=Homo sapiens cathepsin K (pycnodysostosis) (CTSK), mRNA. /FEA=mRNA /GEN=CTSK /PROD=cathepsin K (pycnodysostosis) /DB_XREF=gi:4503 150 /UG=Hs.83942 cathepsin K (pycnodysostosis) /FL=gb:NM_000396

rigule la Co				
214790_at		AK001406	Consensus includes gb:AK001406.1 /DEF=Homo sapiens cDNA FLJ10544 fis, clone NT2RP2001601, highly similar to Homo sapiens mRNA for KIAA0797 protein. /FEA=mRNA /DB_XREF=gi:7022 642 /UG=Hs.27197 SUMO-1-specific protease	
			gb:BC003105.1 /DEF=Homo sapiens, Similar to protein tyrosine phosphatase type IVA, member 3, clone MGC:1950, mRNA, complete cds. /FEA=mRNA /PROD=Similar to protein tyrosine phosphatase typeIVA, member 3 /DB_XREF=gi:1311 1874 /UG=Hs.43666 protein tyrosine phosphatase type	
209695_at		BC003105	IVA, member 3 /FL=gb:BC003105.1	
203030_at		50003103	far upstream	
212847_at	FUBP1	AL036840	element (FUSE) binding protein 1	Hs.118962
214022_s_at	IFITM1	AA749101	interferon induced transmembrane protein 1 (9-27)	Hs.146360

Figure	7a	Cont'd.	
90.0	, .	O O I I C G .	

	 ·		
202393 s_at	NM 005655	gb:NM_005655.1 /DEF=Homo sapiens TGFB inducible early growth response (TIEG), mRNA. /FEA=mRNA /GEN=TIEG /PROD=TGFB inducible early growth response /DB_XREF=gi:5032 176 /UG=Hs.82173 TGFB inducible early growth response /FL=gb:U21847.1 gb:NM_005655.1	
203786 s at	NM 003287	gb:NM_003287.1 /DEF=Homo sapiens tumor protein D52-like 1 (TPD52L1), mRNA. /FEA=mRNA /GEN=TPD52L1 /PROD=tumor protein D52-like 1 /DB_XREF=gi:4507 640 /UG=Hs.16611 tumor protein D52-like 1 /FL=gb:U44427.1 gb:NM_003287.1	

Figure /a Co	nitu.			
218152_at		NM 018200	gb:NM_018200.1 /DEF=Homo sapiens high- mobility group 20A (HMG20A), mRNA. /FEA=mRNA /GEN=HMG20A /PROD=high- mobility group 20A /DB_XREF=gi:8922 632 /UG=Hs.69594 high-mobility group 20A /FL=gb:AF146222.1 gb:NM_018200.1	
			gb:AL136548.1 /DEF=Homo sapiens mRNA; cDNA DKFZp761G18121 (from clone DKFZp761G18121); complete cds. /FEA=mRNA /GEN=DKFZp761G 18121 /PROD=hypothetica I protein /DB_XREF=gi:1205 2731 /UG=Hs.260180 Homo sapiens mRNA; cDNA DKFZp761G18121 (from clone DKFZp761G18121); complete cds	
221626_at		AL136548	/FL=gb:AL136548.1	

Figure 7a CC	nicu.				
			Consensus		ļ
		1	includes		
			gb:NM_000753.1		
			/DEF=Homo		
			sapiens 2,3-cyclic		
			nucleotide 3		
			phosphodiesterase		
		ŀ	(CNP), mRNA.		
			/FEA=CDS		
		·	/GEN=CNP		
			/PROD=2,3-cyclic		
			nucleotide 3		
	:		phosphodiesterase		
			/DB_XREF=gi:4502		į
			924		[
			/UG=Hs.150741		
			2,3-cyclic		
			nucleotide 3		
		İ	phosphodiesterase		
			/FL=gb:NM_000753		·
214582_at		NM_000753	.1		
			Human clone		
			137308 mRNA,		
214657_s_at		AU134977	partial cds		Hs.408944
-					
			gb:NM_021203.1		
		1	/DEF=Homo		
			sapiens APMCF1		
			protein (APMCF1),		
		1	mRNA.		
			/FEA=mRNA		
			/GEN=APMCF1		
			/PROD=APMCF1		
			protein		
			/DB_XREF=gi:1086		
			4014		
			/UG=Hs.12152		
			APMCF1 protein		
			/FL=gb:NM_021203		
218140_x_at		NM_021203	.1 gb:AF141882.1		
	I	LIAIM OF ITOS	1. i gb./\li i= 1002. i	I	l B

					
			gb:NM_012328.1		
			/DEF=Homo		
			sapiens		
			microvascular		
			endothelial		
			differentiation gene	-	
			1 (MDG1), mRNA.	!	
			/FEA=mRNA	-	
			/GEN=MDG1		
			/PROD=microvascu		
			lar endothelial differentiation		
			gene1		
	ļ		/DB_XREF=gi:9558		
			754 /UG=Hs.6790		
			DnaJ (Hsp40)		
			homolog, subfamily		
			B, member 9		
			/FL=gb:AF083247.1		
			gb:AL080081.1		
			gb:AB026908.1		
202843_at		NM_012328	gb:NM_012328.1		
			heterogeneous		
		:	nuclear		
			ribonucleoprotein D		
			(AU-rich element		
224400	LINDDD	DC490044	RNA binding protein		Un 202627
221480_at	HNRPD	BG180941	1, 37kDa) polymerase (RNA)		Hs.303627
			II (DNA directed)	1	
			polypeptide K,		
202634_at	POLR2K	AL558030	7.0kDa		Hs.351475

Figure 7a Co	ont a.	·		
			gb:NM_006979.1	
			/DEF=Homo	
			sapiens HLA class	
			II region	
			expressed gene	
			KE4 (HKE4),	
			mRNA.	
			/FEA=mRNA	
			/GEN=HKE4	
			/PROD=HLA class	
			II region	
			expressed gene	
			KE4	
			/DB_XREF=gi:5901	
			935	
			/UG=Hs.278721	
			HLA class II	
			region expressed	
			gene KE4	
	1		/FL=gb:D82060.1	
202667_s_at		NM_006979	gb:NM_006979.1	
1				
			gb:NM_002890.1	
			/DEF=Homo	:
			sapiens RAS p21	
			protein activator	
			(GTPase activating	
			protein) 1	
			(RASA1), transcript	
			variant 1, mRNA.	
			/FEA=mRNA	
	ĺ		/GEN=RASA1	
			/PROD=RAS p21	
			protein activator 1,	
			lisoform 1	
			1.00.0	
			/DB_XREF=gi:4506	
	1		430 /UG=Hs.758	1
			RAS p21 protein	
			activator (GTPase	
			activating protein)	
			1 /FL=gb:M23379.1	
202677_at		NM_002890	gb:NM_002890.1	
212579 at	KIAA0650	AA868754	KIAA0650 protein	Hs.8118

riguic 7a Oc			,	
221435_x_at		NM_031207	gb:NM_031207.1 /DEF=Homo sapiens hypothetical protein HT036 (HT036), mRNA. /FEA=CDS /GEN=HT036 /PROD=hypothetica I protein HT036 /DB_XREF=gi:1365 4271 /FL=gb:NM_031207	
203404_at		NM_014782	gb:NM_014782.1 /DEF=Homo sapiens KIAA0512 gene product (KIAA0512), mRNA. /FEA=mRNA /GEN=KIAA0512 /PROD=KIAA0512 gene product /DB_XREF=gi:7662 161 /UG=Hs.48924 KIAA0512 gene product; ALEX2 /FL=gb:AB011084.1 gb:NM_014782.1	
221778_at	KIAA1718	BE217882	KIAA1718 protein	Hs.222707

Application of: Liew, et. al. Our Docket #: 4231/2042 Figure 7a Cont'd.

rigule /a Co	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	· 	
209430_at	AJ00	Consensus includes gb:AJ001017.2 /DEF=Homo sapiens partial mRNA for TBP- associated factor 170 (TAFII170) /FEA=mRNA /GEN=TAFII170 /PROD=TBP associated factor /DB_XREF=gi:7018 281 /UG=Hs.180930 TBP-associated factor 172 /FL=gb:AF038362.1	
		gb:D26121.1 /DEF=Human mRNA for ZFM1 protein alternatively spliced product, complete cds. /FEA=mRNA /PROD=ZFM1 protein, alternatively spliced product /DB_XREF=gi:7859 98 /UG=Hs.169303 Human mRNA for ZFM1 protein alternatively spliced product, complete cds	
210172_at	D26	121 /FL=gb:D26121.1	

Figure 7a Co	Jit G.			
			gb:NM_005228.1 /DEF=Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v- erb-b) oncogene homolog) (EGFR), mRNA. /FEA=mRNA /GEN=EGFR /PROD=epidermal growth factor receptor (avianerythroblastic leukemia viral (v- erb-b) oncogene homolog) /DB_XREF=gi:4885 198 /UG=Hs.77432 epidermal growth factor receptor (avian erythroblastic leukemia viral (v- erb-b) oncogene homolog) /FL=gb:NM_005228	
201984_s_at		NM_005228	.1	!
			GrpE-like protein	
212434_at	HMGE	AL542571	cochaperone gb:NM_001856.1	 Hs.151903
			/DEF=Homo sapiens collagen, type XVI, alpha 1 (COL16A1), mRNA. /FEA=mRNA /GEN=COL16A1 /PROD=collagen, type XVI, alpha 1 /DB_XREF=gi:1138 6158 /UG=Hs.26208 collagen, type XVI, alpha 1 /FL=gb:NM_001856	
204345_at		NM_001856	.1 gb:M92642.1	

Figure 7a Co	nt'a.	····		
Figure 7a Co	nra.		gb:AF029750.1 IDEF=Homo sapiens tapasin (NGS-17) mRNA, complete cds. IFEA=mRNA IGEN=NGS-17 IPROD=tapasin IDB_XREF=gi:2587 IUG=Hs.179600 ITAP binding protein (tapasin) IFL=gb:AF314222.1 Igb:AF009510.1	
208829_at			gb:AB010639.1 gb:NM_003190.1	
208863_s_at			gb:M72709.1 /DEF=Human alternative splicing factor mRNA, complete cds. /FEA=mRNA /DB_XREF=gi:1790 /3 /UG=Hs.73737 splicing factor, arginineserine-rich 1 (splicing factor 2, alternate splicing factor) /FL=gb:M72709.1	
240004			gb:NM_017851.1 /DEF=Homo sapiens hypothetical protein FLJ20509 (FLJ20509), mRNA. /FEA=mRNA /GEN=FLJ20509 /PROD=hypothetica I protein FLJ20509 /DB_XREF=gi:8923 470 /UG=Hs.30634 hypothetical protein FLJ20509 /FL=gb:NM_017851	
219034_at	TININI	_017851 .	.1	

Figure /a Co	iit d.		
	NM_00	gb:NM_000142.2 /DEF=Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3), transcript variant 1, mRNA. /FEA=mRNA /GEN=FGFR3 /PROD=fibroblast growth factor receptor 3, isoform 1precursor /DB_XREF=gi:1311 2046 /UG=Hs.1420 fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) /FL=gb:NM_000142 20142 .2 gb:M58051.1	
204379_s_at		gb:NM_001560.1 /DEF=Homo sapiens interleukin 13 receptor, alpha 1 (IL13RA1), mRNA. /FEA=mRNA /GEN=IL13RA1 /PROD=interleukin 13 receptor, alpha 1 /DB_XREF=gi:4504 646 /UG=Hs.285115 interleukin 13 receptor, alpha 1 /FL=gb:NM_001560	
201887_at	NM_00	ד.ד gb:U81379.3	

Application of: Liew, et. al. Our Docket #: 4231/2042 Figure 7a Cont'd.

I igure ra oc	Jiic G.				
209200_at	MEF2C	N22468	MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C) gb:NM_017572.1 /DEF=Homo		Hs.78995
218205_s_at		NM 017572	sapiens G protein-coupled receptor kinase 7 (GPRK7), mRNA. /FEA=mRNA /GEN=GPRK7 /PROD=G protein-coupled receptor kinase 7 /DB_XREF=gi:9994 196 /UG=Hs.261828 G protein-coupled receptor kinase 7 /FL=gb:AF237776.1 gb:AF125532.1 gb:NM 017572.1		
222279 at	HLA-F	Al669379	major histocompatibility complex, class I, F		Hs.377850
215191 at	ILLAST	AW836210	ESTs, Moderately similar to hypothetical protein FLJ20489 [Homo sapiens] [H.sapiens]		Hs.387947
[210191_at	I	7.44000210	III I.Supiciis	l	11.13.007.077

Figure 7a CC	iii u.		,	
219073_s_at 208962_s_at	FADS1	NM_017784 BE540552	gb:NM_017784.1 /DEF=Homo sapiens hypothetical protein FLJ20363 (FLJ20363), mRNA. /FEA=mRNA /GEN=FLJ20363 /PROD=hypothetica I protein FLJ20363 /DB_XREF=gi:8923 336 /UG=Hs.321622 hypothetical protein FLJ20363 /FL=gb:BC003168.1 gb:NM_017784.1 fatty acid desaturase 1 gb:NM_017784.1 fatty acid desaturase 1 gb:NM_006113.2 /DEF=Homo sapiens vav 3 oncogene (VAV3), mRNA. /FEA=mRNA /GEN=VAV3 /PROD=vav 3 oncogene /DB_XREF=gi:7262 390 /UG=Hs.267659 vav 3 oncogene	Hs.132898
			vav 3 oncogene /FL=gb:AF067817.1	

		Consensus includes gb:AW612311 /FEA=EST /DB_XREF=gi:7317 497 /DB_XREF=est:hg9 5e07.x1 /CLONE=IMAGE:29 53380 /UG=Hs.306088 v-crk avian sarcoma virus CT10 oncogene homolog /FL=gb:D10656.1 gb:NM_016823.1		
	AF119855	PRO1847 /FL=gb:AF119855.1		
BRD4	BF718610	bromodomain containing 4		Hs.278675
	NM_005509	gb:NM_005509.2 /DEF=Homo sapiens Dmx-like 1 (DMXL1), mRNA. /FEA=mRNA /GEN=DMXL1 /PROD=Dmx-like 1 /DB_XREF=gi:9961 348 /UG=Hs.181042 Dmx-like 1		
PDE4DIP	AI821791	4D interacting protein (myomegalin)		Hs.265848
	3RD4	AF119855 BF718610 NM_005509	includes gb:AW612311 /FEA=EST /DB_XREF=gi:7317 497 /DB_XREF=est:hg9 5e07.x1 /CLONE=IMAGE:29 53380 /UG=Hs.306088 v- crk avian sarcoma virus CT10 oncogene homolog /FL=gb:D10656.1 NM_016823 gb:NM_016823.1 gb:AF119855.1 /DEF=Homo sapiens PRO1847 mRNA, complete cds. /FEA=mRNA /PROD=PRO1847 //DB_XREF=gi:7770 146 /UG=Hs.285196 hypothetical protein PRO1847 AF119855 /FL=gb:AF119855.1 bromodomain containing 4 gb:NM_005509.2 //DEF=Homo sapiens Dmx-like 1 (DMXL1), mRNA. //FEA=mRNA //GEN=DMXL1 //PROD=Dmx-like 1 //DB_XREF=gi:9961 348 /UG=Hs.181042 Dmx-like 1 //FL=gb:NM_005509 NM_005509 2 phosphodiesterase 4D interacting protein	includes gb:AW612311 //FEA=EST //DB_XREF=gi:7317 497 //DB_XREF=est:hg9 5e07.x1 //CLONE=IMAGE:29 53380 //UG=Hs.306088 v- crk avian sarcoma virus CT10 oncogene homolog //FL=gb:D10656.1 gb:NM_016823.1 gb:AF119855.1 //DEF=Homo sapiens PRO1847 mRNA, complete cds. //FEA=mRNA //PROD=PRO1847 //DB_XREF=gi:7770 146 //UG=Hs.285196 hypothetical protein PRO1847 AF119855 //FL=gb:AF119855.1 srD4 BF718610 gb:NM_005509.2 //DEF=Homo sapiens Dmx-like 1 (DMXL1), mRNA, //FEA=mRNA //GEN=DMXL1 //PROD=Dmx-like 1 //DB_XREF=gi:9961 348 //UG=Hs.181042 Dmx-like 1 //DB_XREF=gi:9961 348 //UG=Hs.181042 Dmx-like 1 //FL=gb:NM_005509 2 phosphodiesterase 4D interacting protein

Application of: Liew, et. al. Our Docket #: 4231/2042 Figure 7a Cont'd.

NM 000532	propionyl Coenzyme A carboxylase, beta polypeptide		
	Consensus includes gb:AW511135 /FEA=EST /DB_XREF=gi:7149 213		
AF191654	3g08.x1 /CLONE=IMAGE:29 12318 /UG=Hs.92381 nudix (nucleoside diphosphate linked moiety X)-type		
	NM_000532 AF191654	includes gb:NM_000532.1 /DEF=Homo sapiens propionyl Coenzyme A carboxylase, beta polypeptide (PCCB), nuclear gene encoding mitochondrial protein, mRNA. /FEA=CDS /GEN=PCCB /PROD=propionyl Coenzyme A carboxylase, betapolypeptide /DB_XREF=gi:4557 043 /UG=Hs.63788 propionyl Coenzyme A carboxylase, beta polypeptide /FL=gb:NM_000532 NM_000532 I Consensus includes gb:AW511135 /FEA=EST /DB_XREF=gi:7149 213 /DB_XREF=gi:7149 213 /DB_XREF=est:hd4 3g08.x1 /CLONE=IMAGE:29 12318 /UG=Hs.92381 nudix (nucleoside diphosphate linked moiety X)-type	includes gb:NM_000532.1 //DEF=Homo sapiens propionyl Coenzyme A carboxylase, beta polypeptide (PCCB), nuclear gene encoding mitochondrial protein, mRNA. //FEA=CDS //GEN=PCCB //PROD=propionyl Coenzyme A carboxylase, betapolypeptide //DB_XREF=gi:4557 043 /UG=Hs.63788 propionyl Coenzyme A carboxylase, beta polypeptide //FL=gb:NM_000532 .1 Consensus includes gb:AW511135 //FEA=EST //DB_XREF=gi:7149 213 //DB_XREF=est:hd4 3g08.x1 //CLONE=IMAGE:29 12318 //UG=Hs.92381 nudix (nucleoside diphosphate linked moiety X)-type

Figure 1a Cor	it d.		
217975 at	NM 016303	gb:NM_016303.1 /DEF=Homo sapiens pp21 homolog (LOC51186), mRNA. /FEA=mRNA /GEN=LOC51186 /PROD=pp21 homolog /DB_XREF=gi:1004 7099 /UG=Hs.15984 pp21 homolog /FL=gb:NM_016303 .1 gb:AF125535.1	
		J	
		gb:NM_024329.1 /DEF=Homo sapiens hypothetical protein MGC4342 (MGC4342), mRNA. /FEA=mRNA /GEN=MGC4342 /PROD=hypothetica I protein MGC4342 /DB_XREF=gi:1344 3015 /UG=Hs.301342 hypothetical protein	
247002 - 01	NIM 024220	MGC4342 /FL=gb:BC003033.1 gb:NM_024329.1	,
217992_s_at	NM_024329	[gb.14101_024329.1	

nica.				
	NIM 012228	gb:NM_013238.1 /DEF=Homo sapiens DNAJ domain-containing (MCJ), mRNA. /FEA=mRNA /GEN=MCJ /PROD=DNAJ domain-containing /DB_XREF=gi:7019 452 /UG=Hs.279884 DNAJ domain-containing /FL=gb:AF126743.1		
	NM_013238			
		/DEF=Homo sapiens clone HQ0310 PRO0310p1 (LOC51203), mRNA. /FEA=mRNA /GEN=LOC51203 /PROD=clone HQ0310 PRO0310p1 /DB_XREF=gi:7705 950 /UG=Hs.279905 clone HQ0310 PRO0310p1 /FL=gb:AF305711.1 gb:BC001308.1 gb:AF290612.1		
	NM 016359	1 ~		
	10.10000			
MGC11308	BF690150	MGC11308		Hs.19210
		NM_016359	gb:NM_013238.1 /DEF=Homo sapiens DNAJ domain-containing (MCJ), mRNA. /FEA=mRNA /GEN=MCJ /PROD=DNAJ domain-containing /DB_XREF=gi:7019 452 /UG=Hs.279884 DNAJ domain- containing /FL=gb:AF126743.1 NM_013238 gb:NM_013238.1 gb:NM_016359.1 /DEF=Homo sapiens clone HQ0310 PRO0310p1 (LOC51203), mRNA. /FEA=mRNA /GEN=LOC51203 /PROD=clone HQ0310 PRO0310p1 /DB_XREF=gi:7705 950 /UG=Hs.279905 clone HQ0310 PRO0310p1 /FL=gb:AF305711.1 gb:BC001308.1 gb:AF290612.1 gb:AF090915.1 lypothetical protein	gb:NM_013238.1 //DEF=Homo sapiens DNAJ domain-containing (MCJ), mRNA. //FEA=mRNA //GEN=MCJ //PROD=DNAJ domain-containing //DB_XREF=gi:7019 452 //UG=Hs.279884 DNAJ domain- containing //FL=gb:AF126743.1 yb:NM_013238.1 gb:NM_013238.1 gb:NM_016359.1 //DEF=Homo sapiens clone HQ0310 PRO0310p1 (LOC51203), mRNA. //FEA=mRNA //GEN=LOC51203 //PROD=clone HQ0310 PRO0310p1 //DB_XREF=gi:7705 950 //UG=Hs.279905 clone HQ0310 PRO0310p1 //DB_XREF=gi:7705 950 //UG=Hs.279905 clone HQ0310 PRO0310p1 //FL=gb:AF305711.1 gb:BC001308.1 gb:AF290612.1 gb:AF290612.1 gb:AF090915.1 NM_016359 hypothetical protein

Figure	7a	Cont'd.
94.0	. ~	O O · · · · · · · · · · · · · · · · · · ·

	nt'd.		
216484_x_at	L24521	Consensus includes gb:L24521.1 /DEF=Human transformation- related protein mRNA, 3 end. /FEA=mRNA /PROD=transformat ion-related protein /DB_XREF=gi:4034 59 /UG=Hs.300705 Human transformation- related protein mRNA, 3 end	
218101_s_at	NM_004549	gb:NM_004549.1 //DEF=Homo sapiens NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2 (14.5kD, B14.5b) (NDUFC2), mRNA. //FEA=mRNA //GEN=NDUFC2 //PROD=NADH dehydrogenase (ubiquinone) 1, subcomplexunknow n, 2 (14.5kD, B14.5b) //DB_XREF=gi:4758 783 //UG=Hs.193313 NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2 (14.5kD, B14.5b) //FL=gb:AF087659.1 gb:NM_004549.1	

Figure 7a CC	THE G.				[· 1
217947 at		NM 017801	gb:NM_017801.1 /DEF=Homo sapiens hypothetical protein FLJ20396 (FLJ20396), mRNA. /FEA=mRNA /GEN=FLJ20396 /PROD=hypothetica I protein FLJ20396 /DB_XREF=gi:8923 369 /UG=Hs.283685 hypothetical protein FLJ20396 /FL=gb:BC002797.1 gb:NM_017801.1	·	
217950_at		NM_015953	gb:NM_015953.1 /DEF=Homo sapiens CGI-25 protein (LOC51070), mRNA. /FEA=mRNA /GEN=LOC51070 /PROD=CGI-25 protein /DB_XREF=gi:7705 715 /UG=Hs.7236 CGI-25 protein /FL=gb:AF132959.1 gb:NM_015953.1		
			tubulin, alpha,		11- 224040
212639_x_at	K-ALPHA-1	AL581768	ubiquitous		Hs.334842
213274_s_at	CTSB	BE875786	cathepsin B		Hs.297939
213278_at	MTMR9	AW014788	myotubularin related protein 9		Hs.48802

I iguie la Ci	One G.			
218049_s_at		NM_014078	gb:NM_014078.1 /DEF=Homo sapiens L13 protein (L13), mRNA. /FEA=mRNA /GEN=L13 /PROD=L13 protein /DB_XREF=gi:7662 495 /UG=Hs.43946 L13 protein /FL=gb:AF112214.1 gb:NM_014078.1	
212490_at	DNAJC8	AA843895	DnaJ (Hsp40) homolog, subfamily C, member 8	Hs.74711
212791_at	FLJ38984	AL042729	hypothetical protein FLJ38984	Hs.112023
201163_s_at		NM_001553	gb:NM_001553.1 /DEF=Homo sapiens insulin-like growth factor binding protein 7 (IGFBP7), mRNA. /FEA=mRNA /GEN=IGFBP7 /PROD=insulin-like growth factor binding protein 7 /DB_XREF=gi:4504 618 /UG=Hs.119206 insulin-like growth factor binding protein 7 /FL=gb:L19182.1 gb:NM_001553.1	

Tiguic ra Ot					
\			gb:U00238.1		
			/DEF=Homo		
			sapiens glutamine		
			PRPP		
			amidotransferase		
			(GPAT) mRNA,		
			complete cds.		
			/FEA=mRNA		
			/GEN=GPAT		
			/PROD=glutamine		
			PRPP		
			amidotransferase		·
}			/DB_XREF=gi:4048		
			60 /UG=Hs.311		
			phosphoribosyl		
			pyrophosphate		
			amidotransferase		
209434_s_at	<u></u>	U00238	/FL=gb:U00238.1		
				,	
				:	
+			gb:AF047695.1		
			/DEF=Homo		
			sapiens cap-		
			binding protein		
			4EHP mRNA,		
			complete cds.	1	
			/FEA=mRNA		
			/PROD=cap-binding		
			protein 4EHP		
			/DB_XREF=gi:3172		
			338 /UG=Hs.19122		
			eukaryotic		
			translation initiation		
			factor 4E-like 3		
			/FL=gb:BC005392.1		
			gb:AF047695.1		
			gb:AF068117.1		
			gb:AF038957.1		
209393_s_at		AF047695	gb:NM_004846.1		
200005_5_at	L	N 077090	195.14141_004040.1	1	L

Figure 7a CC		— ,	
219013 at	NM 022087	gb:NM_022087.1 //DEF=Homo sapiens hypothetical protein FLJ21634 (FLJ21634), mRNA. //FEA=mRNA //GEN=FLJ21634 //PROD=hypothetica I protein FLJ21634 //DB_XREF=gi:1154 5800 //UG=Hs.97056 hypothetical protein FLJ21634 //FL=gb:NM_022087 .1	
210010_ut	1111_022001		
		gb:NM_002592.1 /DEF=Homo sapiens proliferating cell nuclear antigen (PCNA), mRNA. /FEA=mRNA /GEN=PCNA /PROD=proliferating cell nuclear antigen /DB_XREF=gi:4505 640 /UG=Hs.78996 proliferating cell nuclear antigen /FL=gb:BC000491.1 gb:M15796.1	
201202_at	NM_002592	gb:NM_002592.1	

Application of: Liew, et. al. Our Docket #: 4231/2042 Figure 7a Cont'd.

Figure 7a Co			
201205_at	AF006751	Consensus includes gb:AF006751.1 /DEF=Homo sapiens ES130 mRNA, complete cds. /FEA=mRNA /PROD=ES130 /DB_XREF=gi:3299 884 /UG=Hs.98614 ribosome binding protein 1 (dog 180kD homolog) /FL=gb:AF006751.1 gb:NM_004587.1	
		gb:NM_006855.2 /DEF=Homo sapiens KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3 (KDELR3), transcript variant 1, mRNA. /FEA=mRNA /GEN=KDELR3 /PROD=KDEL receptor 3, isoform a /DB_XREF=gi:8051 612 /UG=Hs.250696 KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3 /FL=gb:BC001277.1	
204017_at	NM_006855	gb:NM_006855.2	

Figure /a Co	ilitu.			
riguic 7a co	int d.		gb:BC004817.1 /DEF=Homo sapiens, Ewing sarcoma breakpoint region 1, clone MGC:5432, mRNA, complete cds. /FEA=mRNA /PROD=Ewing sarcoma breakpoint region 1 /DB_XREF=gi:1343 5962 /UG=Hs.129953 Ewing sarcoma breakpoint region 1 /CI=Th:BC004817.1	
209214_s_at		BC004817	/FL=gb:BC004817.1 gb:NM_005243.1	
2002 IT 3_al			gb:NM_005231.1 /DEF=Homo sapiens ems1 sequence (mammary tumor and squamous cell carcinoma- associated (p8085 src substrate) (EMS1), mRNA. /FEA=mRNA /GEN=EMS1 /PROD=cortactin /DB_XREF=gi:4885 204 /UG=Hs.119257 ems1 sequence (mammary tumor and squamous cell carcinoma- associated (p8085 src substrate) /FL=gb:M98343.1	
201059_at		NM_005231	gb:NM_005231.1	
56197_at	PLSCR3	AI783924	phospholipid scramblase 3	Hs.103382

Fluure / a Contu.	Figure	7a	Cont'd.
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				•	
			gb:NM_006379.1		
			/DEF=Homo		
<u> </u>			sapiens sema		
			domain,		
			immunoglobulin		
			domain (Ig), short		
			basic domain,		
	•		secreted,		
	!		(semaphorin) 3C		
			(SEMA3C), mRNA.		
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			/GEN=SEMA3C		
			/PROD=sema		
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			immunoglobulin		
			domain (lg),		
			shortbasic domain,		
			secreted,		
	1		(semaphorin) 3C		
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			047		
			/UG=Hs.171921		
			sema domain,		
	1		immunoglobulin		
			domain (lg), short		
			basic domain,		
			secreted,		
			(semaphorin) 3C		
		l	/FL=gb:AB000220.1		
203789_s_at	<u> </u>	NM_006379	gb:NM_006379.1	<u> </u>	<u> </u>

Tigure 7a Ot	 	·	
203921_at	NM_004267	gb:NM_004267.1 /DEF=Homo sapiens carbohydrate (chondroitin 6keratan) sulfotransferase 2 (CHST2), mRNA. /FEA=mRNA /GEN=CHST2 /PROD=carbohydra te (chondroitin 6keratan)sulfotransferase 2 /DB_XREF=gi:4757 983 /UG=Hs.8786 carbohydrate (chondroitin 6keratan) sulfotransferase 2 /FL=gb:AB021124.1 gb:AB014679.1 gb:AB014680.1 gb:NM_004267.1	
209537_at	AF000416	gb:AF000416.1 /DEF=Homo sapiens EXT-like protein 2 (EXTL2) mRNA, complete cds. /FEA=mRNA /GEN=EXTL2 /PROD=EXT-like protein 2 /DB_XREF=gi:2895 061 /UG=Hs.61152 exostoses (multiple)-like 2 /FL=gb:AB009284.1 gb:AF000416.1	

Figure 7a Co	- T		
207855_s_at	NM 015127	gb:NM_015127.1 /DEF=Homo sapiens KIAA0761 protein (KIAA0761), mRNA. /FEA=mRNA /GEN=KIAA0761 /PROD=KIAA0761 protein /DB_XREF=gi:1319 4194 /UG=Hs.93121 KIAA0761 protein /FL=gb:BC002939.1 gb:NM_015127.1	
 205596_s_at	AY014180	gb:AY014180.1 /DEF=Homo sapiens E3 ubiquitin ligase Smurf2 mRNA, complete cds. /FEA=mRNA /PROD=E3 ubiquitin ligase Smurf2 /DB_XREF=gi:1240 8118 /UG=Hs.194477 E3 ubiquitin ligase SMURF2 /FL=gb:AF301463.1 gb:AF310676.1 gb:NM_022739.1 gb:AY014180.1	
219806_s_at	NM_020179	gb:NM_020179.1 /DEF=Homo sapiens FN5 protein (FN5), mRNA. /FEA=mRNA /GEN=FN5 /PROD=FN5 protein /DB_XREF=gi:9910 225 /UG=Hs.259737 FN5 protein /FL=gb:AF197137.1 gb:NM_020179.1	

Figure 7a C	T	T	hypothetical protein	
201874_at	FLJ21047	BF978611	FLJ21047	Hs.14891
2010/4_at	FLJ21047	B1 970011	1 232 1047	113.14001
			gb:NM_016938.1 /DEF=Homo sapiens EGF- containing fibulin- like extracellular matrix protein 2 (EFEMP2), mRNA. /FEA=mRNA /GEN=EFEMP2 /PROD=EGF- containing fibulin- like extracellular matrixprotein 2 /DB_XREF=gi:8393 298 /UG=Hs.6059 EGF-containing fibulin-like extracellular matrix protein 2 /FL=gb:AF093119.1 gb:AF109121.1	
206580_s_at		NM_016938	gb:NM_016938.1 gb:NM_005627.1 /DEF=Homo sapiens serumglucocorticoid regulated kinase (SGK), mRNA. /FEA=mRNA /GEN=SGK /PROD=serumgluco corticoid regulated kinase /DB_XREF=gi:5032 090 /UG=Hs.296323 serumglucocorticoid regulated kinase /FL=gb:BC001263.1 gb:NM_005637.1	
201739_at		NM_005627	gb:NM_005627.1 gb:AF153609.1	

1	l l			
209509_s_at			gb:BC000325.1 /DEF=Homo sapiens, clone MGC:8482, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:8482) /DB_XREF=gi:1265 3116 /UG=Hs.26433 dolichyl-phosphate (UDP-N- acetylglucosamine) N- acetylglucosaminep hosphotransferase 1 (GlcNAc-1-P transferase) /FL=gb:BC000325.1 gb:NM_001382.1	
202289 s_at		NM 006997	gb:NM_006997.1 /DEF=Homo sapiens transforming, acidic coiled-coil containing protein 2 (TACC2), mRNA. /FEA=mRNA /GEN=TACC2 /PROD=transformin g, acidic coiled-coil containingprotein 2 /DB_XREF=gi:1111 9413 /UG=Hs.272023 transforming, acidic coiled-coil containing protein 2 /FL=gb:AF095791.2 gb:NM_006997.1	

Figure /a Co				
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		gb:NM_001569.2 //DEF=Homo sapiens interleukin- 1 receptor- associated kinase 1 (IRAK1), mRNA. //FEA=mRNA //GEN=IRAK1 //PROD=interleukin- 1 receptor- associated kinase 1 //DB_XREF=gi:4755 143 //UG=Hs.182018 interleukin-1 receptor-associated kinase 1 //FL=gb:L76191.1		
201587_s_at	NM_0015	69 gb:NM_001569.2		

rigule /a Conti	<u>u. </u>			7
		-L-AE454047.4		
		gb:AF154847.1		
		/DEF=Homo		
	1	sapiens 33 kDa		
		Vamp-associated		
		protein (VAMP)		!
		mRNA, complete		
		cds. /FEA=mRNA		
		/GEN=VAMP		
		/PROD=33 kDa		
		Vamp-associated		
		protein		
		/DB_XREF=gi:8099		
		349 /UG=Hs.9006		
		VAMP (vesicle-		
		associated		
		membrane protein)-		
		associated protein		
		A (33kD)		
1		/FL=gb:BC002992.1		
	İ	gb:AF057358.1		
1		gb:AF044670.1		
		gb:AF086627.1		
	İ	gb:NM_003574.1		
208780_x_at	AF154847	gb:AF154847.1		
		gb:BC001669.1		
		/DEF=Homo		
		sapiens, Similar to		
		oxidase		
		(cytochrome c)		
		assembly 1-like,		
-		clone MGC:2171,		
		mRNA, complete		
		cds. /FEA=mRNA		
		/PROD=Similar to		
		oxidase		
	İ	(cytochrome c)		
		assembly1-like		
		/DB_XREF=gi:1280		
		4516		
		/UG=Hs.151134		
		17.1.13-13.131134	I	1
1				
		oxidase		
		oxidase (cytochrome c)		
		oxidase (cytochrome c) assembly 1-like		
208717_at	BC001669	oxidase (cytochrome c)		

	Cont'd.

Figure 7a Cont	(u		 1
		gb:NM_001903.1 /DEF=Homo sapiens catenin (cadherin- associated protein), alpha 1 (102kD) (CTNNA1), mRNA. /FEA=mRNA /GEN=CTNNA1 /PROD=catenin (cadherin- associated protein), alpha 1(102kD) /DB_XREF=gi:4503 126 /UG=Hs.178452 catenin (cadherin- associated protein), alpha 1 (102kD) /FL=gb:L23805.1	
200765_x_at	NM_001903	gb:NM_001903.1 gb:NM_001154.2 /DEF=Homo sapiens annexin A5 (ANXA5), mRNA. /FEA=mRNA /GEN=ANXA5 /PROD=annexin V /DB_XREF=gi:4809 273 /UG=Hs.300711 annexin A5 /FL=gb:BC001429.1 gb:BC004993.1 gb:M18366.1 gb:J03745.1 gb:M21731.1 gb:M19384.1	
	NM_001154	gb:D00172.1 gb:NM_001154.2	

Figure /a Co	inta.		<u> </u>	<u> </u>
202647_s_at		NM_002524	gb:NM_002524.2 /DEF=Homo sapiens neuroblastoma RAS viral (v-ras) oncogene homolog (NRAS), mRNA. /FEA=mRNA /GEN=NRAS /PROD=neuroblasto ma RAS viral (v-ras) oncogenehomolog /DB_XREF=gi:6006 027 /UG=Hs.260523 neuroblastoma RAS viral (v-ras) oncogene homolog /FL=gb:BC005219.1 gb:NM_002524.2	
200021_at		NM_005507	gb:NM_005507.1 /DEF=Homo sapiens cofilin 1 (non-muscle) (CFL1), mRNA. /FEA=mRNA /GEN=CFL1 /PROD=cofilin 1 (non-muscle) /DB_XREF=gi:5031 634 /UG=Hs.180370 cofilin 1 (non-muscle) /FL=gb:NM_005507 .1	
221761_at	ADSS	AA628948	adenylosuccinate synthase	Hs.90011

Figure	7a	Cont'd.	
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I igule la co	// tre ca.			
200710_at		NM 000018	gb:NM_000018.1 /DEF=Homo sapiens acyl- Coenzyme A dehydrogenase, very long chain (ACADVL), nuclear gene encoding mitochondrial protein, mRNA. /FEA=mRNA /GEN=ACADVL /PROD=acyl- Coenzyme A dehydrogenase, very long chainprecursor /DB_XREF=gi:4557 234 /UG=Hs.82208 acyl-Coenzyme A dehydrogenase, very long chain /FL=gb:D43682.1 gb:BC000399.1 gb:NM 000018.1	
211750_x_at		BC005946	gb:BC005946.1 /DEF=Homo sapiens, clone MGC:14580, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:14580) /DB_XREF=gi:1354 3588 /FL=gb:BC005946.1	

Tigulo 74 O				, . · · · · · · · · · · · · · · · · · ·	
203031_s_at	USP4	NM_000375 Al346043	gb:NM_000375.1 /DEF=Homo sapiens uroporphyrinogen III synthase (congenital erythropoietic porphyria) (UROS), mRNA. /FEA=mRNA /GEN=UROS /PROD=uroporphyri nogen III synthase /DB_XREF=gi:4557 872 /UG=Hs.75593 uroporphyrinogen III synthase (congenital erythropoietic porphyria) /FL=gb:BC002573.1 gb:NM_000375.1 ubiquitin specific protease 4 (proto- oncogene)		Hs.77500
202906_s_at	NBS1	AI796269	Nijmegen breakage syndrome 1 (nibrin)		Hs.25812

Figure /a Co	511t d.				
200663_at		NM_001780	gb:NM_001780.1 /DEF=Homo sapiens CD63 antigen (melanoma 1 antigen) (CD63), mRNA. /FEA=mRNA /GEN=CD63 /PROD=CD63 antigen (melanoma 1 antigen) /DB_XREF=gi:4502 678 /UG=Hs.76294 CD63 antigen (melanoma 1 antigen) /FL=gb:BC002349.1 gb:M59907.1 gb:NM_001780.1 peptidylprolyl isomerase A		
211978_x_at	PPIA	AI708767	(cyclophilin A)		Hs.342389
241504 2 25		AB040626	gb:AB049636.1 //DEF=Homo sapiens MRPL9 mRNA for mitochondrial ribosomal protein L9 (L9mt), complete cds. //FEA=mRNA //GEN=MRPL9 //PROD=mitochondr al ribosomal protein L9 (L9mt) //DB_XREF=gi:1355 9362 //FL=gb:AB049636.1		
211594_s_at		AB049636	//FL=gb:ABU49636.1	<u> </u>	L

1 iguie 7 a Oc			,	
202492_at 58994_at	FLJ20241	NM_024085 Al689402	gb:NM_024085.1 /DEF=Homo sapiens hypothetical protein FLJ22169 (FLJ22169), mRNA. /FEA=mRNA /GEN=FLJ22169 /PROD=hypothetica I protein FLJ22169 /DB_XREF=gi:1312 9081 /UG=Hs.323363 hypothetical protein FLJ22169 /FL=gb:BC001206.1 gb:NM_024085.1 hypothetical protein FLJ20241	Hs.181780
		NM_014462	gb:NM_014462.1 /DEF=Homo sapiens Lsm1 protein (LSM1), mRNA. /FEA=mRNA /GEN=LSM1 /PROD=Lsm1 protein /DB_XREF=gi:7657 312 /UG=Hs.111783 Lsm1 protein /FL=gb:BC001767.1 gb:AF000177.1 gb:NM_014462.1	

Figure 7a Co	mu.			-	
			gb:NM_006389.2 /DEF=Homo sapiens oxygen regulated protein (150kD) (ORP150), mRNA. /FEA=mRNA /GEN=ORP150 /PROD=oxygen regulated protein precursor /DB_XREF=gi:1369 9861 /UG=Hs.277704 oxygen regulated protein (150kD) /FL=gb:NM_006389		
200825 s_at		NM 006389	.2 gb:U65785.1		
208638_at	ATP6V1C2	BE910010	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C isoform 2		Hs.372429
			gb:NM_001635.1 /DEF=Homo sapiens amphiphysin (Stiff- Mann syndrome with breast cancer 128kD autoantigen) (AMPH), mRNA. /FEA=mRNA /GEN=AMPH /PROD=amphiphysi n /DB_XREF=gi:4502 080 /UG=Hs.173034 amphiphysin (Stiff- Mann syndrome with breast cancer 128kD autoantigen) /FL=gb:NM_001635		
205257_s_at		NM_001635	.1 gb:U07616.1 Human rearranged		
2465574	A41/1-12	1102706	immunoglobulin heavy chain (A1VH3) gene,		
216557_x_at	A1VH3	U92706	partial cds.	L	<u></u>

	·		
208989_s_at	AF179221	gb:AF179221.1 //DEF=Homo sapiens F-box protein Lilina (LILINA) mRNA, complete cds. //FEA=mRNA //GEN=LILINA //PROD=F-box protein Lilina //DB_XREF=gi:5917 729 //UG=Hs.219614 f- box and leucine- rich repeat protein 11 //FL=gb:AF179221.1	
220842_at	NM_017651	gb:NM_017651.1 /DEF=Homo sapiens hypothetical protein FLJ20069 (FLJ20069), mRNA. /FEA=mRNA /GEN=FLJ20069 /PROD=hypothetica I protein FLJ20069 /DB_XREF=gi:8923 074 /UG=Hs.273294 hypothetical protein FLJ20069 /FL=gb:NM_017651 .1	

Figure 7a CC	nitu.			
201992_s_at	int d.	NM_004521	gb:NM_004521.1 /DEF=Homo sapiens kinesin family member 5B (KIF5B), mRNA. /FEA=mRNA /GEN=KIF5B /PROD=kinesin family member 5B /DB_XREF=gi:4758 647 /UG=Hs.149436 kinesin family member 5B /FL=gb:NM_004521 .1 gb:NM_012264.1 /DEF=Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA. /FEA=mRNA /GEN=C22ORF5 /PROD=chromoso me 22 open reading frame 5 /DB_XREF=gi:7110 634 /UG=Hs.182626 chromosome 22 open reading frame 5 /DB_XREF=gi:7110 634 /UG=Hs.182626 chromosome 22 open reading frame 5 /FL=gb:NM_012264	
202027_at		NM_012264	.1	
			•	

Figure 7a Cont'd.	
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Tigare ra oc	 		
205613_at	NM_016524	gb:NM_016524.1 /DEF=Homo sapiens BK protein (LOC51760), mRNA. /FEA=mRNA /GEN=LOC51760 /PROD=BK protein /DB_XREF=gi:7706 558 /UG=Hs.26971 BK protein /FL=gb:BC004518.1 gb:NK_016524.1	
		gb:NM_001451.1 /DEF=Homo sapiens forkhead	
		box F1 (FOXF1), mRNA.	
		/FEA=mRNA /GEN=FOXF1	
		/PROD=forkhead box F1	
		/DB_XREF=gi:4503	
		732 /UG=Hs.155591	
		forkhead box F1	
205935_at	NM_001451	/FL=gb:U13219.1 gb:NM_001451.1	

Figure /a Co	Jiil u.			,	
219532_at 214284_s_at	FGF18	NM_022726 AA022949	gb:NM_022726.1 /DEF=Homo sapiens Stargardt disease 3 (autosomal dominant) (ELOVL4), mRNA. /FEA=mRNA /GEN=ELOVL4 /PROD=Stargardt disease 3 (autosomal dominant) /DB_XREF=gi:1223 2378 /UG=Hs.101915 Stargardt disease 3 (autosomal dominant) /FL=gb:AF277094.1 gb:NM_022726.1 fibroblast growth factor 18		Hs.49585
- · · · · · · · · · · · · · · · · · · ·			gb:AF123759.1 /DEF=Homo sapiens putative transmembrane protein (CLN8) mRNA, complete cds. /FEA=mRNA /GEN=CLN8 /PROD=putative transmembrane protein /DB_XREF=gi:6467 264 /UG=Hs.127675 ceroid-		
219340_s_at		AF123759	ceroid- lipofuscinosis, neuronal 8 (epilepsy, progressive with mental retardation) /FL=gb:AF123757.1 gb:AF123759.1 gb:AF123760.1 gb:AF123761.1 gb:NM_018941.1		

	onta.				
217770_at		NM_015937	gb:NM_015937.1 /DEF=Homo sapiens CGI-06 protein (LOC51604), mRNA. /FEA=mRNA /GEN=LOC51604 /PROD=CGI-06 protein /DB_XREF=gi:7706 257 /UG=Hs.84038 CGI-06 protein /FL=gb:AF132940.1 gb:NM_015937.1		
208978_at		U36190	gb:U36190.1 /DEF=Human cysteine-rich protein 2 (hCRP2) mRNA, complete cds. /FEA=mRNA /GEN=hCRP2 /PROD=cysteine- rich protein 2 /DB_XREF=gi:1399 027 /UG=Hs.70327 cysteine-rich protein 2 /FL=gb:D42123.1 gb:BC000434.1 gb:BC0001931.1 gb:U36190.1 gb:NM_001312.1	·	
204720_s_at	DNAJC6	AV729634	DnaJ (Hsp40) homolog, subfamily C, member 6		Hs.44896

Figure	7a	Cont'd.	

			.		
214210_at	SLC25A17; PMP34	AL049764	match: proteins: Tr:O43808 Tr:O70579 Tr:O04200 Sw:P39953 Sw:P21245 Sw:Q00319 Sw:P40464 Tr:O22261 Tr:O13660; Human DNA sequence from clone RP3- 362J20 on chromosome 22q13.1-13.31 Contains the 3' part of the gene for peroxisomal integral membrane protein, ESTs, STSs and GSSs, complete sequence.	NM_006358	
			CUG triplet repeat,		
202156_s_at	CUGBP2	N36839	RNA binding protein 2		Hs.211610
			gb:NM_006561.1 /DEF=Homo sapiens CUG triplet repeat, RNA- binding protein 2 (CUGBP2), mRNA. /FEA=mRNA /GEN=CUGBP2 /PROD=CUG triplet repeat, RNA- binding protein 2 /DB_XREF=gi:5729 815 /UG=Hs.211610 CUG triplet repeat, RNA-binding protein 2 /FL=gb:U69546.1		

Figure 7a Co	inta.		·	···	
219779_at			gb:NM_024721.1 /DEF=Homo sapiens hypothetical protein FLJ20980 (FLJ20980), mRNA. /FEA=mRNA /GEN=FLJ20980 /PROD=hypothetica I protein FLJ20980 /DB_XREF=gi:1337 6026 /UG=Hs.109314 hypothetical protein FLJ20980 /FL=gb:NM_024721 .1 gb:NM_003666.1		
			/DEF=Homo sapiens basic leucine zipper nuclear factor 1	;	
			(JEM-1) (BLZF1), mRNA.		
			/FEA=mRNA /GEN=BLZF1 /PROD=basic		
			leucine zipper nuclear factor 1 (JEM-1)		
			/DB_XREF=gi:4504 804		
			/UG=Hs.158205 basic leucine		
			zipper nuclear factor 1 (JEM-1)		
203840_at	N	IM_003666	/FL=gb:U79751.1 gb:NM_003666.1		

Figure 7a Co	ont a.				
217962_at		NM_018648	gb:NM_018648.1 /DEF=Homo sapiens nucleolar protein family A, member 3 (HACA small nucleolar RNPs) (NOLA3), mRNA. /FEA=mRNA /GEN=NOLA3 /PROD=nucleolar protein family A, member 3 (HACAsmall nucleolar RNPs) /DB_XREF=gi:8923 941 /UG=Hs.14317 nucleolar protein family A, member 3 (HACA small nucleolar RNPs) /FL=gb:AB043104.1 gb:NM_018648.1		
214329_x_at	TNFSF10	AW474434	tumor necrosis factor (ligand) superfamily, member 10		Hs.83429
203946_s_at	TINI SI TU	U75667	gb:U75667.1 /DEF=Human arginase II mRNA, complete cds. /FEA=mRNA /PROD=arginase II /DB_XREF=gi:1763 757 /UG=Hs.172851 arginase, type II /FL=gb:NM_001172 .2 gb:BC001350.1 gb:D86724.1 gb:U75667.1 gb:U82256.1		113.00720

Figure 7a Ct	 		,	
216942 s at	D28586	Consensus includes gb:D28586.1 /DEF=Human mRNA for LFA-3(delta D2), partial cds. /FEA=mRNA /PROD=LFA-3(delta D2) /DB_XREF=gi:4665 40 /UG=Hs.75626 CD58 antigen, (lymphocyte function-associated antigen 3)		
200611_s_at	AB010427	gb:AB010427.2 /DEF=Homo sapiens mRNA for NORI-1, complete cds. /FEA=mRNA /PROD=NORI-1 /DB_XREF=gi:5103 672 /UG=Hs.85100 WD repeat domain 1 /FL=gb:BC000201.1 gb:BC002489.1 gb:AF020056.1 gb:AB010427.2 gb:NM_017491.1	-	

	onta.			
222217 6 04		PC003654	Consensus includes gb:BC003654.1 /DEF=Homo sapiens, Similar to hypothetical protein MGC4365, clone IMAGE:3538020, mRNA, partial cds. /FEA=mRNA /PROD=Similar to hypothetical protein MGC4365 /DB_XREF=gi:1317 7768 /UG=Hs.109274 hypothetical protein MGC4365	
222217_s_at		BC003654 AK026980	Consensus includes gb:AK026980.1 //DEF=Homo sapiens cDNA: FLJ23327 fis, clone HEP12630, highly similar to HSZNF37 Homo sapiens ZNF37A mRNA for zinc finger protein. //FEA=mRNA //DB_XREF=gi:1043 9974 //UG=Hs.278064 Homo sapiens cDNA: FLJ23327 fis, clone HEP12630, highly similar to HSZNF37 Homo sapiens ZNF37A mRNA for zinc finger protein	
214725_at	FLJ40021	BE968773	hypothetical protein FLJ40021	Hs.41185

Figure	7a	Cont	d.
		_	_

Figure /a Co	onta.				
			gb:U43784.1		
			/DEF=Human		
			mitogen activated		
			protein kinase		
			activated protein		
			kinase-3 mRNA,		
			complete cds.		
			/FEA=mRNA		
			/PROD=mitogen		
			activated protein		
			kinase		
				•	
			activatedprotein		
			kinase-3		
			/DB_XREF=gi:1256		
			004		
ļ			/UG=Hs.227789		j
			mitogen-activated	•	1
			protein kinase-		
			activated protein		
			kinase 3		
			/FL=gb:U09578.1		
			gb:U43784.1		
			gb:BC001662.1		
202787_s_at		U43784	gb:NM_004635.1	! :	
202707_0_0.			5		
			gb:NM_006278.1		
		1	/DEF=Homo		
			sapiens		
			sialyltransferase		
			4C (beta-		
			galactosidase		
			alpha-2,3-		
			sialytransferase)		
			(SIAT4C), mRNA.		
			/FEA=mRNA		
			/GEN=SIAT4C		
			/PROD=sialyltransf	F	
			erase 4C (beta-		
1		1	galactosidasealpha-		
			2,3-		
		ŀ	sialytransferase)		
			/DB_XREF=gi:5454		
			057 /UG=Hs.75268		İ
			sialyltransferase	ļ	
			4C (beta-		
			galactosidase		
			alpha-2,3-		
1			sialytransferase)		
İ	t	i	Sidiy (i di i Sici doci		
203759_at		NM_006278	/FL=gb:L23767.1 gb:NM_006278.1		

Figure	7a	Cont'd.

Figure /a Cont	. a.	, 	
202009 at	NM_007284	gb:NM_007284.1 /DEF=Homo sapiens protein tyrosine kinase 9- like (A6-related protein) (PTK9L), mRNA. /FEA=mRNA /GEN=PTK9L /PROD=protein tyrosine kinase 9- like (A6- relatedprotein) /DB_XREF=gi:6005 845 /UG=Hs.6780 protein tyrosine kinase 9-like (A6- related protein) /FL=gb:BC000327.1 gb:BC0003161.1 gb:NM_007284.1 gb:AL136773.1	
202009_at		gu.AL 130//3.1	
212339_at	AB002336	Consensus includes gb:AL121895 /DEF=Human DNA sequence from clone RP11-234K24 on chromosome 20 Contains EPB41L1 gene encoding the erythrocyte membrane protein band 4.1-like protein (KIAA0338), a novel gene (CGI-23, DKFZP564N1363), a CpG island, ESTs, STSs and GSSs /FEA=mRNA_1 /DB_XREF=gi:9864 397 /UG=Hs.26395 erythrocyte membrane protein band 4.1-like 1	

Figure 7a Co	JIILU.		abili20657.4		 1
			gb:U39657.1		
			/DEF=Human MAP		
			kinase kinase 6		
			(MKK6) mRNA,		
			complete cds.		
			/FEA=mRNA		
ı			/GEN=MKK6		
			/PROD=MAP		
			kinase kinase 6		
			/DB_XREF=gi:1203		
			817		
			/UG=Hs.118825		
			mitogen-activated		
			protein kinase		
			kinase 6		
			/FL=gb:NM_002758		
İ			.1 gb:U39656.1		
			gb:U39657.1		
			gb:U39065.1		
			gb:U49732.1		
205699 at		U39657	gb:D87905.1		
203016_s_at	KIAA0923	AW136988	KIAA0923 protein		Hs.22587
	1				
			gb:NM_024089.1		
			/DEF=Homo		
			sapiens	•	
			hypothetical protein		
			MGC5302		
			(MGC5302),		
1	•		mRNA.		
			/FEA=mRNA		
			/GEN=MGC5302		
			/PROD=hypothetica		
			I protein MGC5302		
			/DB_XREF=gi:1312		
			9085		
			/UG=Hs.44970		
			endoplasmic		
			reticulum resident]
			protein 58;		
			hypothetical protein		
			MGC5302		
	1	I		1	
	I .		1/CL _~L.D.C.C.4.2.C.7.4	l .	
219479_at		NM_024089	/FL=gb:BC001297.1 gb:NM_024089.1		

Figure 7a Co	Jite G.				
219419_at		NM_024805	gb:NM_024805.1 /DEF=Homo sapiens hypothetical protein FLJ21172 (FLJ21172), mRNA. /FEA=mRNA /GEN=FLJ21172 /PROD=hypothetica I protein FLJ21172 /DB_XREF=gi:1337 6184 /UG=Hs.164207 hypothetical protein FLJ21172 /FL=gb:NM_024805 .1	·	
			Consensus includes		
			gb:NM_005402.1 /DEF=Homo sapiens v-ral		
			simian leukemia viral oncogene		
			homolog A (ras related) (RALA),		
			mRNA. /FEA=CDS /GEN=RALA /PROD=v-ral		
			simian leukemia viral oncogene		
			homolog A(ras related)		
			/DB_XREF=gi:4885 568		
			/UG=Hs.288757 v- ral simian		
			leukemia viral oncogene homolog		
			A (ras related) /FL=gb:M29893.1		
214435_x_at		NM_005402	gb:NM_005402.1		
213290_at	COL6A2	AL531750	collagen, type VI, alpha 2		Hs.159263
				NM_002375; NM_030884;	
			microtubule-	NM_030885;	
243_g_at	MAP4	M64571	associated protein 4	NM_030983	Hs.239298

I igaic ra o	****			
202836_s_at		NM_006701	gb:NM_006701.1 /DEF=Homo sapiens similar to S. pombe dim1+ (DIM1), mRNA. /FEA=mRNA /GEN=DIM1 /PROD=similar to S. pombe dim1+ /DB_XREF=gi:5729 801 /UG=Hs.5074 similar to S. pombe dim1+ /FL=gb:BC001046.1 gb:AF023611.1 gb:NM_006701.1 gb:AF146373.1	
205575_at		NM_006688	gb:NM_006688.1 /DEF=Homo sapiens C1q- related factor (CRF), mRNA. /FEA=mRNA /GEN=CRF /PROD=C1q-related factor /DB_XREF=gi:5729 784 /UG=Hs.134012 C1q-related factor /FL=gb:AF095154.1 gb:NM_006688.1	U. 409754
221840_at		AA775177	ESTs X transporter	Hs.408754
221844_x_at	хтз	AV756161	protein 3	 Hs.107854

Fig	ure	7a	Cont'd.

Figure /a Co	micu.			
203613_s_at	int d.	NM_002493	gb:NM_002493.1 /DEF=Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6 (17kD, B17) (NDUFB6), mRNA. /FEA=mRNA /GEN=NDUFB6 /PROD=NADH dehydrogenase (ubiquinone) 1 betasubcomplex, 6 (17kD, B17) /DB_XREF=gi:4505 364 /UG=Hs.109646 NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6 (17kD, B17) /FB_XREF=gi:4505 364 /UG=Hs.109646 NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6 (17kD, B17) /FL=gb:AF035840.1 gb:NM_002493.1 gb:NM_006810.1	
203857_s_at		NM_006810	gb:NM_006810.1 /DEF=Homo sapiens for protein disulfide isomerase related (PDIR), mRNA. /FEA=mRNA /GEN=PDIR /PROD=for protein disulfide isomerase related /DB_XREF=gi:5803 120 /UG=Hs.76901 for protein disulfide isomerase related /FL=gb:D49490.1 gb:NM_006810.1 G1 to S phase	
215438_x_at	GSPT1	BE906054	transition 1	Hs.2707

Figure 7	'a C	ont'd.
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			gb:BC001288.1		
			/DEF=Homo		
			sapiens, Similar to		
			decay accelerating		
			factor for		
1					
			complement		
			(CD55, Cromer		
			blood group		
			system), clone MGC:5192, mRNA,		
			complete cds. /FEA=mRNA		
			/PROD=Similar to		
			decay accelerating		
			factor		
			forcomplement		
			(CD55, Cromer		
			blood group		
			system)		
			/DB_XREF=gi:1265		
			4888 /UG=Hs.1369		
1			decay accelerating		
			factor for		
	1		complement		
			(CD55, Cromer		
		i	blood group		
			system)		
			/FL=gb:NM 000574		
			.1 gb:BC001288.1		
201926_s_at	1	BC001288	gb:M31516.1		
201920_3_at	<u> </u>	150001200	1920 10 10.1	1	I

Figure	7a	Cont'd.
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1 19010 10 01				
205173_x_at	I OC51668	NM_001779	gb:NM_001779.1 /DEF=Homo sapiens CD58 antigen, (lymphocyte function-associated antigen 3) (CD58), mRNA. /FEA=mRNA /GEN=CD58 /PROD=CD58 antigen, (lymphocyte function- associatedantigen 3) /DB_XREF=gi:4502 676 /UG=Hs.75626 CD58 antigen, (lymphocyte function-associated antigen 3) /FL=gb:NM_001779 .1	Hs.46967
215691_x_at	LOC51668	AV702994	HSPCO34 protein	 HS.46967

		1	1	
			gb:NM_005769.1 /DEF=Homo sapiens carbohydrate (N- acetylglucosamine 6-O) sulfotransferase 4 (CHST4), mRNA. /FEA=mRNA /GEN=CHST4 /PROD=carbohydra te (N- acetylglucosamine 6- O)sulfotransferase 4 /DB_XREF=gi:5031 734 /UG=Hs.251383 carbohydrate (N- acetylglucosamine 6-O) sulfotransferase 4 /FL=gb:AF131235.1	
220446_s_at		NM_005769	gb:NM_005769.1 gb:NM_025158.1 /DEF=Homo sapiens hypothetical protein FLJ22251 (FLJ22251), mRNA. /FEA=mRNA /GEN=FLJ22251 /PROD=hypothetica I protein FLJ22251 /DB_XREF=gi:1337 6756 /UG=Hs.289064 hypothetical protein FLJ22251 /FL=gb:NM_025158 .1	
	OC155066	Al884867	vacuolar proton- ATPase subunit	Hs.351612

Figure /a Co	ont a.			
215283_at		U79248	Consensus includes gb:U79248.1 /DEF=Human clone 23826 mRNA sequence. /FEA=mRNA /DB_XREF=gi:1710 195 /UG=Hs.12484 Human clone 23826 mRNA sequence gb:NM_025262.1 /DEF=Homo sapiens G5C protein (G5C), mRNA. /FEA=mRNA /GEN=G5C /PROD=G5C protein /DB_XREF=gi:1337 6875 /UG=Hs.246845	
			G5C protein /FL=gb:NM_025262	
219860_at		NM_025262	1.1	
201124_at	ITGB5	AL048423	integrin, beta 5	Hs.149846
			hypothetical protein	
212502_at	FLJ14547	AV713053	FLJ14547	 Hs.99821
			gb:U65932.1 /DEF=Human extracellular matrix protein 1 (ECM1) mRNA, complete cds. /FEA=mRNA /GEN=ECM1 /PROD=extracellula r matrix protein 1 /DB_XREF=gi:1488 323 /UG=Hs.81071 extracellular matrix protein 1 /FL=gb:NM_004425 .2 gb:U65932.1	

Figure /a Co	intu.				
218930_s_at			gb:NM_018374.1 /DEF=Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA. /FEA=mRNA /GEN=FLJ11273 /PROD=hypothetica I protein FLJ11273 /DB_XREF=gi:8922 965 /UG=Hs.3542 hypothetical protein FLJ11273 /FL=gb:NM_018374		
		010071		,	
			gb:AF083389.1 /DEF=Homo sapiens putative WHSC1 protein (WHSC1) mRNA, alternative splice product with complete exon 12, complete cds. /FEA=mRNA /GEN=WHSC1 /PROD=putative WHSC1 protein /DB_XREF=gi:4378 016 /UG=Hs.110457 Wolf-Hirschhorn syndrome		
209054_s_at		AF083389	candidate 1 /FL=gb:AF083389.1		

Figure /a Co	Jill G.		Canagaga		
			Consensus		ļ
			includes		
			gb:BF196642		
			/FEA=EST		
			/DB_XREF=gi:1108		
			4786		
			/DB_XREF=est:7m		
			93c12.x1		
			/CLONE=IMAGE:35		
			62750		
			/UG=Hs.108332		
			ubiquitin-		
			conjugating		
			enzyme E2D 2		
			(homologous to		
			yeast UBC45)		
			/FL=gb:U39317.1		
201344 at		NM 003339	gb:NM_003339.1		
			vacuolar protein		
44111_at	VPS33B	AI672363	sorting 33B (yeast)		Hs.26510
_			gb:NM_006082.1		
			/DEF=Homo		
			sapiens tubulin,		
			alpha, ubiquitous		:
			(K-ALPHA-1),		
			mRNA.		
	;		/FEA=mRNA		
			/GEN=K-ALPHA-1	1	
1			/PROD=tubulin,		
			alpha, ubiquitous		
			/DB_XREF=gi:5174		
			476		
			/UG=Hs.278242		
			tubulin, alpha,		
			ubiquitous		
			/FL=gb:BC000696.1		
			gb:BC001128.1		
			gb:BC001209.1		
			gb:K00558.1		
			gb:AF081484.1		
201090_x_at		NM_006082	gb:NM_006082.1		

I igule ra oc	110.			
201338_x_at		NM 002097	gb:NM_002097.1 /DEF=Homo sapiens general transcription factor IIIA (GTF3A), mRNA. /FEA=mRNA /GEN=GTF3A /PROD=general transcription factor IIIA /DB_XREF=gi:4753 158 /UG=Hs.75113 general transcription factor IIIA /FL=gb:D32257.1 gb:NM_002097.1	
		002007	J	
			gb:NM_003746.1 /DEF=Homo sapiens dynein, cytoplasmic, light polypeptide (PIN), mRNA. /FEA=mRNA /GEN=PIN /PROD=dynein, cytoplasmic, light polypeptide /DB_XREF=gi:4505 812 /UG=Hs.5120 dynein, cytoplasmic, light polypeptide /CI	
200703_at		NM_003746	/FL=gb:U32944.1 gb:NM_003746.1	

Figure 7a Co	nitu.				
			gb:NM_003406.1 /DEF=Homo sapiens tyrosine 3- monooxygenasetryp tophan 5- monooxygenase activation protein, zeta polypeptide (YWHAZ), mRNA. /FEA=mRNA /GEN=YWHAZ /PROD=tyrosine 3- monooxygenasetryp tophan5- monooxygenase activation protein, zeta polypeptide /DB_XREF=gi:4507 952 /UG=Hs.75103 tyrosine 3- monooxygenasetryp tophan 5- monooxygenase activation protein, zeta polypeptide /FL=gb:BC003623.1 gb:M86400.1		
200639_s_at		NM 003406	gb:NM_003406.1 gb:U28964.1		
			Consensus includes gb:AB014576.1 /DEF=Homo sapiens mRNA for KIAA0676 protein, partial cds. /FEA=mRNA /GEN=KIAA0676 /PROD=KIAA0676 protein /DB_XREF=gi:3327 165 /UG=Hs.155829		
212052_s_at	L	AB014576	KIAA0676 protein	L	L

Figure /a Co	1		
212313 at	BC004344	Consensus includes gb:BC004344.1 /DEF=Homo sapiens, clone IMAGE:3633354, mRNA, partial cds. /FEA=mRNA /PROD=Unknown (protein for IMAGE:3633354) /DB_XREF=gi:1327 9286 /UG=Hs.5019 Homo sapiens, clone IMAGE:3633354, mRNA, partial cds	
2,2010_dt	50001011	Till to the parties out	
		gb:NM_005620.1 /DEF=Homo sapiens S100 calcium-binding protein A11 (calgizzarin) (S100A11), mRNA. /FEA=mRNA /GEN=S100A11 /PROD=S100 calcium-binding protein A11 /DB_XREF=gi:5032 056	
200660_at	NM_005620	/UG=Hs.256290 S100 calcium- binding protein A11 (calgizzarin) /FL=gb:D49355.1 gb:BC001410.1 gb:D50374.1 gb:NM_005620.1 gb:D38583.1	:

Figure 7a Co	mra.			
211072_x_at		BC006481	gb:BC006481.1 /DEF=Homo sapiens, tubulin alpha 1, clone MGC:4387, mRNA, complete cds. /FEA=mRNA /PROD=tubulin alpha 1 /DB_XREF=gi:1362 3706 /FL=gb:BC006481.1	·
217809_at		NM_014038	gb:NM_014038.1 /DEF=Homo sapiens HSPC028 protein (HSPC028), mRNA. /FEA=mRNA /GEN=HSPC028 /PROD=HSPC028 protein /DB_XREF=gi:7661 743 /UG=Hs.5216 HSPC028 protein /FL=gb:AF110323.1 gb:BC003056.1 gb:AF083246.1 gb:NM_014038.1	
208398_s_at		NM_004865	gb:NM_004865.1 /DEF=Homo sapiens TBP-like 1 (TBPL1), mRNA. /FEA=mRNA /GEN=TBPL1 /PROD=TBP-like 1 /DB_XREF=gi:4759 233 /UG=Hs.13993 TBP-like 1 /FL=gb:AF130312.1 gb:NM_004865.1	

Figure 7a Co	Jili G.			
207812_s_at	·	NM_015530	gb:NM_015530.1 /DEF=Homo sapiens DKFZP434D156 protein (DKFZP434D156), mRNA. /FEA=mRNA /GEN=DKFZP434D 156 /PROD=DKFZP434 D156 protein /DB_XREF=gi:7661 569 /UG=Hs.6880 DKFZP434D156 protein /FL=gb:NM_015530 .1	
 201622_at		 NM_014390	gb:NM_014390.1 /DEF=Homo sapiens EBNA-2 co-activator (100kD) (p100), mRNA. /FEA=mRNA /GEN=p100 /PROD=EBNA-2 co activator (100kD) /DB_XREF=gi:7657 430 /UG=Hs.79093 EBNA-2 co- activator (100kD) /FL=gb:NM_014390 .1 gb:U22055.1	
212959_s_at		AK001821	Consensus includes gb:AK001821.1 /DEF=Homo sapiens cDNA FLJ10959 fis, clone PLACE1000562. /FEA=mRNA /DB_XREF=gi:7023 328 /UG=Hs.7041 hypothetical protein DKFZp762B226	

		abiNIM 000160 1	 ·
		gb:NM_002160.1	
		/DEF=Homo	
		sapiens	
		hexabrachion	
		(tenascin C,	
		cytotactin) (HXB),	
		mRNA.	
		/FEA=mRNA	
		/GEN=HXB	
		/PROD=hexabrachi	
		on (tenascin C,	
		cytotactin)	
1		/DB_XREF=gi:4504	
1		548	
		/UG=Hs.289114	
		hexabrachion	
		(tenascin C,	
		cytotactin)	;
		/FL=gb:M55618.1	
201645_at	NM_002160	gb:NM_002160.1	
		Consensus	
		includes	
		gb:AB033105.1	
		/DEF=Homo	
[sapiens mRNA for	
		KIAA1279 protein,	
		partial cds.	
		/FEA=mRNA	
		/GEN=KIAA1279	
		/PROD=KIAA1279	
		protein	
		/DB_XREF=gi:6331	
		321	
		/UG=Hs.172854	
		DKFZP586B0923	
212453 at	AB033105	protein	

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202657_s_at		gb:NM_014755.1 /DEF=Homo sapiens KIAA0127 gene product (KIAA0127), mRNA. /FEA=mRNA /GEN=KIAA0127 /PROD=KIAA0127 gene product /DB_XREF=gi:7661 925 /UG=Hs.77293 KIAA0127 gene product /FL=gb:D50917.1 gb:NM_014755.1	
207842_s_at	NM 007359	gb:NM_007359.1 /DEF=Homo sapiens MLN51 protein (MLN51), mRNA. /FEA=mRNA /GEN=MLN51 /PROD=MLN51 protein /DB_XREF=gi:6678 887 /UG=Hs.83422 MLN51 protein /FL=gb:NM_007359	

Application of: Liew, et. al. Our Docket #: 4231/2042 Figure 7a Cont'd.

Figure 7a Co	ont a.			· · · · · · · · · · · · · · · · · · ·	
218331_s_at		NM_017782	gb:NM_017782.1 /DEF=Homo sapiens hypothetical protein FLJ20360 (FLJ20360), mRNA. /FEA=mRNA /GEN=FLJ20360 /PROD=hypothetica I protein FLJ20360 /DB_XREF=gi:8923 334 /UG=Hs.26434 hypothetical protein FLJ20360 /FL=gb:BC001759.1 gb:NM_017782.1		
210331 <u>s</u> _at		INII_U17702	gb:NM_025226.1 /DEF=Homo sapiens MSTP032 protein (MSTP032), mRNA. /FEA=mRNA /GEN=MSTP032 /PROD=MSTP032 protein /DB_XREF=gi:1337		
218353_at 213326_at	VAMP1	NM_025226 AU150319	6831 /UG=Hs.274368 MSTP032 protein /FL=gb:AF113212.1 gb:NM_025226.1 vesicle-associated membrane protein 1 (synaptobrevin 1)		Hs.20021

Figure /a Cont	<u>u. </u>	,	
210282_at	AL136621	gb:AL136621.1 /DEF=Homo sapiens mRNA; cDNA DKFZp564B162 (from clone DKFZp564B162); complete cds. /FEA=mRNA /GEN=DKFZp564B 162 /PROD=hypothetica I protein /DB_XREF=gi:1205 2767 /UG=Hs.109526 zinc finger protein 198 /FL=gb:AL136621.1 gb:L22453.1 /DEF=Homo sapiens HIV-1 TAR RNA binding protein (TARBP-b) mRNA, complete cds. /FEA=mRNA /GEN=TARBP-b /DB_XREF=gi:3479 63	
211666_x_at	L22453	/FL=gb:L22453.1	
201738_at	NM_005875	gb:NM_005875.1 /DEF=Homo sapiens translation factor sui1 homolog (GC20), mRNA. /FEA=mRNA /GEN=GC20 /PROD=translation factor sui1 homolog /DB_XREF=gi:5031 710 /UG=Hs.21756 translation factor sui1 homolog /FL=gb:AF064607.1 gb:AF077052.1 gb:NM_005875.1 gb:AF263452.1	

				
203195_s_at			gb:NM_005387.2 /DEF=Homo sapiens nucleoporin 98kD (NUP98), mRNA. /FEA=mRNA /GEN=NUP98 /PROD=nucleoporin 98kD /DB_XREF=gi:1112 0677 /UG=Hs.112255 nucleoporin 98kD /FL=gb:NM_005387 .2 gb:AF071076.1	
200.00_0_ut		· · · · · · · · · · · · · · · · · ·	g	
200899_s_at		NM_012215	gb:NM_012215.1 /DEF=Homo sapiens meningioma expressed antigen 5 (hyaluronidase) (MGEA5), mRNA. /FEA=mRNA /GEN=MGEA5 /PROD=meningiom a expressed antigen 5 (hyaluronidase) /DB_XREF=gi:1102 4697 /UG=Hs.5734 meningioma expressed antigen 5 (hyaluronidase) /FL=gb:AF036144.2 gb:NM_012215.1	

Figure /a Co					
			gb:NM_004733.2		
			/DEF=Homo		
			sapiens acetyl-		
			Coenzyme A		
			transporter		
			(ACATN), mRNA.		
			/FEA=mRNA	-	
			/GEN=ACATN		
			/PROD=acetyl-		
			Coenzyme A		
			transporter		
		ļ	/DB_XREF=gi:6042		
			194		
			/UG=Hs.285176		
			acetyl-Coenzyme A		
			transporter		,
		1	/FL=gb:D88152.1		
203165_s_at		NM_004733	gb:NM_004733.2		
			PRP4 pre-mRNA		
			processing factor 4	•	
209161_at	PRPF4	AI184802	homolog (yeast)		Hs.374973
		L	<u> </u>		
			gb:NM_017745.1		
			gb:NM_017745.1 /DEF=Homo		
			gb:NM_017745.1 /DEF=Homo sapiens		
			gb:NM_017745.1 /DEF=Homo sapiens hypothetical protein		
			gb:NM_017745.1 /DEF=Homo sapiens hypothetical protein FLJ20285		
			gb:NM_017745.1 /DEF=Homo sapiens hypothetical protein FLJ20285 (FLJ20285),		
			gb:NM_017745.1 /DEF=Homo sapiens hypothetical protein FLJ20285 (FLJ20285), mRNA.		
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			gb:NM_017745.1 /DEF=Homo sapiens hypothetical protein FLJ20285 (FLJ20285), mRNA. /FEA=mRNA /GEN=FLJ20285 /PROD=hypothetica I protein FLJ20285		
			gb:NM_017745.1 /DEF=Homo sapiens hypothetical protein FLJ20285 (FLJ20285), mRNA. /FEA=mRNA /GEN=FLJ20285 /PROD=hypothetica I protein FLJ20285 /DB_XREF=gi:8923		
			gb:NM_017745.1 /DEF=Homo sapiens hypothetical protein FLJ20285 (FLJ20285), mRNA. /FEA=mRNA /GEN=FLJ20285 /PROD=hypothetica I protein FLJ20285 /DB_XREF=gi:8923 266		
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219433_at		NM 017745	gb:NM_017745.1 /DEF=Homo sapiens hypothetical protein FLJ20285 (FLJ20285), mRNA. /FEA=mRNA /GEN=FLJ20285 /PROD=hypothetica I protein FLJ20285 /DB_XREF=gi:8923 266 /UG=Hs.278732 hypothetical protein		

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gb:AB002391.2 //DEF=Homo sapiens mRNA for KIAA0393 protein, partial cds. //FEA=mRNA //GEN=KIAA0393 //PROD=KIAA0393 protein //DB_XREF=gi:6683 696 //UG=Hs.266933 hect domain and RLD 2 //DEF=Homo sapiens putative nuclear protein (HRIHFB2122), mRNA. //FEA=mRNA //GEN=HRIHFB2122 //PROD=putative nuclear protein //DB_XREF=gi:1033 4853 //UG=Hs.40342 putative nuclear protein //DB_XREF=gi:1033 4853 //UG=Hs.40342 putative nuclear protein //FL=gb:NM_007032 1 Consensus includes gb:AK026954.1 //DEF=Homo sapiens cDNA: FLJ23301 fis, clone HEP11120. //FEA=mRNA //DB_XREF=gi:1043 9935				Consensus		Ì
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sapiens mRNA for KIAA0393 protein, partial cds. /FEA=mRNA /GEN=KIAA0393 /PROD=KIAA0393 /PROD=KIAA0393 /PROD=KIAA0393 /PROD=KIAA0393 /PROD=KIAA0393 /PROD=KIAA0393 /PROD=KIAA0393 /PROD=KIAA0393 /PROD=MIAD0393 /PROD=JEND /JEF=Homo sapiens putative nuclear protein (HRIHFB2122), mRNA, //FEA=mRNA //GEN=HRIHFB2122 //PROD=putative nuclear protein //DB_XREF=gi:1033 //BS3 //UG=Hs.40342 /PROD=putative nuclear //DB_XREF=gi:1033 //BS3 //UG=Hs.40342 //BS3 //UG=Hs.40342 //DEF=Homo //DB_XREF=gi:1033 //DEF=Homo //DEF				gb:AB002391.2		
KIAA0393 protein, partial cds. FFEA=mRNA FGEA=mRNA FGEN=KIAA0393 FROD=KIAA0393 FRO				/DEF=Homo		
KIAA0393 protein, partial cds. FFEA=mRNA FGEA=mRNA FGEN=KIAA0393 FROD=KIAA0393 FRO				sapiens mRNA for		
partial cds. /FEA=mRNA /GEN=KIAA0393 /PROD=KIAA0393 protein /DB_XREF=gi:6683 696 /UG=Hs.266933 hect domain and RLD 2 gb:NM_007032.1 /DEF=Homo sapiens putative nuclear protein (HRIHFB2122), mRNA /FEA=mRNA /GEN=HRIHFB2122 /PROD=putative nuclear protein nDB_XREF=gi:1033 4853 /UG=Hs.40342 putative nuclear protein /FI=gb:NM_007032 1 Consensus includes gb:AK026954.1 /DEF=Homo sapiens cDNA: FLJ23301 fis, clone HEP11120 /FEA=mRNA /DB_XREF=gi:1043 g935						
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/PROD=KIAA0393 protein /DB_XREF=gi:6683 696 /UG=Hs.266933 hect domain and RLD 2 gb:NM_007032.1 /DEF=Homo sapiens putative nuclear protein (HRIHFB2122), mRNA. /FEA=mRNA /GEN=HRIHFB2122 /PROD=putative nuclear protein /DB_XREF=gi:1033 4853 /UG=Hs.40342 putative nuclear protein (FL=gb:NM_007032 1.1 Consensus includes gb:AK026954.1 //DEF=Homo sapiens cDNA: FLJ23301 fis, clone HEP11120. /FEA=mRNA /DB_XREF=gi:1043 9935						
protein //DB_XREF=gi:6683 696 //UG=Hs.266933 hect domain and RLD 2 gb:NM_007032.1 //DEF=Homo sapiens putative nuclear protein (HRIHFB2122), mRNA. //FEA=mRNA //GEN=HRIHFB2122 //PROD=putative nuclear protein //DB_XREF=gi:1033 4853 //UG=Hs.40342 putative nuclear protein //FL=gb:NM_007032 202795_x_at NM_007032 1 Consensus includes gb:AK026954.1 //DEF=Homo sapiens cDNA: FLJ23301 fis, clone HEP11120. //FEA=mRNA //DB_XREF=gi:1043 9935						
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/UG=Hs.266933 hect domain and RLD 2 gb:NM_007032.1 //DEF=Homo sapiens putative nuclear protein (HRIHFB2122), mRNA. //FEA=mRNA //GEN=HRIHFB2122 //PROD=putative nuclear protein //DB_XREF=gi:1033 4853 //UG=Hs.40342 putative nuclear protein //FL=gb:NM_007032 .1 Consensus includes gb:AK026954.1 //DEF=Homo sapiens cDNA: FLJ23301 fis, clone HEP11120. //FEA=mRNA //DB_XREF=gi:1043 9935						
AB002391 RLD 2						
217317_s_at AB002391 RLD 2 gb:NM_007032.1 //DEF=Homo sapiens putative nuclear protein (HRIHFB2122), mRNA. //FEA=mRNA //GEN=HRIHFB2122 //PROD=putative nuclear protein //DB_XREF=gi:1033 4853 //UG=Hs.40342 putative nuclear protein //FL=gb:NM_007032 .1 Consensus includes gb:AK026954.1 //DEF=Homo sapiens cDNA: FLJ23301 fis, clone HEP11120. //FEA=mRNA //DB_XREF=gi:1043 9935						ł
gb:NM_007032.1 /DEF=Homo sapiens putative nuclear protein (HRIHFB2122), mRNA. /FEA=mRNA /GEN=HRIHFB2122 /PROD=putative nuclear protein /DB_XREF=gi:1033 4853 /UG=Hs.40342 putative nuclear protein /FL=gb:NM_007032 202795_x_at NM_007032 1 Consensus includes gb:AK026954.1 /DEF=Homo sapiens cDNA: FLJ23301 fis, clone HEP11120. /FEA=mRNA /DB_XREF=gi:1043 9935						
gb:NM_007032.1 //DEF=Homo sapiens putative nuclear protein (HRIHFB2122), mRNA. //FEA=mRNA //GEN=HRIHFB2122 //PROD=putative nuclear protein //DB_XREF=gi:1033 4853 //UG=Hs.40342 putative nuclear protein //FL=gb:NM_007032 .1 Consensus includes gb:AK026954.1 //DEF=Homo sapiens cDNA: FLJ23301 fis, clone HEP11120. //FEA=mRNA //DB_XREF=gi:1043 9935	217317_s_at		AB002391	RLD 2		
sapiens putative nuclear protein (HRIHFB2122), mRNA. //FEA=mRNA //GEN=HRIHFB2122 //PROD=putative nuclear protein //DB_XREF=gi:1033 4853 //UG=Hs.40342 putative nuclear protein //FL=gb:NM_007032 202795_x_at NM_007032 1 Consensus includes gb:AK026954.1 //DEF=Homo sapiens cDNA: FLJ23301 fis, clone HEP11120. //FEA=mRNA //DB_XREF=gi:1043 9935				gb:NM_007032.1		
nuclear protein (HRIHFB2122), mRNA. //FEA=mRNA //GEN=HRIHFB2122 //PROD=putative nuclear protein //DB_XREF=gi:1033 4853 //UG=Hs.40342 putative nuclear protein //FL=gb:NM_007032 202795_x_at NM_007032 1 Consensus includes gb:AK026954.1 //DEF=Homo sapiens cDNA: FLJ23301 fis, clone HEP11120. //FEA=mRNA //DB_XREF=gi:1043 9935				/DEF=Homo		
nuclear protein (HRIHFB2122), mRNA. //FEA=mRNA //GEN=HRIHFB2122 //PROD=putative nuclear protein //DB_XREF=gi:1033 4853 //UG=Hs.40342 putative nuclear protein //FL=gb:NM_007032 202795_x_at NM_007032 1 Consensus includes gb:AK026954.1 //DEF=Homo sapiens cDNA: FLJ23301 fis, clone HEP11120. //FEA=mRNA //DB_XREF=gi:1043 9935	,	•		sapiens putative		1
(HRIHFB2122), mRNA. //FEA=mRNA //GEN=HRIHFB2122 //PROD=putative nuclear protein //DB_XREF=gi:1033 4853 //UG=Hs.40342 putative nuclear protein //FL=gb:NM_007032 202795_x_at NM_007032 1 Consensus includes gb:AK026954.1 //DEF=Homo sapiens cDNA: FLJ23301 fis, clone HEP11120. //FEA=mRNA //DB_XREF=gi:1043 9935						
mRNA. //FEA=mRNA //GEN=HRIHFB2122 //PROD=putative nuclear protein //DB_XREF=gi:1033 4853 //UG=Hs.40342 putative nuclear protein //FL=gb:NM_007032 202795_x_at Consensus includes gb:AK026954.1 //DEF=Homo sapiens cDNA: FLJ23301 fis, clone HEP11120. //FEA=mRNA //DB_XREF=gi:1043 9935						
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/GEN=HRIHFB2122 /PROD=putative nuclear protein /DB_XREF=gi:1033 4853 /UG=Hs.40342 putative nuclear protein /FL=gb:NM_007032 202795_x_at Consensus includes gb:AK026954.1 /DEF=Homo sapiens cDNA: FLJ23301 fis, clone HEP11120. /FEA=mRNA /DB_XREF=gi:1043 9935						
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nuclear protein /DB_XREF=gi:1033 4853 /UG=Hs.40342 putative nuclear protein /FL=gb:NM_007032 202795_x_at NM_007032 Consensus includes gb:AK026954.1 /DEF=Homo sapiens cDNA: FLJ23301 fis, clone HEP11120. /FEA=mRNA /DB_XREF=gi:1043 9935				l .		
/DB_XREF=gi:1033 4853 /UG=Hs.40342 putative nuclear protein /FL=gb:NM_007032 202795_x_at NM_007032 Consensus includes gb:AK026954.1 //DEF=Homo sapiens cDNA: FLJ23301 fis, clone HEP11120. /FEA=mRNA /DB_XREF=gi:1043 9935				1		
4853 //UG=Hs.40342 putative nuclear protein /FL=gb:NM_007032 202795_x_at NM_007032 .1 Consensus includes gb:AK026954.1 //DEF=Homo sapiens cDNA: FLJ23301 fis, clone HEP11120. /FEA=mRNA //DB_XREF=gi:1043 9935						
/UG=Hs.40342 putative nuclear protein /FL=gb:NM_007032 202795_x_at NM_007032 1 Consensus includes gb:AK026954.1 /DEF=Homo sapiens cDNA: FLJ23301 fis, clone HEP11120. /FEA=mRNA /DB_XREF=gi:1043 9935						
putative nuclear protein /FL=gb:NM_007032 202795_x_at NM_007032 .1 Consensus includes gb:AK026954.1 /DEF=Homo sapiens cDNA: FLJ23301 fis, clone HEP11120. /FEA=mRNA /DB_XREF=gi:1043 9935						
protein /FL=gb:NM_007032 202795_x_at NM_007032 .1 Consensus includes gb:AK026954.1 //DEF=Homo sapiens cDNA: FLJ23301 fis, clone HEP11120. /FEA=mRNA /DB_XREF=gi:1043 9935				/UG=Hs.40342		
/FL=gb:NM_007032				putative nuclear		
202795_x_at				protein		
202795_x_at				/FL=gb:NM 007032		
Consensus includes gb:AK026954.1 //DEF=Homo sapiens cDNA: FLJ23301 fis, clone HEP11120. //FEA=mRNA //DB_XREF=gi:1043 9935	202795 x at		NM 007032	–		
includes gb:AK026954.1 /DEF=Homo sapiens cDNA: FLJ23301 fis, clone HEP11120. /FEA=mRNA /DB_XREF=gi:1043 9935						
includes gb:AK026954.1 /DEF=Homo sapiens cDNA: FLJ23301 fis, clone HEP11120. /FEA=mRNA /DB_XREF=gi:1043 9935				Consensus		
gb:AK026954.1 //DEF=Homo sapiens cDNA: FLJ23301 fis, clone HEP11120. //FEA=mRNA //DB_XREF=gi:1043 9935				I .		
/DEF=Homo sapiens cDNA: FLJ23301 fis, clone HEP11120. /FEA=mRNA /DB_XREF=gi:1043 9935				1	1]
sapiens cDNA: FLJ23301 fis, clone HEP11120. /FEA=mRNA /DB_XREF=gi:1043 9935			·			
FLJ23301 fis, clone HEP11120. /FEA=mRNA /DB_XREF=gi:1043 9935						
clone HEP11120. /FEA=mRNA /DB_XREF=gi:1043 9935					1	[1
/FEA=mRNA /DB_XREF=gi:1043 9935			1	•		
/DB_XREF=gi:1043 9935						
9935						
				, – •	1	
					1	
			ļ	/UG=Hs.91065		
hypothetical protein					1	
212781_at AK026954 DKFZp761B2423	212781_at		AK026954	DKFZp761B2423		

Application of: Liew, et. al. Our Docket #: 4231/2042 Figure 7a Cont'd.

Consensus includes gb:AB033066.1 /DEF=Homo sapiens mRNA for KIAA1240 protein, partial cds. /FEA=mRNA /GEN=KIAA1240 /PROD=KIAA1240 protein /DB_XREF=gi:6330 790 /UG=Hs.62576 KIAA1240 protein AB033066 213387_at gb:NM_003651.1 /DEF=Homo sapiens cold shock domain protein A (CSDA), mRNA. /FEA=mRNA /GEN=CSDA /PROD=cold shock domain protein A /DB_XREF=gi:4503 070 /UG=Hs.1139 cold shock domain protein A /FL=gb:NM_003651 201161_s_at NM 003651 gb:NM_006393.1 /DEF=Homo sapiens nebulette (NEBL), mRNA. /FEA=mRNA /GEN=NEBL /PROD=nebulette /DB_XREF=gi:5453 757 /UG=Hs.5025 nebulette /FL=gb:NM_006393 NM_006393 203962_s_at RecQ protein-like (DNA helicase Q1-213878 at RECQL AI685944 like) Hs.235069

Figure 7a (Cont'd.
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Figure 7a CC	7716 41.			
r igalo r a o			Consensus includes gb:AL050378.1 //DEF=Homo sapiens mRNA; cDNA DKFZp586I1420 (from clone DKFZp586I1420); partial cds. //FEA=mRNA	
			/GEN=DKFZp586I1 420 /PROD=hypothetica I protein /DB_XREF=gi:4914 581	
-			/UG=Hs.112423 Homo sapiens mRNA; cDNA DKFZp586I1420 (from clone	
213546_at		AL050378	DKFZp586I1420); partial cds	
			gb:U16153.1 /DEF=Human Id- 4H protein mRNA, complete cds. /FEA=mRNA /PROD=Id-4H protein /DB_XREF=gi:6250 95 /UG=Hs.34853 inhibitor of DNA binding 4, dominant negative	
209293_x_at		U16153	helix-loop-helix protein /FL=gb:NM_001546 .1 gb:U16153.1 gb:U28368.1	

Figure /a Cont'd.		
200064 at	AF275719	gb:AF275719.1 /DEF=Homo sapiens isolate Liv chaperone protein HSP90 beta (HSP90BETA) mRNA, complete cds. /FEA=mRNA /GEN=HSP90BETA /PROD=chaperone protein HSP90 beta /DB_XREF=gi:9082 288 /UG=Hs.74335 heat shock 90kD protein 1, beta /FL=gb:BC004928.1 gb:M16660.1 gb:NM_007355.1 gb:AF275719.1
200072_s_at	AF061832	gb:AF061832.1 /DEF=Homo sapiens M4 protein deletion mutant mRNA, complete cds. /FEA=mRNA /PROD=M4 protein deletion mutant /DB_XREF=gi:3126 877 /UG=Hs.79024 heterogeneous nuclear ribonucleoprotein M /FL=gb:AF061832.1

Figure /a Co	nit u.		I-h.NM 005000 4		
:			gb:NM_005336.1 /DEF=Homo		Ì
			sapiens high		
			density lipoprotein		
			binding protein		
	'		(vigilin) (HDLBP),		
			mRNA.		
			/FEA=mRNA		
			/GEN=HDLBP		
			/PROD=high		
			density lipoprotein		
			binding protein		
			/DB_XREF=gi:4885		
			408	:	
			/UG=Hs.177516		
1			high density		
			lipoprotein binding		
	,		protein (vigilin)		
			/FL=gb:BC001179.1		
			gb:M64098.1		
200643_at		NM_005336	gb:NM_005336.1 Consensus		<u> </u>
			lincludes		
			gb:D80000.1		
1			/DEF=Human		
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			KIAA0178 gene,		
			partial cds.		
			/FEA=mRNA		
			/GEN=KIAA0178		
			/DB_XREF=gi:1136		
	·		415		
			/UG=Hs.211602		
			SMC1 (structural		
			maintenance of		
			chromosomes 1,		
			yeast)-like 1 /FL=gb:NM_006306		
201500 01		D80000	1.1		
201589_at 41644_at	KIAA0790	AB018333	KIAA0790 protein	NM_015278	Hs.12002
7 1077_at	11/0/01/30	7.2010333	MAP/microtubule	14141_010270	110.12002
			affinity-regulating		
202568 s at	MARK3	AI745639	kinase 3		Hs.172766
			seven in absentia		
			homolog 1		į i
221834_at	SIAH1 KIAA1332	U70056 AA836114	(Drosophila) KIAA1332 protein		Hs.295923 Hs.62767

r iguic 7a O	1		gb:NM_001085.2		
			/DEF=Homo		
			sapiens serine (or		
				i	
			cysteine)	i	
			proteinase		
			inhibitor, clade A		
			(alpha-1		
			antiproteinase,		
			antitrypsin),		
			member 3		
			(SERPINA3),		
			mRNA.		
			/FEA=mRNA		
			/GEN=SERPINA3		
			/PROD=alpha-1-		
			antichymotrypsin,		:
	•		precursor		
			/DB_XREF=gi:9665		
			246		
			/UG=Hs.234726		
			serine (or		
			cysteine)		
			proteinase		
			inhibitor, clade A		
			(alpha-1		
			antiproteinase,		
			antitrypsin),		
			member 3		
			/FL=gb:BC003559.1		
			gb:K01500.1		
202376_at		NM_001085	gb:NM_001085.2		
202010_4			hypothetical protein		
222163_s_at	MGC5347	BE890973	MGC5347		Hs.5555
at	1	1223000.0	1	l	

Figure	7a	Cont'd.

gb:AF114013.1 //DEF=Homo sapiens tumor necrosis factor- related death ligand-1gamma mRNA, complete cds. /FEA=mRNA //PROD=tumor necrosis factor- related deathiligand- 1gamma //DB_XREF=gi:7328 557 //UG=Hs.54673 tumor necrosis factor (ligand) superfamily, member 13 /FL=gb:AF136294.1 gb:AF114013.1 gb:NM_001884.1 //DEF=Homo sapiens cartilage linking protein 1 (CRTL1), mRNA. //FEA=mRNA //GEN=CRTL1 //PROD=cartilage linking protein 1 //DB_XREF=gi:4503 052 //UG=Hs.2799 cartilage linking	/DEF=Homo sapiens tumor necrosis factor- related death ligand-1gamma mRNA, complete cds. /FEA=mRNA //PROD=tumor necrosis factor- related deathligand- 1gamma //DB_XREF=gi.7328 557 /UG=Hs.54673 tumor necrosis factor (ligand) superfamily, member 13 //FL=gb:AF136294.1 gb:AF114013.1 gb:NM_001884.1 //DEF=Homo sapiens cartilage linking protein 1 (CRTL1), mRNA. //FEA=mRNA //GEN=CRTL1 //PROD=cartilage linking protein 1 //DB_XREF=gi.4503 052 /UG=Hs.2799 cartilage linking protein 1	 	 	
gb:NM_001884.1 /DEF=Homo sapiens cartilage linking protein 1 (CRTL1), mRNA. /FEA=mRNA /GEN=CRTL1 /PROD=cartilage linking protein 1 /DB_XREF=gi:4503 052 /UG=Hs.2799 cartilage linking	210314_x_at AF114013 gb:AF114013.1 gb:NM_001884.1 //DEF=Homo sapiens cartilage linking protein 1 (CRTL1), mRNA. //FEA=mRNA //GEN=CRTL1 //PROD=cartilage linking protein 1 //DB_XREF=gi:4503 052 /UG=Hs.2799 cartilage linking protein 1		/DEF=Homo sapiens tumor necrosis factor- related death ligand-1gamma mRNA, complete cds. /FEA=mRNA /PROD=tumor necrosis factor- related deathligand- 1gamma /DB_XREF=gi:7328 557 /UG=Hs.54673 tumor necrosis factor (ligand) superfamily, member 13	
protein 1			gb:NM_001884.1 /DEF=Homo sapiens cartilage linking protein 1 (CRTL1), mRNA. /FEA=mRNA /GEN=CRTL1 /PROD=cartilage linking protein 1 /DB_XREF=gi:4503 052 /UG=Hs.2799 cartilage linking protein 1 /FL=gb:U43328.1	

Figure /a Co	nta.			
204215_at			gb:NM_024315.1 /DEF=Homo sapiens hypothetical protein MGC4175 (MGC4175), mRNA. /FEA=mRNA /GEN=MGC4175 /PROD=hypothetica I protein MGC4175 /DB_XREF=gi:1323 6556 /UG=Hs.322404 hypothetical protein MGC4175 /FL=gb:BC002837.1 gb:NM_024315.1	
220890_s_at		 NM_016355	gb:NM_016355.1 /DEF=Homo sapiens hqp0256 protein (LOC51202), mRNA. /FEA=mRNA /GEN=LOC51202 /PROD=hqp0256 protein /DB_XREF=gi:1004 7107 /UG=Hs.284288 hqp0256 protein /FL=gb:NM_016355 .1 gb:AF078843.1	

Figure /a Co	Jiit G.		T	
219717_at		NM_017741	gb:NM_017741.1 //DEF=Homo sapiens hypothetical protein FLJ20280 (FLJ20280), mRNA. //FEA=mRNA //GEN=FLJ20280 //PROD=hypothetica I protein FLJ20280 //DB_XREF=gi:8923 256 //UG=Hs.270134 hypothetical protein FLJ20280 //FL=gb:NM_017741 .1	
			SON DNA binding	
213538_at	SON	AI936458	protein	Hs.92909
205089_at		NM_003416	gb:NM_003416.1 /DEF=Homo sapiens zinc finger protein 7 (KOX 4, clone HF.16) (ZNF7), mRNA. /FEA=mRNA /GEN=ZNF7 /PROD=zinc finger protein 7 (KOX 4, clone HF.16) /DB_XREF=gi:4508 034 /UG=Hs.2076 zinc finger protein 7 (KOX 4, clone HF.16) /FL=gb:M29580.1 gb:NM_003416.1	

Figure 7a Co	illu.		F	
208691_at		BC001188	gb:BC001188.1 /DEF=Homo sapiens, transferrin receptor (p90, CD71), clone MGC:3151, mRNA, complete cds. /FEA=mRNA /PROD=transferrin receptor (p90, CD71) /DB_XREF=gi:1265 4696 /UG=Hs.77356 transferrin receptor (p90, CD71) /FL=gb:BC001188.1 gb:M11507.1	
209170_s_at		AF016004	gb:AF016004.1 /DEF=Homo sapiens m6b1 mRNA, complete cds. /FEA=mRNA /GEN=m6b1 /DB_XREF=gi:3387 766 /UG=Hs.5422 glycoprotein M6B /FL=gb:AF016004.1	
209167_at		AF016004	Consensus includes gb:Al419030 /FEA=EST /DB_XREF=gi:4264 961 /DB_XREF=est:tf53 b01.x1 /CLONE=IMAGE:21 02953 /UG=Hs.5422 glycoprotein M6B /FL=gb:AF016004.1	

I igure /a co	 		 · · · · · · · · · · · · · · · · · · ·
218134_s_at	NM_018047	gb:NM_018047.1 /DEF=Homo sapiens hypothetical protein FLJ10290 (FLJ10290), mRNA. /FEA=mRNA /GEN=FLJ10290 /PROD=hypothetica I protein FLJ10290 /DB_XREF=gi:8922 327 /UG=Hs.25516 hypothetical protein FLJ10290 /FL=gb:AL136933.1 gb:NM_018047.1 gb:NM_018047.1 gb:NM_018047.1 /DEF=Homo sapiens zinc finger protein 263 (ZNF263), mRNA. /FEA=mRNA /GEN=ZNF263 /PROD=zinc finger protein 263 /PROD=zinc finger protein 263 /PROD=zinc finger protein 263 /PROD=zinc finger protein 263 /PROD=zinc finger protein 263 /FL=gb:D88827.1	
203707_at	 NM_005741	gb:NM_005741.1	

Figure	7a	Cont'd.

gb:NM_018357.1 //DEF=Homo sapiens hypothetical protein FI_J11196 (FLJ11196), mRNA. //EA=mRNA //EA=mRNA //EB=j:8922 933 /UG=Hs.6166 hypothetical protein FI_J11196 //PCO=hypothetical I protein FI_J11196 //PCD=hypothetical I protein FI_J11196 //DE_Hs.6166 hypothetical protein FI_J11196 //EL=gb:NM_018357 1 gb:NM_018357	Figure /a Co	inte.			
/DEF=Homo sapiens TG- interacting factor (TALE family homeobox) (TGIF), mRNA. /FEA=mRNA /GEN=TGIF /PROD=TG- interacting factor (TALE family homeobox) /DB_XREF=gi:4507 472 /UG=Hs.90077 TG-interacting factor (TALE family homeobox) /FL=gb:BC000814.1 gb:NM_003244.1	218651_s_at		NM_018357	/DEF=Homo sapiens hypothetical protein FLJ11196 (FLJ11196), mRNA. /FEA=mRNA /GEN=FLJ11196 /PROD=hypothetica I protein FLJ11196 /DB_XREF=gi:8922 933 /UG=Hs.6166 hypothetical protein FLJ11196 /FL=gb:NM_018357	
/DEF=Homo sapiens TG- interacting factor (TALE family homeobox) (TGIF), mRNA. /FEA=mRNA /GEN=TGIF /PROD=TG- interacting factor (TALE family homeobox) /DB_XREF=gi:4507 472 /UG=Hs.90077 TG-interacting factor (TALE family homeobox) /FL=gb:BC000814.1 gb:NM_003244.1					
1203333 6 St INM 1032777 10034-1799013 1	203313_s_at		NM_003244	/DEF=Homo sapiens TG-interacting factor (TALE family homeobox) (TGIF), mRNA. /FEA=mRNA /GEN=TGIF /PROD=TG-interacting factor (TALE family homeobox) /DB_XREF=gi:4507 472 /UG=Hs.90077 TG-interacting factor (TALE family homeobox) /FL=gb:BC000814.1	

Figure 7a CC	 		
218429_s_at	NM_018381	gb:NM_018381.1 /DEF=Homo sapiens hypothetical protein FLJ11286 (FLJ11286), mRNA. /FEA=mRNA /GEN=FLJ11286 /PROD=hypothetica I protein FLJ11286 /DB_XREF=gi:8922 978 /UG=Hs.12151 hypothetical protein FLJ11286 /FL=gb:NM_018381 .1	
210723_3_at	0 10001		
		gb:NM_001243.1 /DEF=Homo sapiens tumor necrosis factor receptor superfamily, member 8 (TNFRSF8), mRNA. /FEA=mRNA /GEN=TNFRSF8 /PROD=CD30 antigen (Ki-1 antigen) /DB_XREF=gi:4507 588 /UG=Hs.1314 tumor necrosis factor receptor superfamily, member 8 /FL=gb:D86042.1 gb:M83554.1	
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Figure /a Contd.			
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	Ì	sapiens, clone	
		IMAGE:3940843,	
		mRNA, partial cds.	
		/FEA=mRNA	
		/PROD=Unknown	
1		·	
		(protein for	
]		IMAGE:3940843)	
		/DB_XREF=gi:1280	
1		4044	
	1	/UG=Hs.274149	
		proline and	
		glutamic acid rich	
215354_s_at	BC002875	nuclear protein	
		gb:NM_016657.1	
1		/DEF=Homo	
		sapiens KDEL	
1		(Lys-Asp-Glu-Leu)	
		endoplasmic	
		reticulum protein	
		retention receptor	
		3 (KDELR3),	
		transcript variant	
	1	2, mRNA.	
		/FEA=mRNA	
		/GEN=KDELR3	
		/PROD=KDEL	
		F I	
		receptor 3, isoform	
		b vpcc:-0054	
		/DB_XREF=gi:8051	
		610	
	1	/UG=Hs.250696	
		KDEL (Lys-Asp-	
	1	Glu-Leu)	
		endoplasmic	
		reticulum protein	
		retention receptor	
		3	
		/FL=gb:NM_016657	
207264_at	NM_016657	.1	

Figure 7a Co	Jin u.				
			gb:NM_018660.1 /DEF=Homo sapiens papillomavirus regulatory factor PRF-1 (LOC55893), mRNA. /FEA=mRNA /GEN=LOC55893 /PROD=papillomavi rus regulatory factor PRF-1 /DB_XREF=gi:8923 886 /UG=Hs.27410 papillomavirus regulatory factor PRF-1 /FL=gb:AF263928.1		
221123_x_at		NM_018660	gb:NM_018660.1 acyl-Coenzyme A		
	ŀ		dehydrogenase,		
206068_s_at	ACADL	Al367275	long chain		Hs.1209
		A16000004	Consensus includes gb:AK023621.1 /DEF=Homo sapiens cDNA FLJ13559 fis, clone PLACE1007852, highly similar to Homo sapiens mRNA for KIAA0878 protein. /FEA=mRNA /DB_XREF=gi:1043 5602 /UG=Hs.188006		
216048_s_at 212776_s_at	KIAA0657	AK023621 AI978623	KIAA0878 protein KIAA0657 protein		Hs.6654
212110_S_at	TVINA0001	M1910052	Triavoos, bioreiu	L	113.0004

Figure 7a Conf	ťd	
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Figure 1a Co	517C G.			
201531 at		NM 003407	gb:NM_003407.1 /DEF=Homo sapiens zinc finger protein homologous to Zfp- 36 in mouse (ZFP36), mRNA. /FEA=mRNA /GEN=ZFP36 /PROD=zinc finger protein homologous to Zfp- 36 inmouse /DB_XREF=gi:4507 960 /UG=Hs.1665 zinc finger protein homologous to Zfp- 36 in mouse /FL=gb:M92843.1 gb:M63625.1 gb:NM_003407.1	
201001_at		14W_003407	gb.14141_005+07.1	
			gb:NM_004867.1 /DEF=Homo sapiens integral membrane protein 2A (ITM2A), mRNA. /FEA=mRNA /GEN=ITM2A /PROD=integral membrane protein 2A /DB_XREF=gi:4758 223 /UG=Hs.17109 integral membrane protein 2A /FL=gb:AF038953.1	
202747_s_at		NM_004867	gb:NM_004867.1	
			CCAAT/enhancer binding protein	
213006_at	CEBPD	AV655640	(C/EBP), delta	Hs.76722

Application of: Liew, et. al. Our Docket #: 4231/2042 Figure 7a Cont'd.

Figure 7a Co	ont'd.			
	· - · · · · · · · · · · · · · · · · · ·		gb:AF078077.1	
			/DEF=Homo	
			sapiens growth	
			arrest and DNA-	
			damage-inducible	
			protein	
			GADD45beta	
			mRNA, complete	
i.			cds. /FEA=mRNA	
			/PROD=growth	
			arrest and DNA-	
			damage-inducible	
			proteinGADD45bet	
			a	
			/DB_XREF=gi:3978	
			391	
			/UG=Hs.110571	}
			growth arrest and	
			DNA-damage-	
			inducible, beta	
			/FL=gb:AF087853.1	
209305_s_at		AF078077	gb:AF078077.1	
		7.0.00	.	
			gb:NM_015675.1	
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			sapiens growth	
			arrest and DNA-	
			damage-inducible,	
			beta (GADD45B),	
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1			/FEA=mRNA	
			/GEN=GADD45B	
1			/PROD=DKFZP566	
			B133 protein	
}			/DB_XREF=gi:9945	
			331	
			/UG=Hs.110571	
			growth arrest and	
[DNA-damage-	
			inducible, beta	
			/FL=gb:AF090950.1	
207574_s_at		NM_015675	gb:NM_015675.1	
222041_at	t	BG235929	ESTs	 Hs.391830

Figure 7a Co	onta.	·	·	·	
204377_s_at		NM_014703	gb:NM_014703.1 /DEF=Homo sapiens KIAA0800 gene product (KIAA0800), mRNA. /FEA=mRNA /GEN=KIAA0800 /PROD=KIAA0800 gene product /DB_XREF=gi:7662 315 /UG=Hs.118738 KIAA0800 gene product /FL=gb:AB018343.1 gb:NM_014703.1		He 2776
217741_s_at	ZNF216	AW471220	gb:NM_000655.2 /DEF=Homo sapiens selectin L (lymphocyte adhesion molecule 1) (SELL), mRNA.		Hs.3776
204563 at		NM 000655	/FEA=mRNA /GEN=SELL /PROD=selectin L /DB_XREF=gi:5713 320 /UG=Hs.82848 selectin L (lymphocyte adhesion molecule 1) /FL=gb:M25280.1 gb:NM_000655.2		

Figure 7a	Cont'd.
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204406_at	NM 002019	gb:NM_002019.1 /DEF=Homo sapiens fms- related tyrosine kinase 1 (vascular endothelial growth factorvascular permeability factor receptor) (FLT1), mRNA. /FEA=mRNA /GEN=FLT1 /PROD=fms-related tyrosine kinase 1 (vascularendothelial growth factorvascular permeability factorreceptor) /DB_XREF=gi:4503 748 /UG=Hs.138671 fms-related tyrosine kinase 1 (vascular endothelial growth factorvascular permeability factor receptor) /FL=gb:AF063657.1 gb:NM 002019.1	
205976_at	NM_014929	gb:NM_014929.1 /DEF=Homo sapiens KIAA0971 protein (KIAA0971), mRNA. /FEA=mRNA /GEN=KIAA0971 /PROD=KIAA0971 protein /DB_XREF=gi:7662 421 /UG=Hs.84429 KIAA0971 protein /FL=gb:AB023188.1 gb:NM_014929.1	

Figure 7a Co	inta.		,		
			gb:NM_004327.2 /DEF=Homo sapiens breakpoint cluster region (BCR), transcript variant 1, mRNA. /FEA=mRNA /GEN=BCR /PROD=breakpoint cluster region, isoform 1 /DB_XREF=gi:1103 8638 /UG=Hs.234799 breakpoint cluster region /FL=gb:NM_004327		
202315_s_at		NM_004327	.2		
			gb:BC001425.1 /DEF=Homo sapiens, Similar to differential display and activated by p53, clone MGC:1780, mRNA, complete cds. /FEA=mRNA /PROD=Similar to differential display and activated byp53 /DB_XREF=gi:1265 5140 /UG=Hs.77550 CDC28 protein kinase 1 /FL=gb:BC001425.1 gb:AF274941.1 gb:AF279897.1		
201896_s_at		BC001425	gb:NM_001826.1		
			tumor necrosis		
			factor, alpha-		
206025_s_at	TNFAIP6	AW188198	induced protein 6		Hs.29352
64942_at		Al937160	ESTs, Weakly similar to A43932 mucin 2 precursor, intestinal - human (fragments) [H.sapiens]		Hs.7967
07372_at	<u>L</u>	1,4901 100	III i.sapiciisj	L	15. / 55 /

Application of: Liew, et. al. Our Docket #: 4231/2042 Figure 7a Cont'd.

Figure 7a Co	onta.			 1
211343_s_at		M33653	gb:M33653.1 /DEF=Human (clones HT- 125,133) alpha-2 type IV collagen (COL4A2) mRNA, complete cds. /FEA=mRNA /GEN=COL4A2 /PROD=alpha-2 type IV collagen /DB_XREF=gi:1808 28 /UG=Hs.211933 collagen, type XIII, alpha 1 /FL=gb:M33653.1	
211040_3_dt		14.00000	FK506 binding	
214119_s_at	FKBP1A	AI936769	protein 1A, 12kDa	 Hs.380080
247772		NIM 014242	gb:NM_014342.1 /DEF=Homo sapiens mitochondrial carrier homolog 2 (MTCH2), nuclear gene encoding mitochondrial protein, mRNA. /FEA=mRNA /GEN=MTCH2 /PROD=mitochondri al carrier homolog 2 /DB_XREF=gi:7657 346 /UG=Hs.279609 mitochondrial carrier homolog 2 /FL=gb:BC000875.1 gb:AF085361.1 gb:AF176008.1 gb:NM_014342.1	
217772_s_at	<u></u>	NM_014342	gb:NM_014342.1	

Figure 7a Co	T		gb:BC000296.1		-
			/DEF=Homo		
			sapiens, Similar to		
:			KIAA0772 gene		
			product, clone		
			MGC:8342, mRNA,		
			complete cds.		
			/FEA=mRNA		
			/PROD=Similar to		
	İ		KIAA0772 gene		
			product		
			/DB_XREF=gi:1265		
			3062		
			/UG=Hs.15519		
			KIAA0772 gene		
			product		
			/FL=gb:BC000296.1		
209222_s_at		BC000296	gb:BC004455.1	!	
	[calcium/calmodulin-		
			dependent protein	=	
	·		kinase kinase 2,		
212252 at	CAMKK2	AA181179	beta		Hs.108708
	****			<u> </u>	
			gb:NM_001718.2		
			/DEF=Homo		
			sapiens bone		
			morphogenetic		
			protein 6 (BMP6),		
			mRNA.		
			/FEA=mRNA		
			/GEN=BMP6		
			/PROD=bone		
			morphogenetic	,	
			protein 6 precursor		
		-	/DB XREF=gi:4809		
			281		
			/UG=Hs.285671		
			bone		
			morphogenetic		
			protein 6		
	1		/FL=gb:M60315.1		
206176_at	1	NM_001718	gb:NM_001718.2		
213030_s_at	PLXNA2	Al688418	plexin A2		Hs.300622
∠13030_S_at	JPLXNA2	JA1000418	Thiexin Az	L	IDS.30002Z

Figure 7a Co	Jit a.			
208912_s_at		BC001362	gb:BC001362.1 /DEF=Homo sapiens, 2,3-cyclic nucleotide 3 phosphodiesterase, clone MGC:2262, mRNA, complete cds. /FEA=mRNA /PROD=2,3-cyclic nucleotide 3 phosphodiesterase /DB_XREF=gi:1265 5028 /UG=Hs.150741 2,3-cyclic nucleotide 3 phosphodiesterase /FL=gb:BC001362.1 gb:M19650.1	
220432_s_at		NM_016593	gb:NM_016593.1 /DEF=Homo sapiens oxysterol 7alpha-hydroxylase (CYP39A1), mRNA. /FEA=mRNA /GEN=CYP39A1 /PROD=oxysterol 7alpha-hydroxylase /DB_XREF=gi:7706 128 /UG=Hs.20766 oxysterol 7alpha- hydroxylase /FL=gb:AF237982.1 gb:NM_016593.1	

Figure 7a Co	JIIL G.		NIM OCCASS 4	1	 -
			gb:NM_006455.1 /DEF=Homo	1	
			sapiens nucleolar		
			autoantigen (55kD) similar to rat		
	·		synaptonemal		
			complex protein (SC65), mRNA.		
			/FEA=mRNA		
			/GEN=SC65		
			/PROD=nucleolar		
			autoantigen (55kD)		
			similar to		
			ratsynaptonemal		
			complex protein		
			/DB XREF=gi:5454		
			037		
			/UG=Hs.207251		
	1		nucleolar		
			autoantigen (55kD)		
			similar to rat		
1			synaptonemal		
			complex protein		
			/FL=gb:BC001047.1		
			gb:U47621.1	į	
204078_at		NM_006455	gb:NM_006455.1		
221987_s_at	SRR	AI803633	serine racemase		Hs.204501
			gb:NM_018153.1		
			/DEF=Homo		
			sapiens		
	•		hypothetical protein FLJ10601		
			(FLJ10601),		
			mRNA.		
1			/FEA=mRNA		
			/GEN=FLJ10601		
	1		/PROD=hypothetica		
			I protein FLJ10601	,	
			/DB_XREF=gi:8922		ĺ
	l .	I	. –		
		l .	545		
			/UG=Hs.257174		
			/UG=Hs.257174		
			/UG=Hs.257174 hypothetical protein		

rigule ra Oc	in a.			
209715_at		L07515	gb:L07515.1 /DEF=Human heterochromatin protein homologue (HP1) mRNA, complete cds. /FEA=mRNA /DB_XREF=gi:1843 10 /UG=Hs.89232 chromobox homolog 5 (Drosophila HP1 alpha) /FL=gb:L07515.1 gb:NM_012117.1	
213069 at	KIAA1237	AI148659	KIAA1237 protein	Hs.10491
			Consensus includes gb:Al357376 /FEA=EST /DB_XREF=gi:4108 997 /DB_XREF=est:qy1 3a06.x1 /CLONE=IMAGE:20 11858 /UG=Hs.12017 homolog of yeast ubiquitin-protein ligase Rsp5; potential epithelial sodium channel	
212445 s at		AB007899	regulator	
209197_at	SYT11	AA626780	synaptotagmin XI	Hs.380439

Figure	7а	Cont	<u>'d.</u>

I Iguic 7 a Oc					
220603_s_at		NM_018349	gb:NM_018349.1 /DEF=Homo sapiens hypothetical protein FLJ11175 (FLJ11175), mRNA. /FEA=mRNA /GEN=FLJ11175 /PROD=hypothetica I protein FLJ11175 /DB_XREF=gi:8922 916 /UG=Hs.33368 hypothetical protein FLJ11175 /FL=gb:NM_018349 .1		
218534_s_at		NM_018046	gb:NM_018046.1 /DEF=Homo sapiens hypothetical protein FLJ10283 (FLJ10283), mRNA. /FEA=mRNA /GEN=FLJ10283 /PROD=hypothetica I protein FLJ10283 /DB_XREF=gi:8922 325 /UG=Hs.284216 hypothetical protein FLJ10283 /FL=gb:NM_018046 .1	·	
			seven in absentia		11- 005000
221833_at	SIAH1	U70056	(Drosophila)	L	Hs.295923

ga.o 7 a o	 			
221508 at	AF181985	gb:AF181985.1 /DEF=Homo sapiens serinethreonine kinase (KDS) mRNA, complete cds. /FEA=mRNA /GEN=KDS /PROD=serinethreo nine kinase /DB_XREF=gi:6708 149 /UG=Hs.12040 STE20-like kinase /FL=gb:BC002756.1 gb:AF181985.1		
221691_x_at	AB042278	gb:AB042278.1 /DEF=Homo sapiens mRNA for nucleophosminB23. 2, complete cds. /FEA=mRNA /PROD=nucleophos minB23.2 /DB_XREF=gi:1353 6990 /FL=gb:AB042278.1		

Consensus includes gb:AL121903 //DEF=Human DNA sequence from clone RP1-155G6 on chromosome 20 Contains part of the gene for brefeldin A- inhibited guanine nucleotide- exchange protein 2, part of the gene for CSE1L (chromosome segregation 1 (yeast homolog)- like), ESTs, STSs, GSSs and a //FEA=mRNA //DB_XREF=gi:7330 682 //LIG=Hs 118249		ure 7a Cont'd.	Figure 7a Co
brefeldin A- inhibited guanine nucleotide- exchange protein 2 //FL=gb:AF084521.1	includes gb:AL121903 //DEF=Human DNA sequence from clone RP1-155G6 on chromosome 20 Contains part of the gene for brefeldin A- inhibited guanine nucleotide- exchange protein 2, part of the gene for CSE1L (chromosome segregation 1 (yeast homolog)- like), ESTs, STSs, GSSs and a //FEA=mRNA //DB_XREF=gi:7330 682 //UG=Hs.118249 brefeldin A- inhibited guanine nucleotide- exchange protein 2		
218098_at NM_006420 gb:NM_006420.1	1 - 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	98 at NM 006420	218098 at
gb:NM_018297.1 /DEF=Homo sapiens hypothetical protein FLJ11005 (FLJ11005), mRNA. /FEA=mRNA /GEN=FLJ11005 /PROD=hypothetica I protein FLJ11005 /DB_XREF=gi:8922 817 /UG=Hs.63657 hypothetical protein FLJ11005 /FL=gb:NM_018297 220742_s_at NM_018297 .1	gb:NM_018297.1 //DEF=Homo sapiens hypothetical protein FLJ11005 (FLJ11005), mRNA. //FEA=mRNA //GEN=FLJ11005 //PROD=hypothetica I protein FLJ11005 //DB_XREF=gi:8922 817 /UG=Hs.63657		

Figure 7a Co	onta.	···			
			nuclear		
			transcription factor		
218127_at	NFYB	AI804118	Y, beta		Hs.84928
210121_at	INI TO	71007110	1, 50.6		110.01020
			gb:NM_012456.1		
			/DEF=Homo		
			sapiens		
			translocase of		
			inner mitochondrial		
			membrane 10		
			(yeast) homolog		
			(TIMM10), mRNA.		
			/FEA=mRNA		
			/GEN=TIMM10		
			/PROD=translocase		1
			of inner		
			mitochondrial		[
			membrane		
			10(yeast) homolog		
	,		/DB_XREF=gi:6912		
1			707		
		1	/UG=Hs.109571		
			translocase of		
			inner mitochondrial		
			membrane 10		
			(yeast) homolog	<u>'</u>	
			/FL=gb:AF150089.1]
			gb:AF152354.1		
218408_at		NM_012456	gb:NM_012456.1		
210700_at		1.111_0.12.100	3-1-1-1-1-1		
		1	-b.AE200204 4		
			gb:AF288391.1		
			/DEF=Homo		
!			sapiens C1orf24		
			mRNA, complete		
1	1		cds. /FEA=mRNA		
	1		/PROD=C1orf24		
	1		1		
			/DB_XREF=gi:1262		
	1		0191]
			/UG=Hs.48778		
	1	I	niban protein		
1	1	1			
		1	/FL=gb:AB050477.1		
	1	1	gb:NM_022083.1		
217967_s_at		AF288391	gb:AF288391.1		<u> </u>
				NM_015242;	
34206_at	CENTD2	AB018325	centaurin, delta 2	NM_139181	Hs.21264
07200_al	IOPINIO5	[ADD 10020	Tochtaum, delta Z	100101	1.10.2.1207

Figure 7a Co	Jill G.			
218364_at			gb:NM_017724.1 /DEF=Homo sapiens leucine rich repeat (in FLII) interacting protein 2 (LRRFIP2), mRNA. /FEA=mRNA /GEN=LRRFIP2 /PROD=leucine rich repeat (in FLII) interactingprotein 2 /DB_XREF=gi:8923 223 /UG=Hs.57672 leucine rich repeat (in FLII) interacting protein 2 /FL=gb:NM_017724 .1	
219544_at		NM_024808	gb:NM_024808.1 /DEF=Homo sapiens hypothetical protein FLJ22624 (FLJ22624), mRNA. /FEA=mRNA /GEN=FLJ22624 /PROD=hypothetica I protein FLJ22624 /DB_XREF=gi:1337 6190 /UG=Hs.166425 hypothetical protein FLJ22624 /FL=gb:NM_024808 .1	

Figure 7a Co	 		
219037_at	NM_016052	gb:NM_016052.1 /DEF=Homo sapiens CGI-115 protein (LOC51018), mRNA. /FEA=mRNA /GEN=LOC51018 /PROD=CGI-115 protein /DB_XREF=gi:7705 619 /UG=Hs.56043 CGI-115 protein /FL=gb:AF151873.1 gb:NM_016052.1	
219434_at	NM_018643	gb:NM_018643.1 /DEF=Homo sapiens triggering receptor expressed on myeloid cells 1 (TREM1), mRNA. /FEA=mRNA /GEN=TREM1 /PROD=triggering receptor expressed on myeloid cells1 /DB_XREF=gi:8924 261 /UG=Hs.283022 triggering receptor expressed on myeloid cells 1 /FL=gb:AF196329.1 gb:NM_018643.1 gb:AF287008.1	

Figure 7a C	Ontu.				
218041_x_at		NM_018573	gb:NM_018573.1 /DEF=Homo sapiens hypothetical protein PRO1068 (PRO1068), mRNA. /FEA=mRNA /GEN=PRO1068 /PROD=hypothetica I protein PRO1068 /DB_XREF=gi:8924 006 /UG=Hs.321158 hypothetical protein PRO1068 /FL=gb:AF116620.1 gb:NM_018573.1		
218313_s_at		NM_017423	gb:NM_017423.1 /DEF=Homo sapiens UDP-N- acetyl-alpha-D- galactosamine:poly peptide N- acetylgalactosaminy ltransferase 7 (GalNAc-T7) (GALNT7), mRNA. /FEA=mRNA /GEN=GALNT7 /PROD=polypeptide N- acetylgalactosaminy ltransferase 7 /DB_XREF=gi:8393 408 /UG=Hs.246315 UDP-N-acetyl-alpha-D- galactosamine:poly peptide N- acetylgalactosaminy ltransferase 7 (GalNAc-T7) /FL=gb:NM_017423 .1		
212354_at	KIAA1077	AW043713	sulfatase FP		Hs.70823

Figure /a Co	ii. d.	[O
	1	Consensus
		includes
		gb:AU118026
		/FEA=EST
		/DB_XREF=gi:1093
		3043
	i	/DB_XREF=est:AU
		118026
		/CLONE=HEMBA10
		02729
		/UG=Hs.289068
		Homo sapiens
ļ,		cDNA FLJ11918
	 	fis, clone
040005	AK004000	
212385_at	AK021980	HEMBB1000272
		Consensus
		includes
		gb:AW001101
		/FEA=EST
_		/DB_XREF=gi:5848
		017
		/DB_XREF=est:wu2
	!	4c05.x1
		/CLONE=IMAGE:25
		20968
		/UG=Hs.3852
212428_at	AB002366	KIAA0368 protein
		gb:NM_003417.1
		/DEF=Homo
		sapiens zinc finger
		protein 264
		(ZNF264), mRNA.
		/FEA=mRNA
		/GEN=ZNF264
		/PROD=zinc finger
		protein 264
		/DB_XREF=gi:4585
		1642
		/UG=Hs.117077
		zinc finger protein
		264
		/FL=gb:NM_003417
205917_at	NM_003417	[.1

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Figure 7a Co	nicu.	,		1	
206026_s_at		NM_007115	gb:NM_007115.1 /DEF=Homo sapiens tumor necrosis factor, alpha-induced protein 6 (TNFAIP6), mRNA. /FEA=mRNA /GEN=TNFAIP6 /PROD=tumor necrosis factor, alpha-induced protein 6 /DB_XREF=gi:6005 905 /UG=Hs.29352 tumor necrosis factor, alpha- induced protein 6 /FL=gb:NM_007115 .1		
208025_s_at		NM_003483	gb:NM_003483.2 /DEF=Homo sapiens high- mobility group (nonhistone chromosomal) protein isoform I-C (HMGIC), mRNA. /FEA=mRNA /GEN=HMGIC /PROD=high- mobility group (nonhistone chromosomal)protei n isoform I-C /DB_XREF=gi:6631 086 /FL=gb:NM_003483 2		

Figure 7a Co	Jit u.				
gara	Jil d.		Consensus includes gb:AA902326 /FEA=EST /DB_XREF=gi:3037 233 /DB_XREF=est:ok9 2b01.s1 /CLONE=IMAGE:15		
212176_at		AL080186	21385 /UG=Hs.18368 DKFZP564B0769 protein		
212353_at	KIAA1077	AW043713	sulfatase FP		Hs.70823
206284_x_at		NM_001834	gb:NM_001834.1 /DEF=Homo sapiens clathrin, light polypeptide (Lcb) (CLTB), transcript variant nonbrain, mRNA. /FEA=mRNA /GEN=CLTB /PROD=clathrin, light polypeptide B (Lcb) isoform a /DB_XREF=gi:4502 900 /UG=Hs.73919 clathrin, light polypeptide (Lcb) /FL=gb:M20470.1 gb:NM_001834.1		
212299_at		AL117502	Consensus includes gb:AL117502.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434D0935 (from clone DKFZp434D0935). /FEA=mRNA /DB_XREF=gi:5912 009 /UG=Hs.7200 Homo sapiens mRNA; cDNA DKFZp434D0935 (from clone DKFZp434D0935)		
_ ,at	1	1, 12111002	12.11 Ep 10-10-0000/	L	<u> </u>

Figure 7a Co	Jill G.		 	
204774 at		NM 014210	gb:NM_014210.1 /DEF=Homo sapiens ecotropic viral integration site 2A (EVI2A), mRNA. /FEA=mRNA /GEN=EVI2A /PROD=ecotropic viral integration site 2A /DB_XREF=gi:7657 074 /UG=Hs.70499 ecotropic viral integration site 2A /FL=gb:NM_014210 .1	
204774_4			gb:NM_002526.1	
			/DEF=Homo	
			sapiens 5 nucleotidase	
			(CD73) (NT5),	
			mRNA.	
			/FEA=mRNA	
		1	/GEN=NT5 /PROD=5	
			nucleotidase	
			/DB_XREF=gi:4505	
			466	
			/UG=Hs.153952 5	
			nucleotidase (CD73)	
			/FL=gb:NM_002526	ļ
203939_at		NM_002526	.1	
212725_s_at		N37081	ESTs	Hs.409222
	:			
			solute carrier family 1 (glutamate/neutral	
			amino acid	
			transporter),	
212810_s_at	SLC1A4	BG032165	member 4	 Hs.323878
212765_at	KIAA1078	AW593213	KIAA1078 protein	Hs.23585

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gb:NM_004808.1 /DEF=Homo sapiens Nmyristoyltransferase 2 (NMT2), mRNA. /FEA=mRNA /GEN=NMT2 /PROD=glycylpeptid e Ntetradecanoyltransf erase 2 /DB_XREF=gi:4758 815 /UG=Hs.122647 Nmyristoyltransferase /FL=gb:AF043325.1 205006_s_at NM 004808 gb:NM_004808.1 gb:AL136842.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434A0530 (from clone DKFZp434A0530); complete cds. /FEA=mRNA /GEN=DKFZp434A 0530 /PROD=hypothetica I protein /DB_XREF=gi:6807 668 /UG=Hs.260024 Cdc42 effector protein 3 /FL=gb:AF094521.1 gb:AF104857.1 gb:NM_006449.1 gb:AF164118.1 209288_s_at AL136842 gb:AL136842.1

Spi-BC-000433-1 I/DEF=Homo Sapiens, mitogen-activated protein Kinase 13, clone MGC:8364, mRNA, complete des. I/EA=mRNA I/PROD=mitogen-activated protein Kinase 13 I/DB_XREF=gi:1265 3328 I/G=Hs.178695 mitogen-activated protein Kinase 13 I/EL_gb.BC000433.1 gb.BC001641.1 gb.BC000433.1 gb.BC001641.1 gb.BC0004428.1 gb:AF016256.1 gb:J83232.1 gb:MM_002754.1 gb:AF016256.1 gb:J83232.1 gb:MM_002754.1 gb:AF016256.1 gb:J83232.1 gb:MM_002754.1 gb:AF016256.1 misulin receptor substrate 2 Hs.143648 I/DEF=Homo sapiens tumor necrosis factor-related death iligand-1beta mRNA, complete cds. I/EA=mRNA I/PROD=tumor necrosis factor-related death iligand-1beta mRNA, complete cds. I/EA=mRNA I/PROD=tumor necrosis factor-related death iligand-1beta mRNA, complete cds. I/EA=mRNA I/PROD=tumor necrosis factor-related death iligand-1beta mRNA, complete cds. I/EA=mRNA I/PROD=tumor necrosis factor-related death iligand-1beta mRNA, complete cds. I/EA=mRNA I/PROD=tumor necrosis factor-related death iligand-1beta mRNA, complete cds. I/EA=mRNA I/PROD=tumor necrosis factor-related death iligand-1beta I/DB_XREF=gi:7328 555 I/JG=Hs.54673 tumor necrosis factor filestore factor filestore factor filestore factor filestore factor filestore factor filestore factor filestore factor filestore factor filestore factor filestore factor filestore factor filestore factor filestore factor filestore factor filestore factor filestore factor filestore factor fac	Figure 7a Co	onicu.		L D00004004		
sapiens, mitogen-activated protein kinase 13, clone MGC:8364, mRNA, complete cds. /FEA=mRNA /PROD=mitogen-activated protein kinase 13 /DB_XREF=gi:1265 3328 /UG=Hs.178695 mitogen-activated protein kinase 13 /FL=gb:BC000433.1 gb:BC001641.1 gb:BC004428.1 gb:AF004709.1 gb:AF004709.1 gb:AF004709.1 gb:AF004709.1 gb:AF004709.1 gb:AF004709.1 gb:AF002754.1 gb:AF002754.1 gb:AF002754.1 gb:AF002754.1 gb:AF002754.1 gb:AF002754.1 gb:AF002754.1 gb:AF002754.1 gb:AF002754.1 gb:AF002754.1 gb:AF002754.1 gb:AF002754.1 gb:AF002754.1 gb:AF002754.1 gb:AF002754.1 gb:AF100546.1 insulin receptor substrate 2 Hs.143648 209184_s_at IRS2 BF700086 substrate 2 Hs.143648 BF700086 substrate 2 Hs.143648 209184_s_at IRS2 BF700086 substrate 2 Hs.143648 209184_s_at IRS2 BF700086 substrate 2 Hs.143648				gb:BC000433.1		
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mRNA, complete cds. /FEA=mRNA /PROD=tumor necrosis factor- related deathligand- 1beta /DB_XREF=gi:7328 555 /UG=Hs.54673 tumor necrosis factor (ligand) superfamily, member 13 209500_x_at AF114012 /FL=gb:AF114012.1 oxysterol binding	209184_s_at	IRS2	BF700086	gb:AF114012.1 /DEF=Homo sapiens tumor necrosis factor-		Hs.143648
cds. /FEA=mRNA /PROD=tumor necrosis factor- related deathligand- 1beta /DB_XREF=gi:7328 555 /UG=Hs.54673 tumor necrosis factor (ligand) superfamily, member 13 209500_x_at AF114012 /FL=gb:AF114012.1 oxysterol binding	209184_s_at	IRS2	BF700086	gb:AF114012.1 /DEF=Homo sapiens tumor necrosis factor- related death		Hs.143648
/PROD=tumor necrosis factor- related deathligand- 1beta /DB_XREF=gi:7328 555 /UG=Hs.54673 tumor necrosis factor (ligand) superfamily, member 13 209500_x_at AF114012 /FL=gb:AF114012.1 oxysterol binding	209184_s_at	IRS2	BF700086	gb:AF114012.1 /DEF=Homo sapiens tumor necrosis factor- related death ligand-1beta		Hs.143648
necrosis factor- related deathligand- 1beta /DB_XREF=gi:7328 555 /UG=Hs.54673 tumor necrosis factor (ligand) superfamily, member 13 209500_x_at AF114012 /FL=gb:AF114012.1 oxysterol binding	209184_s_at	IRS2	BF700086	gb:AF114012.1 /DEF=Homo sapiens tumor necrosis factor- related death ligand-1beta mRNA, complete		Hs.143648
related deathligand- 1beta /DB_XREF=gi:7328 555 /UG=Hs.54673 tumor necrosis factor (ligand) superfamily, member 13 209500_x_at AF114012 /FL=gb:AF114012.1 oxysterol binding	209184_s_at	IRS2	BF700086	gb:AF114012.1 /DEF=Homo sapiens tumor necrosis factor- related death ligand-1beta mRNA, complete cds. /FEA=mRNA		Hs.143648
1beta //DB_XREF=gi:7328 555 /UG=Hs.54673 tumor necrosis factor (ligand) superfamily, member 13 209500_x_at AF114012 /FL=gb:AF114012.1 oxysterol binding	209184_s_at	IRS2	BF700086	gb:AF114012.1 /DEF=Homo sapiens tumor necrosis factor- related death ligand-1beta mRNA, complete cds. /FEA=mRNA /PROD=tumor		Hs.143648
/DB_XREF=gi:7328 555 /UG=Hs.54673 tumor necrosis factor (ligand) superfamily, member 13 209500_x_at AF114012 /FL=gb:AF114012.1 oxysterol binding	209184_s_at	IRS2	BF700086	gb:AF114012.1 /DEF=Homo sapiens tumor necrosis factor- related death ligand-1beta mRNA, complete cds. /FEA=mRNA /PROD=tumor necrosis factor-		Hs.143648
555 /UG=Hs.54673 tumor necrosis factor (ligand) superfamily, member 13 209500_x_at	209184_s_at	IRS2	BF700086	gb:AF114012.1 /DEF=Homo sapiens tumor necrosis factor- related death ligand-1beta mRNA, complete cds. /FEA=mRNA /PROD=tumor necrosis factor- related deathligand-		Hs.143648
555 /UG=Hs.54673 tumor necrosis factor (ligand) superfamily, member 13 209500_x_at	209184_s_at	IRS2	BF700086	gb:AF114012.1 /DEF=Homo sapiens tumor necrosis factor- related death ligand-1beta mRNA, complete cds. /FEA=mRNA /PROD=tumor necrosis factor- related deathligand-		Hs.143648
tumor necrosis factor (ligand) superfamily, member 13 209500_x_at	209184_s_at	IRS2	BF700086	gb:AF114012.1 /DEF=Homo sapiens tumor necrosis factor- related death ligand-1beta mRNA, complete cds. /FEA=mRNA /PROD=tumor necrosis factor- related deathligand- 1beta		Hs.143648
factor (ligand) superfamily, member 13 209500_x_at	209184_s_at	IRS2	BF700086	gb:AF114012.1 /DEF=Homo sapiens tumor necrosis factor- related death ligand-1beta mRNA, complete cds. /FEA=mRNA /PROD=tumor necrosis factor- related deathligand- 1beta /DB_XREF=gi:7328		Hs.143648
superfamily, member 13 209500_x_at	209184_s_at	IRS2	BF700086	gb:AF114012.1 /DEF=Homo sapiens tumor necrosis factor- related death ligand-1beta mRNA, complete cds. /FEA=mRNA /PROD=tumor necrosis factor- related deathligand- 1beta /DB_XREF=gi:7328 555 /UG=Hs.54673		Hs.143648
member 13 209500_x_at	209184_s_at	IRS2	BF700086	gb:AF114012.1 /DEF=Homo sapiens tumor necrosis factor- related death ligand-1beta mRNA, complete cds. /FEA=mRNA /PROD=tumor necrosis factor- related deathligand- 1beta /DB_XREF=gi:7328 555 /UG=Hs.54673 tumor necrosis		Hs.143648
209500_x_at	209184_s_at	IRS2	BF700086	gb:AF114012.1 /DEF=Homo sapiens tumor necrosis factor- related death ligand-1beta mRNA, complete cds. /FEA=mRNA /PROD=tumor necrosis factor- related deathligand- 1beta /DB_XREF=gi:7328 555 /UG=Hs.54673 tumor necrosis factor (ligand)		Hs.143648
oxysterol binding	209184_s_at	IRS2	BF700086	gb:AF114012.1 /DEF=Homo sapiens tumor necrosis factor- related death ligand-1beta mRNA, complete cds. /FEA=mRNA /PROD=tumor necrosis factor- related deathligand- 1beta /DB_XREF=gi:7328 555 /UG=Hs.54673 tumor necrosis factor (ligand) superfamily,		Hs.143648
l		IRS2		gb:AF114012.1 /DEF=Homo sapiens tumor necrosis factor- related death ligand-1beta mRNA, complete cds. /FEA=mRNA /PROD=tumor necrosis factor- related deathligand- 1beta /DB_XREF=gi:7328 555 /UG=Hs.54673 tumor necrosis factor (ligand) superfamily, member 13		Hs.143648
209485 s at OSBPL1A W19983 protein-like 1A Hs.252716		IRS2		gb:AF114012.1 /DEF=Homo sapiens tumor necrosis factor- related death ligand-1beta mRNA, complete cds. /FEA=mRNA /PROD=tumor necrosis factor- related deathligand- 1beta /DB_XREF=gi:7328 555 /UG=Hs.54673 tumor necrosis factor (ligand) superfamily, member 13 /FL=gb:AF114012.1		Hs.143648
	209500_x_at		AF114012	gb:AF114012.1 /DEF=Homo sapiens tumor necrosis factor- related death ligand-1beta mRNA, complete cds. /FEA=mRNA /PROD=tumor necrosis factor- related deathligand- 1beta /DB_XREF=gi:7328 555 /UG=Hs.54673 tumor necrosis factor (ligand) superfamily, member 13 /FL=gb:AF114012.1 oxysterol binding		

Figure 7a Cont'd.			
209360 s at	D43968	gb:D43968.1 /DEF=Human AML1 mRNA for AML1b protein (alternatively spliced product), complete cds. /FEA=mRNA /GEN=AML1 /PROD=AML1b protein /DB_XREF=gi:9669 96 /UG=Hs.129914 runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) /FL=gb:L34598.1 gb:D43968.1	
200000_5_at	D40900	190.04000.1	
209967_s_at	D14826	gb:D14826.1 /DEF=Human mRNA for hCREM (cyclic AMP- responsive element modulator) type 2 protein, complete cds. /FEA=mRNA /GEN=hCREM-2; hCREM-2; hCREM-2 /PROD=hCREM 2beta-b protein; hCREM 2beta-a protein; hCREM 2alpha-b protein; hCREM 2alpha-a protein /DB_XREF=gi:5320 36 /UG=Hs.155924 cAMP responsive element modulator /FL=gb:AF069065.1 gb:D14826.1	

Figure /a Cont'd.		10		
		Consensus		
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1		mRNA for		
		KIAA0230 gene,		
	1	partial cds.		
1		/FEA=mRNA		
1		/GEN=KIAA0230		
1		/DB_XREF=gi:1504		
		039]
		/UG=Hs.118893		
		Melanoma		
212013_at	AF200348	associated gene		
		Consensus		
	1	includes		
		gb:X98743.1		
1		/DEF=H.sapiens		
		mRNA for RNA		
		helicase (Myc-		
		regulated dead		;
		box protein).		
		/FEA=mRNA		
		/PROD=RNA		
		helicase		
		/DB_XREF=gi:1498		
		228		
	1	/UG=Hs.100555]
		DEADH (Asp-Glu-		
		Ala-AspHis) box		
		polypeptide 18		
		(Myc-regulated)		
		/FL=gb:BC001238.1		
208896_at	BC003360	gb:BC003360.1		
		Consensus		
		includes		
		gb:BE552421		
		/FEA=EST		
		/DB_XREF=gi:9794		
		113		
		/DB_XREF=est:hw2		
		6b02.x1		
		/CLONE=IMAGE:31	1	
		84011		
		/UG=Hs.7946		
212095_s_at	AL096842	KIAA1288 protein	j	1

Figure /a Co	nica.				
208708_x_at		AL080102	gb:AL080102.1 /DEF=Homo sapiens mRNA; cDNA DKFZp564N1916 (from clone DKFZp564N1916); complete cds. /FEA=mRNA /GEN=DKFZp564N 1916 /PROD=hypothetica I protein /DB_XREF=gi:5262 526 /UG=Hs.286236 eukaryotic translation initiation factor 5 /FL=gb:AL080102.1		
211615_s_at		M92439	gb:M92439.1 /DEF=Human leucine-rich protein mRNA, complete cds. /FEA=mRNA /PROD=leucine-rich protein; leucine- rich protein /DB_XREF=gi:1771 09 /FL=gb:M92439.1		
208952_s_at		BC003381	Consensus includes gb:AA811923 /FEA=EST /DB_XREF=gi:2881 534 /DB_XREF=est:ob7 2f05.s1 /CLONE=IMAGE:13 36929 /UG=Hs.78851 KIAA0217 protein /FL=gb:BC003381.1		

rigule /a Contu.		1 1114 045057 4	·····	`
	[gb:NM_015057.1		
		/DEF=Homo		
		sapiens KIAA0916		
		protein		
		(KIAA0916),		
		mRNA.		
!		/FEA=mRNA		
		/GEN=KIAA0916		
1		/PROD=KIAA0916		
		protein		
		/DB_XREF=gi:7662		
		379		
		/UG=Hs.151411		
		KIAA0916 protein		
1		/FL=gb:AF075587.1		
		gb:AF083244.1		
201960_s_at	NM_015057	gb:NM_015057.1		
		gb:NM_002229.1		
		/DEF=Homo		1
		sapiens jun B		
	1	proto-oncogene		
		(JUNB), mRNA.		
1		/FEA=mRNA		
		/GEN=JUNB		
		/PROD=jun B		
		proto-oncogene		
		/DB_XREF=gi:4504		
		808		
		/UG=Hs.198951		
		jun B proto-		
		oncogene		
		/FL=gb:BC004250.1		
201473_at	NM 002229	gb:NM_002229.1		

Figure 7a CC	JIR G.				
201324_at		NM_001423	gb:NM_001423.1 /DEF=Homo sapiens epithelial membrane protein 1 (EMP1), mRNA. /FEA=mRNA /GEN=EMP1 /PROD=epithelial membrane protein 1 /DB_XREF=gi:4503 558 /UG=Hs.79368 epithelial membrane protein 1 /FL=gb:U77085.1 gb:U43916.1 gb:NM_001423.1		
		_			
201554_x_at		NM_004130	gb:NM_004130.1 /DEF=Homo sapiens glycogenin (GYG), mRNA. /FEA=mRNA /GEN=GYG /PROD=glycogenin /DB_XREF=gi:4758 491 /UG=Hs.174071 glycogenin /FL=gb:U44131.1 gb:BC000033.1 gb:NM_004130.1 gb:U31525.1		,
201502_s_at	NFKBIA	AI078167	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha		Hs.81328
-01002_0_at	La ISON	1, 110, 010,	In andicor, diprid	<u> </u>	

Figure 7a Cont'd.

		gb:NM_003252.2	
		/DEF=Homo	
	:	sapiens TIA1	
		cytotoxic granule-	
		associated RNA-	
		binding protein-like	
		1 (TIAL1),	
		transcript variant	
		1, mRNA.	
		/FEA=mRNA	
		/GEN=TIAL1	
		/PROD=TIA1	
		cytotoxic granule-	
1		associated RNA-	
		bindingprotein-like	
		1, isoform 1	
		/DB_XREF=gi:1343	
		5392	
		/UG=Hs.182741	
		TIA1 cytotoxic	
		granule-associated	
		RNA-binding	
		protein-like 1	
		/FL=gb:NM_003252	
202406_s_at	 NM_003252	.2 gb:M96954.1	

Figure /a Co	nica.				-
202418_at			gb:NM_020470.1 /DEF=Homo sapiens putative transmembrane protein; homolog of yeast Golgi membrane protein Yif1p (Yip1p- interacting factor) (54TM), mRNA. /FEA=mRNA /GEN=54TM /PROD=putative transmembrane protein; homolog of yeastGolgi membrane protein Yif1p (Yip1p- interacting factor) /DB_XREF=gi:9994 168 /UG=Hs.5809 putative transmembrane protein; homolog of yeast Golgi membrane protein Yif1p (Yip1p- interacting factor) /FB_SEG001299.1 gb:AF004876.1 gb:NM 020470.1		
214280_x_at		X79536	Consensus includes gb:X79536.1 /DEF=H.sapiens mRNA for hnRNPcore protein A1. /FEA=mRNA /PROD=hnRNPcore protein A1 /DB_XREF=gi:4968 97 /UG=Hs.249495 heterogeneous nuclear ribonucleoprotein A1		

Figure 7a Co	illu.				
202163_s_at		NM_004779	gb:NM_004779.1 /DEF=Homo sapiens CCR4- NOT transcription complex, subunit 8 (CNOT8), mRNA. /FEA=mRNA /GEN=CNOT8 /PROD=CCR4-NOT transcription complex, subunit 8 /DB_XREF=gi:4758 945 /UG=Hs.26703 CCR4-NOT transcription complex, subunit 8 /FL=gb:AF053318.1 gb:NM_004779.1 gb:AL122045.1 gb:AF180476.1 gb:AF180476.1 gb:AF180476.1 gb:AF183421.1 /DEF=Homo sapiens small GTP-binding protein rab22b mRNA, complete cds. /FEA=mRNA /PROD=small GTP-binding protein rab22b /DB_XREF=gi:9963 780 /UG=Hs.223025 RAR31 member		
			protein rab22b mRNA, complete cds. /FEA=mRNA /PROD=small GTP- binding protein		
			/DB_XREF=gi:9963 780 /UG=Hs.223025 RAB31, member RAS oncogene		
			family /FL=gb:AF234995.1 gb:BC001148.1 gb:U59877.1 gb:U57091.1 gb:NM_006868.1		
217764_s_at		AF183421	gb:AF183421.1	<u> </u>	

I iguic 7a oc	nica.			
217643_x_at		AA443771	ESTs, Weakly similar to hypothetical protein FLJ20378 [Homo sapiens] [H.sapiens]	Hs.368762
200872 at		NM 002966	gb:NM_002966.1 /DEF=Homo sapiens S100 calcium-binding protein A10 (annexin II ligand, calpactin I, light polypeptide (p11)) (S100A10), mRNA. /FEA=mRNA /GEN=S100A10 /PROD=S100 calcium-binding protein A10 /DB_XREF=gi:4506 760 /UG=Hs.119301 S100 calcium- binding protein A10 (annexin II ligand, calpactin I, light polypeptide (p11)) /FL=gb:M81457.1 gb:M38591.1 gb:NM_002966.1	
200872_at		MM_005900	anti-oxidant protein 2 (non-selenium glutathione peroxidase, acidic	
200844_s_at	AOP2	BE869583	calcium- independent phospholipase A2)	Hs.120

		gb:NM_018253.1 /DEF=Homo sapiens hypothetical protein FLJ10875 (FLJ10875), mRNA. /FEA=mRNA /GEN=FLJ10875 /PROD=hypothetica I protein FLJ10875 /DB_XREF=gi:8922 730 /UG=Hs.18851 hypothetical protein FLJ10875 /FL=gb:BC001655.1 gb:BC001843.1		
		mRNA. /FEA=mRNA /GEN=FLJ10875 /PROD=hypothetica I protein FLJ10875 /DB_XREF=gi:8922 730 /UG=Hs.18851 hypothetical protein		
		1		
		gb:BC001843.1		
217836_s_at	 NM_018253	gb:NM_018253.1		
		gb:NM_024811.1 /DEF=Homo sapiens hypothetical protein FLJ12529 (FLJ12529), mRNA. /FEA=mRNA /GEN=FLJ12529 /PROD=hypothetica I protein FLJ12529 /DB_XREF=gi:1337		
		6196 /UG=Hs.169100 hypothetical protein FLJ12529		
047000	NA 004044	/FL=gb:NM_024811		
217866_at	 NM_024811	<u>.1 </u>	l	<u></u>

Figure 7a CC					
201194_at		NM_003009	gb:NM_003009.1 /DEF=Homo sapiens selenoprotein W, 1 (SEPW1), mRNA. /FEA=mRNA /GEN=SEPW1 /PROD=selenoprote in W, 1 /DB_XREF=gi:4506 886 /UG=Hs.14231 selenoprotein W, 1 /FL=gb:U67171.1 gb:AF015283.1 gb:NM_003009.1		
215483 at		AK000270	Consensus includes gb:AK000270.1 /DEF=Homo sapiens cDNA FLJ20263 fis, clone COLF7804, highly similar to AJ131693 Homo sapiens mRNA for AKAP450 protein. /FEA=mRNA /DB_XREF=gi:7020 239 /UG=Hs.164036 Homo sapiens AKAP350C mRNA sequence, alternatively spliced		
215483_at		AK000270	signal sequence		
200900+	SSR1	AI016620	receptor, alpha (translocon- associated protein alpha)		Hs.250773
200890_s_at	JOON I	1710 10020	laihiia)	<u></u>	113.200770

Figure 7a Co	, , , , , , , , , , , , , , , , , , ,		·	
203150_at		NM_005833	gb:NM_005833.1 /DEF=Homo sapiens Rab9 effector p40 (RAB9P40), mRNA. /FEA=mRNA /GEN=RAB9P40 /PROD=Rab9 effector p40 /DB_XREF=gi:5032 014 /UG=Hs.19012 Rab9 effector p40 /FL=gb:BC000503.1 gb:Z97074.1 gb:NM_005833.1	
200,100_ut				 -
			gb:NM_006876.1	
			/DEF=Homo	
			sapiens i-beta-1,3-	
			N	
			acetylglucosaminyltr	
			ansferase	
			(BETA3GNTI),	
			mRNA. /FEA=mRNA	
			/GEN=BETA3GNTI	
			/PROD=i-beta-1,3-	
			N-	
		1	acetylglucosaminyltr	
			ansferase	
			/DB_XREF=gi:5802	
			983 /UG=Hs.8526	
			i-beta-1,3-N-	
		l	acetylglucosaminyltr	
			ansferase	
			/FL=gb:AF029893.1	
203188_at		NM_006876	gb:NM_006876.1	

Figure 7a Co	inta.		,	
203477_at		NM_001855	gb:NM_001855.1 /DEF=Homo sapiens collagen, type XV, alpha 1 (COL15A1), mRNA. /FEA=mRNA /GEN=COL15A1 /PROD=collagen, type XV, alpha 1 /DB_XREF=gi:4502 940 /UG=Hs.83164 collagen, type XV, alpha 1 /FL=gb:NM_001855 .1 gb:L25286.1	U- 207020
213275_x_at	CTSB	BE875786	cathepsin B	 Hs.297939
203411_s_at		NM_005572	gb:NM_005572.1 /DEF=Homo sapiens lamin AC (LMNA), mRNA. /FEA=mRNA /GEN=LMNA /PROD=lamin AC /DB_XREF=gi:5031 874 /UG=Hs.77886 lamin AC /FL=gb:BC000511.1 gb:BC003162.1 gb:M13451.1 gb:NM_005572.1	
202595_s_at		AF161461	gb:AF161461.1 /DEF=Homo sapiens HSPC112 mRNA, complete cds. /FEA=mRNA /PROD=HSPC112 /DB_XREF=gi:6841 445 /UG=Hs.11000 leptin receptor overlapping transcript-like 1 /FL=gb:BC000642.1 gb:AF063605.1 gb:AF161461.1 gb:NM_015344.1	

Figure 7a Co	inta.		· · · · · · · · · · · · · · · · · · ·	
221421_s_at	int u.	NM_030955	gb:NM_030955.1 /DEF=Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 12 (ADAMTS12), mRNA. /FEA=CDS /GEN=ADAMTS12 /PROD=a disintegrin-like and metalloprotease(rep rolysin type) with thrombospondin type 1 motif, 12 /DB_XREF=gi:1356 9927 /FL=gb:NM_030955 .1 gb:NM_013392.1 /DEF=Homo sapiens nuclear receptor binding protein (NRBP), mRNA. /FEA=mRNA /GEN=NRBP /PROD=nuclear receptor binding protein /DB_XREF=gi:7019 332	
			/DB_XREF=gi:7019 332 /UG=Hs.272736 nuclear receptor	
217765_at		NM_013392	binding protein /FL=gb:BC001221.1 gb:AF113249.1 gb:NM_013392.1 Thy-1 cell surface	
213869_x_at	THY1	AA218868	antigen	Hs.125359

	 r**-		
205256 at	NM_014830	gb:NM_014830.1 /DEF=Homo sapiens KIAA0352 gene product (KIAA0352), mRNA. /FEA=mRNA /GEN=KIAA0352 /PROD=KIAA0352 gene product /DB_XREF=gi:7662 071 /UG=Hs.17262 KIAA0352 gene product /FL=gb:AB002350.1 gb:NM_014830.1	
206027_at	NM_002960	gb:NM_002960.1 /DEF=Homo sapiens S100 calcium-binding protein A3 (S100A3), mRNA. /FEA=mRNA /GEN=S100A3 /PROD=S100 calcium-binding protein A3 /DB_XREF=gi:4506 762 /UG=Hs.2961 S100 calcium- binding protein A3 /FL=gb:NM_002960 .1	

rigule la Contu.				
220391_at	NM 024784	gb:NM_024784.1 /DEF=Homo sapiens hypothetical protein FLJ23392 (FLJ23392), mRNA. /FEA=mRNA /GEN=FLJ23392 /PROD=hypothetica I protein FLJ23392 /DB_XREF=gi:1337 6145 /UG=Hs.147554 hypothetical protein FLJ23392 /FL=gb:NM_024784 .1		
209198_s_at	BC004291	gb:BC004291.1 /DEF=Homo sapiens, Similar to synaptotagmin 11, clone MGC:10881, mRNA, complete cds. /FEA=mRNA /PROD=Similar to synaptotagmin 11 /DB_XREF=gi:1327 9139 /UG=Hs.74554 KIAA0080 protein /FL=gb:BC004291.1	-	

Figure 7a Co	onta.			 · · · · · ·
219915_s_at 214337_at	COPA	NM_018593 Al621079	gb:NM_018593.1 /DEF=Homo sapiens hypothetical protein PRO0813 (PRO0813), mRNA. /FEA=mRNA /GEN=PRO0813 /PROD=hypothetica I protein PRO0813 /DB_XREF=gi:8923 980 /UG=Hs.270087 hypothetical protein PRO0813 /FL=gb:AF116652.1 gb:NM_018593.1 coatomer protein complex, subunit alpha gb:NM_030965.1 /DEF=Homo sapiens similar to sialyltransferase 7 ((alpha-N- acetylneuraminyl 2,3-betagalactosyl- 1,3)-N-acetyl galactosaminide alpha-2,6- sialyltransferase) E (MGC3184), mRNA. /FEA=mRNA /GEN=MGC3184 /PROD=similar to sialyltransferase 7((alpha-N- acetylneuraminyl2,3 betagalactosyl-1,3)- N-acetyl galactosaminidealp	Hs.75887
220979_s_at		NM_030965	galactosaminidealp ha-2,6- sialyltransferase) E /DB_XREF=gi:1356 9937 /FL=gb:NM_030965 .1	

Application of: Liew, et. al. Our Docket #: 4231/2042 Figure 7a Cont'd.

- 1 igui o 7 a o o	 T		
		/DEF=Homo	
		sapiens	
		hypothetical protein	
		FLJ12615 similar	
		to membrane	
		protein,	
		palmitoylated 3	
	•	(MAGUK p55	
		subfamily member	
		5) (FLJ12615),	
		mRNA.	
1		/FEA=mRNA	
		/GEN=FLJ12615	
		/PROD=hypothetica	
		I protein FLJ12615	
	1	similar	
		tomembrane	
		protein,	
		palmitoylated 3	
		(MAGUK p55	
		subfamilymember	
		5)	
		/DB_XREF=gi:1196	
-		8024	
		/UG=Hs.306219	
		hypothetical protein	
		FLJ12615 similar	
		to membrane	
		protein,	
		palmitoylated 3	
		(MAGUK p55	
219321_at	NM_022474	subfamily member	
			

Figure /a Co	Jill G.			
rigure 7a oc	Jil d.		gb:NM_001995.1 /DEF=Homo sapiens fatty-acid- Coenzyme A ligase, long-chain 1 (FACL1), nuclear gene encoding mitochondrial protein, mRNA. /FEA=mRNA /GEN=FACL1 /PROD=long-chain fatty-acid-coenzyme A ligase 1 /DB_XREF=gi:4503 650 /UG=Hs.278333 fatty-acid- Coenzyme A ligase, long-chain 1 /FL=gb:L09229.1	
207275_s_at		NM_001995	gb:NM_001995.1 gb:NM_020657.1 /DEF=Homo sapiens zinc finger protein 304 (ZNF304), mRNA. /FEA=mRNA /GEN=ZNF304 /PROD=zinc finger protein 304 /DB_XREF=gi:1019	
207753_at 202438_x_at	IDS	NM_020657 BF346014	0695 /UG=Hs.287374 zinc finger protein 304 /FL=gb:NM_020657 .1 iduronate 2- sulfatase (Hunter syndrome)	Hs.172458

Figure 7a Co	7716 94.	 	
205200_at		gb:NM_003278.1 /DEF=Homo sapiens tetranectin (plasminogen- binding protein) (TNA), mRNA. /FEA=mRNA /GEN=TNA /PROD=tetranectin (plasminogen- binding protein) /DB_XREF=gi:4507 556 /UG=Hs.65424 tetranectin (plasminogen- binding protein) /FB=gb:NM_003278 .1	
214838_at		Consensus includes gb:AL035297.1 /DEF=H.sapiens gene from PAC 747L4. /FEA=mRNA /PROD=hypothetica I protein /DB_XREF=gi:4200 248 /UG=Hs.119254 H.sapiens gene from PAC 747L4	

Figure 7a Co	ont'd.				
			gb:NM_017425.1	i	
			/DEF=Homo		
			sapiens sperm		
:			autoantigenic		
			protein 17		
			(SPA17), mRNA.		
			/FEA=mRNA	}	
			/GEN=SPA17		
			/PROD=sperm		
		•	autoantigenic		
			protein 17		
			/DB_XREF=gi:8394		
			342		
			/UG=Hs.286233		
			sperm		
			autoantigenic		
			protein 17		
			/FL=gb:NM_017425		
205406 s at		NM_017425	.1		
			zinc finger protein		
78330_at	ZNF335	AA845577	335		Hs.165983
		i	gb:NM_001110.1		
	1		/DEF=Homo		
			sapiens a		
			disintegrin and		
			metalloproteinase		
			domain 10		
			(ADAM10), mRNA.		
			/FEA=mRNA		
			/GEN=ADAM10		
			/PROD=a		-
			disintegrin and		
			metalloprotease		
			domain 10		
			/DB_XREF=gi:4557		
			250		
			/UG=Hs.172028 a		
			disintegrin and		
			metalloproteinase		
			domain 10		
			/FL=gb:AF009615.1		
202604_x_at	1	NM_001110	gb:NM_001110.1		
			aquaporin 1		
			(channel-forming		
			integral protein,		j l
209047_at	AQP1	AL518391	28kDa)		Hs.74602
			1	I	

Application of: Liew, et. al. Our Docket #: 4231/2042 Figure 7a Cont'd.

gb:NM_007023.1 /DEF=Homo sapiens cAMPregulated guanine nucleotide exchange factor II (CAMP-GEFII), mRNA. /FEA=mRNA /GEN=CAMP-GEFII /PROD=cAMPregulated guanine nucleotide exchangefactor II /DB_XREF=gi:5901 913 /UG=Hs.91971 cAMP-regulated guanine nucleotide exchange factor II /FL=gb:U78516.1 NM_007023 gb:NM_007023.1 205651 x at gb:NM_001930.2 /DEF=Homo. sapiens deoxyhypusine synthase (DHPS), transcript variant 1, mRNA. /FEA=mRNA /GEN=DHPS /PROD=deoxyhypu sine synthase isoform a /DB_XREF=gi:7108 341 /UG=Hs.79064 deoxyhypusine synthase /FL=gb:U40579.1 gb:BC000333.1 gb:U32178.1 gb:U79262.1 gb:NM_001930.2 gb:L39068.1 202802_at NM_001930

Figure /a Co	iit d.		
208623_s_at	J05021	gb:J05021.1 /DEF=Human cytovillin 2 (VIL2) mRNA, complete cds. /FEA=mRNA /GEN=VIL2 /DB_XREF=gi:3402 16 /UG=Hs.155191 villin 2 (ezrin) /FL=gb:J05021.1 gb:AL162086.1 gb:NM_003379.2	·
219620_x_at	NM_017	gb:NM_017723.1 /DEF=Homo sapiens hypothetical protein FLJ20245 (FLJ20245), mRNA. /FEA=mRNA /GEN=FLJ20245 /PROD=hypothetica I protein FLJ20245 /DB_XREF=gi:8923 220 /UG=Hs.169758 hypothetical protein FLJ20245 /FL=gb:NM_017723 .1	
204451_at	NM_003	gb:NM_003505.1 /DEF=Homo sapiens frizzled (Drosophila) homolog 1 (FZD1), mRNA. /FEA=mRNA /GEN=FZD1 /PROD=frizzled 1 /DB_XREF=gi:4503 824 /UG=Hs.94234 frizzled (Drosophila) homolog 1 /FL=gb:AB017363.1 gb:NM_003505.1	

1 igule 7a oc	TIL G.		, 	
209621_s_at		AF002280	gb:AF002280.1 /DEF=Homo sapiens alpha- actinin-2 associated LIM protein mRNA, alternatively spliced product, complete cds. /FEA=mRNA /PROD=alpha- actinin-2 associated LIM protein /DB_XREF=gi:3138 919 /UG=Hs.135281 alpha-actinin-2- associated LIM protein /FL=gb:AF039018.1 gb:AF002280.1 gb:NM_014476.1	
201826_s_at		NM_016002	gb:NM_016002.1 /DEF=Homo sapiens CGI-49 protein (LOC51097), mRNA. /FEA=mRNA /GEN=LOC51097 /PROD=CGI-49 protein /DB_XREF=gi:7705 766 /UG=Hs.238126 CGI-49 protein /FL=gb:AF151807.1 gb:NM_016002.1	

I iguic 7 a oc				
209057_x_at		AB007892	gb:AB007892.1 /DEF=Homo sapiens KIAA0432 mRNA, complete cds. /FEA=mRNA /GEN=KIAA0432 /DB_XREF=gi:2887 434 /UG=Hs.155174 CDC5 (cell division cycle 5, S. pombe, homolog)-like /FL=gb:NM_001253 .1 gb:U86753.1 gb:AB007892.1	
	1			
			gb:NM_017606.1 /DEF=Homo sapiens hypothetical protein DKFZp434K1210 (DKFZp434K1210), mRNA. /FEA=mRNA /GEN=DKFZp434K 1210 /PROD=hypothetica I protein DKFZp434K1210 /DB_XREF=gi:8922 146 /UG=Hs.32352 hypothetical protein DKFZp434K1210 /FL=gb:NM_017606	
218149_s_at		NM_017606	.1	

Figure 7a Co	Jrita.		T	· · · · · · ·	
202609_at		NM_004447	gb:NM_004447.1 /DEF=Homo sapiens epidermal growth factor receptor pathway substrate 8 (EPS8), mRNA. /FEA=mRNA /GEN=EPS8 /PROD=epidermal growth factor receptor pathwaysubstrate 8 /DB_XREF=gi:4758 295 /UG=Hs.2132 epidermal growth factor receptor pathway substrate 8 /FL=gb:NM_004447 .1 gb:U12535.1 ubiquitin activating enzyme E1-like		
214004_s_at	GSA7	A1806207	protein		Hs.278607
213909_at		AU147799	ESTs		Hs.409224
			gb:NM_004753.1 /DEF=Homo sapiens short-chain dehydrogenaseredu ctase 1 (SDR1), mRNA. /FEA=mRNA /GEN=SDR1 /PROD=short-chain dehydrogenaseredu ctase 1 /DB_XREF=gi:4759 083 /UG=Hs.17144 short-chain dehydrogenaseredu ctase 1 /FL=gb:BC002730.1 gb:AF061741.1		
202481_at	<u> </u>	NM_004753	gb:NM_004753.1		

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gb:NM_000293.1 //DEF=Homo sapiens phosphorylase kinase, beta (PHKB), mRNA. //FEA=mRNA //GEN=PHKB //PROD=phosphoryl ase kinase, beta //DB_XREF=gi:4505 782 /UG=Hs.78060 phosphorylase kinase, beta //FL=gb:NM_000293 202739_s_at NM_000293 .1	Figure 7a Ci	711. G.	
	202739_s_at	NM_000	/DEF=Homo sapiens phosphorylase kinase, beta (PHKB), mRNA. /FEA=mRNA /GEN=PHKB /PROD=phosphoryl ase kinase, beta /DB_XREF=gi:4505 782 /UG=Hs.78060 phosphorylase kinase, beta /FL=gb:NM_000293
gb:NM_004199.1 //DEF=Homo sapiens procollagen-proline, 2-oxoglutarate 4- dioxygenase (proline 4- hydroxylase), alpha polypeptide II (P4HA2), mRNA. //FEA=mRNA //GEN=P4HA2 //PROD=procollagen proline, 2- oxoglutarate4- dioxygenase (proline 4- hydroxylase), alpha polypeptideII //DB_XREF=gi:4758 867 //UG=Hs.3622 procollagen-proline, 2-oxoglutarate 4- dioxygenase (proline 4- hydroxylase), alpha polypeptideII //DB_XREF=gi:4758 867 //UG=Hs.3622 procollagen-proline, 2-oxoglutarate 4- dioxygenase (proline 4- hydroxylase), alpha polypeptide II //FL=gb:U90441.1 //FL=gb:U90441.1			/DEF=Homo sapiens procollagen-proline, 2-oxoglutarate 4- dioxygenase (proline 4- hydroxylase), alpha polypeptide II (P4HA2), mRNA. /FEA=mRNA /GEN=P4HA2 /PROD=procollagen- proline, 2- oxoglutarate4- dioxygenase (proline 4- hydroxylase), alpha polypeptideII /DB_XREF=gi:4758 867 /UG=Hs.3622 procollagen-proline, 2-oxoglutarate 4- dioxygenase (proline 4- hydroxylase), alpha polypeptide II /FL=gb:U90441.1

Figure /a Co	nicu.				
221730_at		NM_000393	Consensus includes gb:NM_000393.1 /DEF=Homo sapiens collagen, type V, alpha 2 (COL5A2), mRNA. /FEA=CDS /GEN=COL5A2 /PROD=collagen, type V, alpha 2 /DB_XREF=gi:4502 958 /UG=Hs.82985 collagen, type V, alpha 2 /FL=gb:NM_000393.1		
202746_at	ITM2A; E25A	AL021786	Human DNA sequence from clone RP4-696H22 on chromosome Xq21.1-21.2, complete sequence.	NM_004867	
221737_at		NM 007353	Consensus includes gb:AK024696.1 //DEF=Homo sapiens cDNA: FLJ21043 fis, clone CAE11633. //FEA=mRNA //DB_XREF=gi:1043 7043 //UG=Hs.182874 guanine nucleotide binding protein (G protein) alpha 12 //FL=gb:L01694.1 gb:NM_007353.1		
221737_at		NM_007353 AW575374	gb:NM_00/353.1 ESTs, Highly similar to A48765 G protein coupled receptor kinase (EC 2.7.1) 6 - human [H.sapiens]		Hs.409176

	0.11. u.			
213902_at	ASAH1	AI379338	N-acylsphingosine amidohydrolase (acid ceramidase) 1 ESTs, Weakly similar to A53959 thromboxane A-2 receptor, endothelial - human	Hs.75811 Hs.389813
202321_at		AW299507	[H.sapiens] ESTs, Moderately similar to cytokine receptor-like factor 2; cytokine receptor CRL2 precusor [Homo sapiens] [H.sapiens]	Hs.356467
202220 at		NM 014949	gb:NM_014949.1 /DEF=Homo sapiens KIAA0907 protein (KIAA0907), mRNA. /FEA=mRNA /GEN=KIAA0907 /PROD=KIAA0907 protein /DB_XREF=gi:7662 371 /UG=Hs.24656 KIAA0907 protein /FL=gb:AB020714.1 gb:NM 014949.1	

Figure 7a Cont'd.			
202164_s_at	AF180476	gb:AF180476.1 /DEF=Homo sapiens CALIFp (CALIF) mRNA, complete cds. /FEA=mRNA /GEN=CALIF /PROD=CALIFp /DB_XREF=gi:6856 208 /UG=Hs.26703 CCR4-NOT transcription complex, subunit 8 /FL=gb:AF053318.1 gb:NM_004779.1 gb:AL122045.1 gb:AF180476.1 Consensus	
		includes gb:AK022014.1	
		/DEF=Homo	
		sapiens cDNA	
		FLJ11952 fis,	
		clone HEMBB1000831,	
		weakly similar to	
		Homo sapiens	
		breast cancer	1
		nuclear receptor-	
		binding auxiliary	
		protein (BRX) mRNA.	
		/FEA=mRNA	
		/DB_XREF=gi:1043	
		3327	
		/UG=Hs.306619 Homo sapiens	
		cDNA FLJ11952	
		fis, clone	
		HEMBB1000831,	
		weakly similar to	
		Homo sapiens	
		breast cancer nuclear receptor-	
		binding auxiliary	
		protein (BRX)	
222024_s_at	AK022014	mRNA	

Figure /a Co	onta.			
			ceroid-	
			lipofuscinosis,	
214252_s_at	CLN5	AV700514	neuronal 5	Hs.30213
			far upstream	
			element (FUSE)	
214093_s_at	FUBP1	AA156865	binding protein 1	Hs.118962
			hypothetical protein	
221897_at	MGC16175	AA205660	MGC16175	Hs.334638
-			gb:NM_018579.1 /DEF=Homo sapiens mitochondrial solute carrier (LOC51312), mRNA. /FEA=mRNA /GEN=LOC51312 /PROD=hypothetica I protein PRO1278 /DB_XREF=gi:8924 027 /UG=Hs.300496 mitochondrial solute carrier	
			/FL=gb:AF155660.1	
			gb:AF116630.1	
218136_s_at		NM_018579	gb:NM_018579.1	
	0.400		GDP-mannose 4,6-	405405
214106_s_at	GMDS	AI762113	dehydratase	 Hs.105435
218139_s_at		NM 018229	gb:NM_018229.1 /DEF=Homo sapiens hypothetical protein FLJ10813 (FLJ10813), mRNA. /FEA=mRNA /GEN=FLJ10813 /PROD=hypothetica I protein FLJ10813 /DB_XREF=gi:8922 687 /UG=Hs.106210 hypothetical protein FLJ10813 /FL=gb:AL136685.1 gb:NM_018229.1	

Figure 7a Co	Jiit G.			
202404 s at		NM_000089	gb:NM_000089.1 /DEF=Homo sapiens collagen, type I, alpha 2 (COL1A2), mRNA. /FEA=mRNA /GEN=COL1A2 /PROD=collagen, type I, alpha 2 /DB_XREF=gi:4502 946 /UG=Hs.179573 collagen, type I, alpha 2 /FL=gb:J03464.1 gb:NM_000089.1	
			collagen, type V,	
203325_s_at	COL5A1	Al130969	alpha 1	 Hs.146428
			gb:NM_020120.1 /DEF=Homo sapiens UDP- glucose:glycoprotei n glucosyltransferase 1 (HUGT1), mRNA. /FEA=mRNA /GEN=HUGT1 /PROD=UDP- glucose:glycoprotei n glucosyltransferase 1 /DB_XREF=gi:9910 279 /UG=Hs.105794 UDP- glucose:glycoprotei n glucosyltransferase 1 /FL=gb:AF227905.1	
218257_s_at		NM_020120	gb:NM_020120.1	

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203380_x_at

gb:NM_005524.2 /DEF=Homo sapiens hairy (Drosophila)homolog (HRY), mRNA. /FEA=mRNA /GEN=HRY /PROD=hairy (Drosophila)homolog /DB_XREF=gi:8400 709 /UG=Hs.250666 hairy (Drosophila)homolog /FL=gb:AF264785.1 NM_005524 gb:NM_005524.2 203395_s_at gb:NM_006925.1 /DEF=Homo sapiens splicing factor, arginineserine-rich 5 (SFRS5), mRNA. /FEA=mRNA /GEN=SFRS5 /PROD=splicing factor, arginineserine-rich /DB_XREF=gi:5902 077 /UG=Hs.166975 splicing factor, arginineserine-rich 5 /FL=gb:U30827.1

NM_006925

gb:NM_006925.1

Figure 7a Co	711. 0.			r	
213524_s_at	NA		Consensus includes gb:NM_015714.1 //DEF=Homo sapiens putative lymphocyte G0G1 switch gene (G0S2), mRNA. //FEA=CDS //GEN=G0S2 //PROD=putative lymphocyte G0G1 switch gene //DB_XREF=gi:7657 103 //UG=Hs.95910 putative lymphocyte G0G1 switch gene //FL=gb:NM_015714 .1		
213524_S_at	INIV	1_015/14	. 1		
221517_s_at	AF	105421	gb:AF105421.1 //DEF=Homo sapiens vitamin D3 receptor interacting protein (DRIP80) mRNA, complete cds. //FEA=mRNA //GEN=DRIP80 //PROD=vitamin D3 receptor interacting protein //DB_XREF=gi:4838 128 //UG=Hs.22630 cofactor required for Sp1 transcriptional activation, subunit 6 (77kD) //FL=gb:AF105421.1		

Figure 7a Cont'd.

	·		gb:NM_002767.1 /DEF=Homo		
203537_at		NM_002767	sapiens phosphoribosyl pyrophosphate synthetase- associated protein 2 (PRPSAP2), mRNA. /FEA=mRNA /GEN=PRPSAP2 /PROD=phosphorib osyl pyrophosphatesynth etase-associated protein 2 /DB_XREF=gi:4506 132 /UG=Hs.13339 phosphoribosyl pyrophosphate synthetase- associated protein 2 /FL=gb:AB007851.1 gb:NM_002767.1		
213455_at	LOC92689	W87466	hypothetical protein BC001096		Hs.352406
213392_at	MGC35048	AW070229	hypothetical protein MGC35048		Hs.367493
221718_s_at		M90360	gb:M90360.1 /DEF=Human type II cAMP-dependent protein kinase (Ht31) mRNA, complete cds. /FEA=CDS /GEN=Ht31 /PROD=protein kinase /DB_XREF=gi:1844 34 /FL=gb:M90360.1	·	

Figure 7a Co	Jile G.			 · · · · · · · · · · · · · · · · · · ·
202887_s_at		NM 019058	gb:NM_019058.1 /DEF=Homo sapiens hypothetical protein (FLJ20500), mRNA. /FEA=mRNA /GEN=FLJ20500 /PROD=hypothetica I protein /DB_XREF=gi:9506 686 /UG=Hs.111244 hypothetical protein /FL=gb:AL136668.1 gb:NM_019058.1	
202814_s_at	HIS1	AW193511	HMBA-inducible	 Hs.15299
202017_3_dt		7.00071	Consensus includes gb:AL575735 /FEA=EST /DB_XREF=gi:1293 7190 /DB_XREF=est:AL5 75735 /CLONE=CS0DI070 YK23 (3 prime) /UG=Hs.82985 collagen, type V, alpha 2 /FL=gb:NM_000393	
221729_at		NM_000393	.1	
202403_s_at	COL1A2	AA788711	collagen, type I, alpha 2	Hs.179573

Jitu.				
	NM_002318	gb:NM_002318.1 /DEF=Homo sapiens lysyl oxidase-like 2 (LOXL2), mRNA. /FEA=mRNA /GEN=LOXL2 /PROD=lysyl oxidase-like 2 /DB_XREF=gi:4505 010 /UG=Hs.83354 lysyl oxidase-like 2 /FL=gb:BC000594.1 gb:U89942.1 gb:NM_002318.1 gb:AF117949.1		
MAGED2	AI924630			Hs.4943
	NM_001124	gb:NM_001124.1 /DEF=Homo sapiens adrenomedullin (ADM), mRNA. /FEA=mRNA /GEN=ADM /PROD=adrenomed ullin /DB_XREF=gi:4501 944 /UG=Hs.394 adrenomedullin /FL=gb:NM_001124 .1 gb:D14874.1		
M6A	AW069290	putative methyltransferase		Hs.268149
	MAGED2	NM_002318 MAGED2 Al924630 NM_001124	gb:NM_002318.1 //DEF=Homo sapiens lysyl oxidase-like 2 (LOXL2), mRNA. //FEA=mRNA //GEN=LOXL2 //PROD=lysyl oxidase-like 2 //DB_XREF=gi:4505 010 //UG=Hs.83354 lysyl oxidase-like 2 //FL=gb:BC000594.1 gb:U89942.1 gb:NM_002318.1 gb:NM_002318.1 melanoma antigen, family D, 2 gb:NM_001124.1 //DEF=Homo sapiens adrenomedullin (ADM), mRNA. //FEA=mRNA //GEN=ADM //PROD=adrenomed ullin //DB_XREF=gi:4501 944 //UG=Hs.394 adrenomedullin //FL=gb:NM_001124 NM_001124 1 gb:D14874.1 putative	gb:NM_002318.1 //DEF=Homo sapiens lysyl oxidase-like 2 (LOXL2), mRNA. //FEA=mRNA //GEN=LOXL2 //PROD=lysyl oxidase-like 2 //DB_XREF=gi:4505 010 //UG=Hs.83354 lysyl oxidase-like 2 //FL=gb:BC000594.1 gb:NM_002318.1 gb:NM_002318.1 gb:NM_002318.1 melanoma antigen, family D, 2 gb:NM_001124.1 //DEF=Homo sapiens adrenomedullin (ADM), mRNA. //FEA=mRNA //GEN=ADM //PROD=adrenomed ullin //DB_XREF=gi:4501 944 //UG=Hs.394 adrenomedullin //FL=gb:NM_001124 NM_001124 1. gb:D14874.1 putative

Figure 7a CC	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	L-1-NIM 000 400 0	r	
		gb:NM_002406.2 /DEF=Homo	:	
		.		
		sapiens mannosyl		
		(alpha-1,3-)-		
		glycoprotein beta-		
		1,2-N-		
		acetylglucosaminyltr		
		ansferase		
		(MGAT1), mRNA.		
		/FEA=mRNA		
		/GEN=MGAT1		
		/PROD=mannosyl		
		(alpha-1,3-)-		
		glycoproteinbeta-		
		1,2-N-		
		acetylglucosaminyltr		
		ansferase		•
		/DB_XREF=gi:6031		
		182		
		/UG=Hs.151513		
ŀ		mannosyl (alpha-		
		1,3-)-glycoprotein		
		beta-1,2-N-		
		acetylglucosaminyltr		
		ansferase		
004400		/FL=gb:M55621.1		
201126_s_at	NM_00	2406 gb:NM_002406.2		•
		Consensus		
		includes		
		gb:Al741392		
		/FEA=EST	,	
		/DB_XREF=gi:5109]	
		680		
		/DB_XREF=est:wg2		
		7b08.x1		
		/CLONE=IMAGE:23		
		66295		
		/UG=Hs.5151 RAN		
		binding protein 7		
		/FL=gb:AF098799.1		
200005 at	AL1373			
200995_at	JAL 137	555 [gb.ivivi_00591.1		

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. 19410 74 04					
			Consensus		
			includes		
			gb:U95822.1		
			/DEF=Human		
			putative		
			transmembrane		
			GTPase mRNA,		
			partial cds.		
			/FEA=mRNA		
			/GEN=fzo		
			/PROD=putative		
			transmembrane		
			GTPase		
			/DB_XREF=gi:2252		
			803		
	:		/UG=Hs.197877	:	
			hypothetical protein		
217043_s_at		U95822	FLJ20693		
218032 at		AF070673	gb:AF070673.1 /DEF=Homo sapiens stannin mRNA, complete cds. /FEA=mRNA /PROD=stannin /DB_XREF=gi:3978 241 /UG=Hs.76691 stannin /FL=gb:AF030196.1 gb:AF070673.1 gb:NM_003498.1 gb:AL161976.1		·
2.0002_dt		5 55. 5	J		
			v-ets		
			erythroblastosis		
-			virus E26 oncogene		1
201328_at	ETS2	AL575509	homolog 2 (avian)		Hs.85146

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201204_s_at

gb:NM_002775.1 /DEF=Homo sapiens protease, serine, 11 (IGF binding) (PRSS11), mRNA. /FEA=mRNA /GEN=PRSS11 /PROD=protease, serine, 11 (IGF binding) /DB_XREF=gi:4506 140 /UG=Hs.75111 protease, serine, 11 (IGF binding) /FL=gb:D87258.1 gb:NM_002775.1 NM_002775 201185_at Consensus includes gb:N31913 /FEA=EST /DB_XREF=gi:1152 312 /DB_XREF=est:yy2 1f10.s1 /CLONE=IMAGE:27 1915 /UG=Hs.28578 muscleblind (Drosophila)-like /FL=gb:NM_021038 .1 gb:AB007888.1 NM_021038 201152_s_at ribosome binding protein 1 homolog RRBP1 Hs.98614

AI921320

180kDa (dog)

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Figure 7a CC	int d.				
217771_at		NM_016548	gb:NM_016548.1 /DEF=Homo sapiens golgi membrane protein GP73 (LOC51280), mRNA. /FEA=mRNA /GEN=LOC51280 /PROD=golgi membrane protein GP73 /DB_XREF=gi:7706 084 /UG=Hs.182793 golgi membrane protein GP73 /FL=gb:BC001740.1 gb:AF236056.1 gb:NM_016548.1		
21777_dt			gb:NM_001386.1		
			/DEF=Homo		:
			sapiens		
			dihydropyrimidinase		
			like 2 (DPYSL2),		
			mRNA.		
			/FEA=mRNA		
			/GEN=DPYSL2		
			/PROD=dihydropyri		
			midinase-like 2		
			/DB_XREF=gi:4503		
			376	1	
			/UG=Hs.173381		
			dihydropyrimidinase	1	
			/FL=gb:U17279.1		
			gb:D78013.1		
			gb:U97105.1		
200762_at		NM_001386	gb:NM_001386.1		

Figure 7a Cont d.	_ 		
217949 s at	NM 024006	gb:NM_024006.1 /DEF=Homo sapiens hypothetical protein IMAGE3455200 (IMAGE3455200), mRNA. /FEA=mRNA /GEN=IMAGE3455 200 /PROD=hypothetica l protein IMAGE3455200 /DB_XREF=gi:1312 4769 /UG=Hs.324844 hypothetical protein IMAGE3455200 /FL=gb:BC002911.1 gb:NM_024006.1	
217911_s_at	NM_004281	gb:NM_004281.1 /DEF=Homo sapiens BCL2- associated athanogene 3 (BAG3), mRNA. /FEA=mRNA /GEN=BAG3 /PROD=BCL2- associated athanogene 3 /DB_XREF=gi:6631 072 /UG=Hs.15259 BCL2-associated athanogene 3 /FL=gb:AF095193.2 gb:NM_004281.1 gb:AF127139.1 gb:AF071218.2	

Figure /a Co	ill a.		7	
200069_at		NM_014706	Consensus includes gb:Al656011 /FEA=EST /DB_XREF=gi:4739 990 /DB_XREF=est:tt42 e08.x1 /CLONE=IMAGE:22 43462 /UG=Hs.116875 KIAA0156 gene product /FL=gb:AB020880.1 gb:NM_014706.1 gb:D63879.1	
200069_at		NM_014706	gb:D63879.1 gb:NM_002394.1 /DEF=Homo sapiens solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2 (SLC3A2), mRNA. /FEA=mRNA /GEN=SLC3A2 /PROD=antigen identified by monoclonal antibodies 4F2,TRA1.10, TROP4, and T43 /DB_XREF=gi:4505 140 /UG=Hs.79748 solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2 /FL=gb:BC001061.1	
200924_s_at		NM_002394	gb:J02769.1 gb:J03569.1 gb:NM_002394.1 gb:AB018010.1	
44783_s_at	HEY1	R61374	hairy/enhancer-of- split related with YRPW motif 1	Hs.234434

Figure 7a Co	ont a.		,		
200994_at	int d.	AL137335	Consensus includes gb:BG291787 /FEA=EST /DB_XREF=gi:1305 0002 /DB_XREF=est:602 386007F1 /CLONE=IMAGE:45 15240 /UG=Hs.5151 RAN binding protein 7 /FL=gb:AF098799.1 gb:NM_006391.1 gb:NM_00062.1 /DEF=Homo sapiens serine (or cysteine) proteinase inhibitor, clade G (C1 inhibitor), member 1 (SERPING1), mRNA. /FEA=mRNA /GEN=SERPING1 /PROD=complement component 1 inhibitor precursor /DB_XREF=gi:4557 378 /UG=Hs.151242 serine (or cysteine) proteinase inhibitor, clade G (C1 inhibitor), member 1		
	,		/FL=gb:M13690.1 gb:M13656.1		
200986_at		NM_000062	gb:NM_000062.1	L_,	L

I Iguic 1 a o				
217161_x_at		X17406	Consensus includes gb:X17406.1 //DEF=Human mRNA for cartilage specific proteoglycan. //FEA=mRNA //PROD=cartilage specific proteoglycan (600 AA) //DB_XREF=gi:3024 8 //UG=Hs.2159 aggrecan 1 (chondroitin sulfate proteoglycan 1, large aggregating proteoglycan, antigen identified by monoclonal antibody A0122)	
<u> </u>		,,,,,,,	elongation of very	
			long chain fatty	
			acids (FEN1/Elo2,	
57163 at	ELOVL1	H93026	SUR4/Elo3, yeast)-	Hs.25597
101 103_at	ICLOALI	Į 133020	luve i	113.20091

Figure 7a Co	110.			
217127_at	AL354872			
222303_at	AV700891	I ESTs	1,,,,,,,	Hs.202273
201880_at	NM 0057	Consensus includes gb:AL040708 /FEA=EST /DB_XREF=gi:5409 654 /DB_XREF=est:DK FZp434A1015_s1 /CLONE=DKFZp43 4A1015 /UG=Hs.181461 ariadne (Drosophila) homolog, ubiquitin- conjugating enzyme E2-binding protein, 1 /FL=gb:AF072832.1		

Figure /a Co	micu.			
201735_s_at		NM_001829	gb:NM_001829.1 /DEF=Homo sapiens chloride channel 3 (CLCN3), mRNA. /FEA=mRNA /GEN=CLCN3 /PROD=chloride channel 3 /DB_XREF=gi:4502 868 /UG=Hs.174139 chloride channel 3 /FL=gb:AF029346.1 gb:NM_001829.1 gb:AF172729.1	
201735_S_at		14141_001025	95.74 172720.1	
201829_at	NET1	AW263232	neuroepithelial cell transforming gene 1	Hs.25155
218062_x_at		NM_012121	gb:NM_012121.2 /DEF=Homo sapiens Cdc42 effector protein 4; binder of Rho GTPases 4 (CEP4), mRNA. /FEA=mRNA /GEN=CEP4 /PROD=Cdc42 effector protein 4; binder of Rho GTPases4 /DB_XREF=gi:1378 6126 /UG=Hs.3903 Cdc42 effector protein 4; binder of Rho GTPases 4 /FL=gb:AB042237.1 gb:NM_012121.2 gb:AF099664.1	

Figure 7a CC		1	
		Consensus	
		includes	
		gb:AK026674.1	
		/DEF=Homo	
		sapiens cDNA:	
		FLJ23021 fis,	
		cione LNG01014,	
		highly similar to	
		HUMSEF21B	
		Human SEF2-1B	
		protein (SEF2-1B)	
		mRNA.	
		/FEA=mRNA	
		/DB_XREF=gi:1043	
		9577	
		/UG=Hs.326198	
		transcription factor	
222446	AK026674	4	
222146_s_at	ANU20074		
İ		gb:NM_015001.1	
		/DEF=Homo	
		sapiens KIAA0929	
		protein Msx2	
		interacting nuclear	
		target (MINT)	
		homolog	
		(KIAA0929),	
		1'	
		mRNA.	
		/FEA=mRNA	
		/GEN=KIAA0929	
]		/PROD=KIAA0929	
		protein Msx2	
		interacting nuclear	
		target(MINT)	
		homolog	
		•	
	l	/DB_XREF=gi:7657	
	ŀ	266	
		/UG=Hs.184245	
		KIAA0929 protein	
		Msx2 interacting	
	l	nuclear target	
		(MINT) homolog	
		/FL=gb:NM_015001	
201997_s_at	NM_015001	.1	
201991_5_at	10001 _ININI_	[.]	 L

Application of: Liew, et. al. Our Docket #: 4231/2042 Figure 7a Cont'd.

Figure /a Co	Jitt d.	, 	γ		y
214440_at		NM_000662	Consensus includes gb:NM_000662.1 /DEF=Homo sapiens N-acetyltransferase 1 (arylamine N-acetyltransferase) (NAT1), mRNA. /FEA=CDS /GEN=NAT1 /PROD=N-acetyltransferase 1 /DB_XREF=gi:4505 334 /UG=Hs.155956 N-acetyltransferase 1 (arylamine N-acetyltransferase) /FL=gb:NM_000662 .1 FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1		
004040 -4	EADD4	DE040070	(chondrocyte-		H- 400700
201910_at	FARP1	BF213279	derived)		Hs.183738
214721 × at		AI 162074	Consensus includes gb:AL162074.1 //DEF=Homo sapiens mRNA; cDNA DKFZp762L106 (from clone DKFZp762L106); partial cds. //FEA=mRNA //GEN=DKFZp762L106 //PROD=hypothetica I protein //DB_XREF=gi:7328 153 //UG=Hs.3903 Cdc42 effector protein 4; binder of Rho GTPases 4		
214721_x_at 214606_at	TSPAN-2	AL162074 BF129969	tetraspan 2		Hs.234863
	•	<u> </u>	 	·	•————

Figure 7a C	one a.	Υ			
			capping protein		
			(actin filament)		
201949_x_at	CAPZB	AL572341	muscle Z-line, beta		Hs.333417
			collagen, type III,		
			alpha 1 (Ehlers-		
			Danlos syndrome		
			type IV, autosomal		
215076_s_at	COL3A1	AU144167	dominant)		Hs.119571
210070_0_ut	0020/11	7.07.11.61	period homolog 1		
36829_at	PER1	AF022991	(Drosophila)	NM_002616	Hs.68398
30023_at	LIKI	711 022001	mitochondrial	14141_002010	113.00000
			Itranslational		
045004	NATIES	DE540045			116 75440
215091_s_at	MTIF3	BE542815	initiation factor 3		Hs.75113
			gb:NM_005776.1		
			/DEF=Homo		
<u>.</u>			sapiens cornichon-		
			like (CNIL),		
			mRNA.		
			/FEA=mRNA		
			/GEN=CNIL		
			/PROD=cornichon-		
			like		
			/DB_XREF=gi:5031		
			638		
	1		/UG=Hs.201673		
	ļ				
			cornichon-like		
		1	/FL=gb:AF104398.1		
			gb:AF070654.1		
			gb:AF031379.1		
201653_at		NM_005776	gb:NM_005776.1		
			gb:NM_004927.1		
			/DEF=Homo		
			sapiens		
1			chromosome 11		
			open reading		
		1	frame 4		
			(C110RF4),		
		1	mRNA.		
			/FEA=mRNA		
		1	/GEN=C11ORF4		,
			/PROD=chromoso		
			ľ		
			me 11 open		
			reading frame 4		
			/DB_XREF=gi:4826		
			648 /UG=Hs.75859		
		1	chromosome 11		
		1	open reading		
		1	frame 4		
		1	/FL=gb:U39400.1		
			gb:BC004378.1		
201717_at		NM_004927	gb:NM_004927.1		
201111_at	<u> </u>	11111 007321	192.1411_007327.1	L	L

Figure 7a Cont'd.

rigule ra Co	 		
201525_at	NM_001647	gb:NM_001647.1 /DEF=Homo sapiens apolipoprotein D (APOD), mRNA. /FEA=mRNA /GEN=APOD /PROD=apolipoprot ein D precursor /DB_XREF=gi:4502 162 /UG=Hs.75736 apolipoprotein D /FL=gb:J02611.1 gb:NM_001647.1	
201506_at	NM_000358	gb:NM_000358.1 /DEF=Homo sapiens transforming growth factor, beta- induced, 68kD (TGFBI), mRNA. /FEA=mRNA /GEN=TGFBI /PROD=transformin g growth factor, beta-induced, 68kD /DB_XREF=gi:4507 466 /UG=Hs.118787 transforming growth factor, beta- induced, 68kD /FL=gb:BC000097.1 gb:BC004972.1 gb:NM_000358.1	

gb:AL136943.1 //DEF=Homo sapiens mRNA; cDNA DKFZp586G1024 (from clone DKFZp586G1024); complete cds. //FEA=mRNA //GEN=DKFZp586G 1024 //PROD=hypothetica I protein //DB_XREF=gi:1205 3380 //UG=Hs.301226 KIAA1085 protein //El=gb:AL136943.1 gb:BC005057.1 //DEF=Homo sapiens, eukaryotic translation initiation factor 4E binding protein 2, clone MGC:12944, mRNA, complete cds. //FEA=mRNA //PROD=eukaryotic translation initiation factor 4E binding protein 2 //DB_XREF=gi:1347 7190 //UG=Hs.278712	Figure 7a Co	nta.			
/DEF=Homo sapiens, eukaryotic translation initiation factor 4E binding protein 2, clone MGC:12944, mRNA, complete cds. /FEA=mRNA /PROD=eukaryotic translation initiation factor 4Ebinding protein 2 /DB_XREF=gi:1347 7190 /UG=Hs.278712	208773_s_at			/DEF=Homo sapiens mRNA; cDNA DKFZp586G1024 (from clone DKFZp586G1024); complete cds. /FEA=mRNA /GEN=DKFZp586G1024 /PROD=hypothetica I protein /DB_XREF=gi:12053380 /UG=Hs.301226 KIAA1085 protein	
eukaryotic translation initiation factor 4E binding protein 2 /FL=gb:BC005057.1 gb:NM_004096.1 208770_s_at BC005057 gb:L36056.1	208770 s at		BC005057	/DEF=Homo sapiens, eukaryotic translation initiation factor 4E binding protein 2, clone MGC:12944, mRNA, complete cds. /FEA=mRNA /PROD=eukaryotic translation initiation factor 4Ebinding protein 2 /DB_XREF=gi:1347 7190 /UG=Hs.278712 eukaryotic translation initiation factor 4E binding protein 2 /FL=gb:BC005057.1 gb:NM_004096.1	

Application of: Liew, et. al. Our Docket #: 4231/2042 Figure 7a Cont'd.

Figure 7a CC	Trees.			
208763_s_at		AL110191	gb:AL110191.1 /DEF=Homo sapiens mRNA; cDNA DKFZp566A093 (from clone DKFZp566A093); complete cds. /FEA=mRNA /GEN=DKFZp566A 093 /PROD=hypothetica I protein /DB_XREF=gi:5817 105 /UG=Hs.75450 delta sleep inducing peptide, immunoreactor /FL=gb:AF228339.1 gb:AF153603.1 gb:AF183393.1	
208/63_s_at		AL110191	gb.AF 183393.1	
218643_s_at		NM_014171	gb:NM_014171.1 /DEF=Homo sapiens postsynaptic protein CRIPT (CRIPT), mRNA. /FEA=mRNA /GEN=CRIPT /PROD=HSPC139 protein /DB_XREF=gi:7661 797 /UG=Hs.39733 postsynaptic protein CRIPT /FL=gb:AF161488.1 gb:NM_014171.1	
208980_s_at		M26880	gb:M26880.1 /DEF=Human ubiquitin mRNA, complete cds. /FEA=mRNA /DB_XREF=gi:3400 67 /UG=Hs.183704 ubiquitin C /FL=gb:M17597.1 gb:M26880.1	

rigule 7a Cont	.u.		
208898_at	AF077614	gb:AF077614.1 //DEF=Homo sapiens vacuolar ATP synthase subunit D homolog (VATD) mRNA, complete cds. //FEA=mRNA //GEN=VATD //PROD=vacuolar ATP synthase subunit D homolog //DB_XREF=gi:1199 9089 //UG=Hs.272630 vacuolar proton pump delta polypeptide //FL=gb:AF104629.1 gb:AF077614.1 gb:AF145316.1 gb:AF100741.1 gb:NM_015994.1	
208833_s_at	AF119662	gb:AF119662.1 /DEF=Homo sapiens E46 protein mRNA, complete cds. /FEA=mRNA /PROD=E46 protein /DB_XREF=gi:6563 249 /UG=Hs.13493 like mouse brain protein E46 /FL=gb:AL050282.1 gb:AF119662.1 gb:NM_013236.1	

Figure /a Co	лка	· 	
219526_at	NM_024644	gb:NM_024644.1 /DEF=Homo sapiens hypothetical protein FLJ21802 (FLJ21802), mRNA. /FEA=mRNA /GEN=FLJ21802 /PROD=hypothetica I protein FLJ21802 /DB_XREF=gi:1337 5884 /UG=Hs.48938 hypothetical protein FLJ21802 /FL=gb:NM_024644 .1	-
		gb:NM_001135.1 /DEF=Homo sapiens aggrecan 1 (chondroitin sulfate proteoglycan 1, large aggregating proteoglycan, antigen identified by monoclonal antibody A0122) (AGC1), transcript variant 1, mRNA. /FEA=mRNA /GEN=AGC1 /PROD=aggrecan 1, isoform 1 precursor /DB_XREF=gi:4501 990 /UG=Hs.2159 aggrecan 1 (chondroitin sulfate proteoglycan, antigen identified by monoclonal antibody A0122) /FL=gb:M55172.1	
207692_s_at	NM_001135	gb:NM_001135.1	

rigure ra oc	 	,	
207614_s_at	NM_003592	gb:NM_003592.1 /DEF=Homo sapiens cullin 1 (CUL1), mRNA. /FEA=mRNA /GEN=CUL1 /PROD=cullin 1 /DB_XREF=gi:4503 160 /UG=Hs.14541 cullin 1 /FL=gb:U58087.1 gb:NM_003592.1	
		Consensus includes gb:AL049943.1 //DEF=Homo sapiens mRNA; cDNA DKFZp564F0522 (from clone DKFZp564F0522). //FEA=mRNA //GEN=DKFZp564F0522 //PROD=hypothetica I protein //DB_XREF=gi:4884187 //UG=Hs.23060 DKFZP564F0522	
212333_at	 AL049943	protein ESTs, Weakly	
212063_at	BE903880	similar to TRHY_HUMAN Trichohyalin [H.sapiens]	Hs.408878

Figure 7a	Cont'd.
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Figure 7a Co	····			
211998_at	NM_005324	Consensus includes gb:AW138159 /FEA=EST /DB_XREF=gi:6142 559 /DB_XREF=est:UI-H-BI1-acy-d-03-0-UI.s1 /CLONE=IMAGE:27 16060 /UG=Hs.180877 H3 histone, family 3B (H3.3B) /FL=gb:NM_005324 .1		
208712_at	M73554	gb:M73554.1 /DEF=Human bcl-1 mRNA, complete CDS. /FEA=mRNA /GEN=bcl-1 /PROD=bcl-1 /DB_XREF=gi:1793 64 /UG=Hs.82932 cyclin D1 (PRAD1: parathyroid adenomatosis 1) /FL=gb:BC000076.1 gb:M73554.1		
208290_s_at	NM_001969	gb:NM_001969.1 /DEF=Homo sapiens eukaryotic translation initiation factor 5 (EIF5), mRNA. /FEA=mRNA /GEN=EIF5 /PROD=eukaryotic translation initiation factor 5 /DB_XREF=gi:4503 542 /UG=Hs.286236 eukaryotic translation initiation factor 5 /FL=gb:U49436.1 gb:NM_001969.1		

Figure 7a C	Ont G.			
	ļ		chromosome 7	
			open reading frame	
212247_at	C7orf14	AW008531	14	Hs.84790
			splicing factor,	
			arginine/serine-rich	1
212266_s_at	SFRS5	AW084582	5	Hs.409118
212200_3_at	01100	7111004002	gb:NM_004038.1	110.100110
			/DEF=Homo	
			1	
			sapiens amylase,	
			alpha 1A; salivary	
			(AMY1A), mRNA.	1
	1		/FEA=CDS	1
			/GEN=AMY1A	
			/PROD=amylase,	
			alpha 1A; salivary	
			/DB_XREF=gi:4757	
			749	
		·	/UG=Hs.274376	
			amylase, alpha	<u> </u>
			1A; salivary	
			/FL=gb:NM_004038	
208498_s_at		NM_004038	.1	
			i i	
			1	
			i	ļ
			gb:AF084513.1	
	1		/DEF=Homo	
	1		1	
			sapiens DNA	
			repair exonuclease	
			(REC1) mRNA,	
			alternatively spliced	
	1		product, complete	
			cds. /FEA=mRNA	
	1		/GEN=REC1	
			/PROD=DNA repair	
1			exonuclease	
			/DB_XREF=gi:3600	
			078 /UG=Hs.7179	
			RAD1 (S. pombe)	
			homolog	
			/FL=gb:AF084513.1	
210216_x_at		AF084513	gb:AF090170.1	
<u></u>	<u> </u>	1, 11 00-10 10	13-" " 000 0. 1	

gb:AF114488.1 //DEF=Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds. //EEA=mRNA //GEN=ITSN //PROD=intersectin short isoform //DB_XREF=gi:4808 824 //UG=Hs.68392 intersectin 1 (SH3 domain protein) //FL=gb:AF064243.1 gb:AF114488.1 209298_s_at AF114488 gb:AF114488.1 gb:NM_022490.1 //DEF=Homo sapiens hypothetical protein FJJ13390 similar to PAF53 (/FLA=mRNA //GEN=FLJ13390 similar to PAF63 //DB_XREF=gi:1196 8046 //UG=Hs.24884 hypothetical protein FJJ13390 similar to PAF63 //DB_XREF=gi:1196 8046 //UG=Hs.24884 hypothetical protein FJJ13390 similar to PAF63 //DB_XREF=gi:1196 8046 //UG=Hs.24884 hypothetical protein FJJ13390 similar to PAF63 //DB_XREF=gi:1196 8046 //UG=Hs.24884 hypothetical protein FJJ13390 similar to PAF63 //DB_XREF=gi:1196 8046 //UG=Hs.24884 hypothetical protein FJJ13390 similar to PAF63 //DB_XREF=gi:1196 8046 //UG=Hs.24884 hypothetical protein FJJ13390 similar to PAF63 //DB_XREF=gi:1196 8046 //UG=Hs.24884 hypothetical protein FJJ13390 similar to PAF63 //DB_XREF=gi:1196 8046 //UG=Hs.24884 hypothetical protein FJJ13390 similar to PAF63 //DB_XREF=gi:1196 8046 //UG=Hs.24884 hypothetical protein FJJ13390 similar to PAF63 //DB_XREF=gi:1196 8046 //UG=Hs.24884	I iguie 7a Oc	 		
gb:NM_022490.1 //DEF=Homo sapiens hypothetical protein FLJ13390 similar to PAF53 (FLJ13390), mRNA. //FEA=mRNA //GEN=FLJ13390 //PROD=hypothetica I protein FLJ13390 similar to PAF53 //DB_XREF=gi:1196 8046 //UG=Hs.24884 hypothetical protein FLJ13390 similar to PAF53 //FL=gb:NM_022490	209298 s at	AF114488	/DEF=Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds. /FEA=mRNA /GEN=ITSN /PROD=intersectin short isoform /DB_XREF=gi:4808 824 /UG=Hs.66392 intersectin 1 (SH3 domain protein) /FL=gb:AF064243.1	
/DEF=Homo sapiens hypothetical protein FLJ13390 similar to PAF53 (FLJ13390), mRNA. /FEA=mRNA /GEN=FLJ13390 /PROD=hypothetica I protein FLJ13390 similar to PAF53 /DB_XREF=gi:1196 8046 /UG=Hs.24884 hypothetical protein FLJ13390 similar to PAF53 /FL=gb:NM_022490	200200_0_dt	711100	J	
	218997 at	NM 022490	/DEF=Homo sapiens hypothetical protein FLJ13390 similar to PAF53 (FLJ13390), mRNA. /FEA=mRNA /GEN=FLJ13390 /PROD=hypothetica I protein FLJ13390 similar to PAF53 /DB_XREF=gi:1196 8046 /UG=Hs.24884 hypothetical protein FLJ13390 similar to PAF53	

Figure 7a Co				
219002_at			gb:NM_024622.1 /DEF=Homo sapiens hypothetical protein FLJ21901 (FLJ21901), mRNA. /FEA=mRNA /GEN=FLJ21901 /PROD=hypothetica I protein FLJ21901 /DB_XREF=gi:1337 5843 /UG=Hs.32646 hypothetical protein FLJ21901 /FL=gb:NM_024622 .1	
2 13002_at		7441_027022		
210275_s_at		AF062347	gb:AF062347.1 /DEF=Homo sapiens zinc finger protein 216 splice variant 2 (ZNF216) mRNA, complete cds. /FEA=mRNA /GEN=ZNF216 /PROD=zinc finger protein 216 splice variant 2 /DB_XREF=gi:3643 810 /UG=Hs.3776 zinc finger protein 216 /FL=gb:AF062347.1	
2102/5_s_at		Aru6234/	[/FL=gb:AFU62347.1	

Figure 7a CC	int G.		
209803_s_at	AF00	gb:AF001294.1 //DEF=Homo sapiens IPL (IPL) mRNA, complete cds. /FEA=mRNA //GEN=IPL //PROD=IPL //DB_XREF=gi:2150 049 //UG=Hs.154036 tumor suppressing subtransferable candidate 3 //FL=gb:BC005034.1 gb:AF001294.1 gb:AF019953.1 gb:AF035444.1	
209409_at	D8696	gb:D86962.1 /DEF=Human mRNA for KIAA0207 gene, complete cds. /FEA=mRNA /GEN=KIAA0207 /DB_XREF=gi:1503 997 /UG=Hs.81875 growth factor receptor-bound protein 10 /FL=gb:D86962.1	
209596_at	AF24	gb:AF245505.1 /DEF=Homo sapiens adlican mRNA, complete cds. /FEA=mRNA /PROD=adlican /DB_XREF=gi:9280 404 /UG=Hs.72157 DKFZP564I1922 protein 5505 /FL=gb:AF245505.1	

Figure 7a Co	iii di.		
209561_at	L38969	gb:L38969.1 /DEF=Homo sapiens thrombospondin 3 (THBS3) mRNA, complete cds. /FEA=mRNA /GEN=THBS3 /PROD=thrombosp ondin 3 /DB_XREF=gi:8862 98 /UG=Hs.169875 thrombospondin 3 /FL=gb:NM_007112 .1 gb:L38969.1	
209972_s_at	AF116615	gb:AF116615.1 /DEF=Homo sapiens PRO0992 mRNA, complete cds. /FEA=mRNA /PROD=PRO0992 /DB_XREF=gi:7959 732 /UG=Hs.258730 heme-regulated initiation factor 2- alpha kinase /FL=gb:AF116615.1	
211161_s_at	AF130082	gb:AF130082.1 /DEF=Homo sapiens clone FLC1492 PRO3121 mRNA, complete cds. /FEA=mRNA /PROD=PRO3121 /DB_XREF=gi:1149 3468 /UG=Hs.119571 collagen, type III, alpha 1 (Ehlers- Danlos syndrome type IV, autosomal dominant) /FL=gb:AF130082.1	

Figure /a Co	inta.			
rigule 74 oc		Consensus includes gb:BE504689 /FEA=EST /DB_XREF=gi:9707 097 /DB_XREF=est:hz3 0h07.x1 /CLONE=IMAGE:32 09533 /UG=Hs.166563 replication factor C (activator 1) 1		
209084_s_at	L149	(145kD) /FL=gb:AF040250.1 22 gb:L14922.1		
209076_s_at	BC00	gb:BC000974.2 //DEF=Homo sapiens, Similar to hypothetical protein 628, clone MGC:5116, mRNA, complete cds. //FEA=mRNA //PROD=Similar to hypothetical protein 628 //DB_XREF=gi:1280 3025 //UG=Hs.181349 hypothetical protein 628 //FL=gb:BC000974.2		
209014_at		gb:AF217963.1 /DEF=Homo sapiens NRAGE mRNA, complete cds. /FEA=mRNA /PROD=NRAGE /DB_XREF=gi:9963 809 /UG=Hs.177556 melanoma antigen, family D, 1 /FL=gb:AF132205.1 gb:AF124440.1 gb:NM_006986.1 7963 gb:AF217963.1		

Figure /a Co				· · · · · · · · · · · · · · · · · · ·	
212240_s_at	M6	1906	Consensus includes gb:Al679268 /FEA=EST /DB_XREF=gi:4889 450 /DB_XREF=est:tu6 2e04.x1 /CLONE=IMAGE:22 55646 /UG=Hs.6241 phosphoinositide-3-kinase, regulatory subunit, polypeptide 1 (p85 alpha)		
209025_s_at	AF (037448	gb:AF037448.1 //DEF=Homo sapiens RRM RNA binding protein Gry rbp (GRY-RBP) mRNA, complete cds. /FEA=mRNA //GEN=GRY-RBP //PROD=Gry-rbp //DB_XREF=gi:3037 012 //UG=Hs.155489 NS1-associated protein 1 //FL=gb:AF037448.1		
219038_at		_024657	gb:NM_024657.1 /DEF=Homo sapiens hypothetical protein FLJ11565 (FLJ11565), mRNA. /FEA=mRNA /GEN=FLJ11565 /PROD=hypothetica I protein FLJ11565 /DB_XREF=gi:1337 5906 /UG=Hs.61763 hypothetical protein FLJ11565 /FL=gb:NM_024657 .1		

I iguic ru oc	 	,	 , — . — . — . — . — . — . — . — . — . —
209183_s_at	AL136653	gb:AL136653.1 /DEF=Homo sapiens mRNA; cDNA DKFZp564P1263 (from clone DKFZp564P1263); complete cds. /FEA=mRNA /GEN=DKFZp564P 1263 /PROD=hypothetica I protein /DB_XREF=gi:6807 650 /UG=Hs.93675 decidual protein induced by progesterone /FL=gb:AB022718.1 gb:NM_007021.1 gb:AL136653.1	
209185_s_at	AF073310	gb:AF073310.1 /DEF=Homo sapiens insulin receptor substrate- 2 (IRS2) mRNA, complete cds. /FEA=mRNA /GEN=IRS2 /PROD=insulin receptor substrate- 2 /DB_XREF=gi:4511 968 /UG=Hs.143648 insulin receptor substrate 2 /FL=gb:NM_003749 .1 gb:AF073310.1	

Figure /a CC	iii u.		
211058_x_at	BC006379	gb:BC006379.1 /DEF=Homo sapiens, tubulin alpha 1, clone MGC:12832, mRNA, complete cds. /FEA=mRNA /PROD=tubulin alpha 1 /DB_XREF=gi:1362 3540 /FL=gb:BC006379.1	
209118_s_at	AF141347	gb:AF141347.1 /DEF=Homo sapiens hum-a- tub2 alpha-tubulin mRNA, complete cds. /FEA=mRNA /PROD=alpha- tubulin /DB_XREF=gi:4929 133 /UG=Hs.272897 Tubulin, alpha, brain-specific /FL=gb:AF141347.1 gb:NM_006009.1	·
209106_at	U19179	Consensus includes gb:BF576458 /FEA=EST /DB_XREF=gi:1165 0170 /DB_XREF=est:602 133875F1 /CLONE=IMAGE:42 88891 /UG=Hs.74002 nuclear receptor coactivator 1 /FL=gb:U19179.1	

Figure 7a Co	int d.		
209169_at	AF016004	Consensus includes gb:N63576 /FEA=EST /DB_XREF=gi:1211 405 /DB_XREF=est:yy6 3f07.s1 /CLONE=IMAGE:27 8245 /UG=Hs.5422 glycoprotein M6B /FL=gb:AF016004.1	
209168_at	AF016004	Consensus includes gb:AW148844 /FEA=EST /DB_XREF=gi:6196 740 /DB_XREF=est:xf0 5c06.x1 /CLONE=IMAGE:26 17162 /UG=Hs.5422 glycoprotein M6B /FL=gb:AF016004.1	
211063_s_at	BC006403	gb:BC006403.1 /DEF=Homo sapiens, NCK adaptor protein 1, clone MGC:12668, mRNA, complete cds. /FEA=mRNA /PROD=NCK adaptor protein 1 /DB_XREF=gi:1362 3576 /FL=gb:BC006403.1	

Figure /a Co	ont a.		I.S.		
			Consensus		
			includes		
			gb:AI074333		
			/FEA=EST		
			/DB_XREF=gi:3400		
			977		
			/DB_XREF=est:oz8		
			4a09.x1		
			/CLONE=IMAGE:16		
			82008	!	
			/UG=Hs.8025		
			Homo sapiens		
			clone 23767 and		
]		23782 mRNA		
213004_at		AF007150	sequences		
			gb:NM_005195.1		
			/DEF=Homo		
			sapiens		ı
			CCAATenhancer		
!			binding protein		
			(CEBP), delta		
			(CEBPD), mRNA.		
			/FEA=mRNA		
			/GEN=CEBPD		
			/PROD=CCAATenh		
			ancer binding		
			protein (CEBP),		
			delta		
			/DB_XREF=gi:4885		
			130 /UG=Hs.76722		
			CCAATenhancer		
			binding protein		
			(CEBP), delta		
	1		/FL=gb:M83667.1		
203973_s_at		NM_005195	gb:NM_005195.1		
213068_at	DPT	AI146848	dermatopontin		Hs.80552
			RecQ protein-like		
242048 -+	BECOL	DE040004	(DNA helicase Q1-		110 005000
212918_at	RECQL	BF219234	like)		Hs.235069

	nitu.			
204615_x_at		NM_004508	gb:NM_004508.1 /DEF=Homo sapiens isopentenyl- diphosphate delta isomerase (IDI1), mRNA. /FEA=mRNA /GEN=IDI1 /PROD=isopentenyl- diphosphate delta isomerase /DB_XREF=gi:4758 583 /UG=Hs.76038 isopentenyl- diphosphate delta isomerase /FL=gb:NM_004508 .1	
			gb:NM_022443.1	
204784_s_at		NM_022443	/DEF=Homo sapiens myeloid leukemia factor 1 (MLF1), mRNA. /FEA=mRNA /GEN=MLF1 /PROD=myeloid leukemia factor 1 /DB_XREF=gi:1196 7974 /UG=Hs.85195 myeloid leukemia factor 1 /FL=gb:NM_022443 .1	
204478_s_at		NM_002871	gb:NM_002871.1 /DEF=Homo sapiens RAB interacting factor (RABIF), mRNA. /FEA=mRNA /GEN=RABIF /PROD=RAB interacting factor /DB_XREF=gi:4506 378 /UG=Hs.90875 RAB interacting factor /FL=gb:U74324.1 gb:NM_002871.1	

Figure 7a Co	J. 1. C G.		,	
213001_at		AF007150	Consensus includes gb:AF007150.1 /DEF=Homo sapiens clone 23767 and 23782 mRNA sequences. /FEA=mRNA /DB_XREF=gi:2852 628 /UG=Hs.8025 Homo sapiens clone 23767 and 23782 mRNA sequences	
204594_s_at		NM_013298	gb:NM_013298.1 /DEF=Homo sapiens hypothetical protein (HSU79252), mRNA. /FEA=mRNA /GEN=HSU79252 /PROD=hypothetica I protein /DB_XREF=gi:9558 736 /UG=Hs.240062 hypothetical protein /FL=gb:U79252.1 gb:NM_013298.1	
203659_s_at		NM_005798	gb:NM_005798.1 /DEF=Homo sapiens ret finger protein 2 (RFP2), mRNA. /FEA=mRNA /GEN=RFP2 /PROD=ret finger protein 2 /DB_XREF=gi:5031 860 /UG=Hs.151428 ret finger protein 2 /FL=gb:AF220127.1 gb:AF220128.1 gb:NM_005798.1 gb:AF241850.1	

gb:NM_016408.1 /DEF=Homo sapiens CGI-05 protein (LOC51654), mRNA. /FEA=mRNA /GEN=LOC51654 /PROD=hypothetica I protein HSPC167 /DB_XREF=gi:7705 484 /UG=Hs.306044 CGI-05 protein /FL=qb:AF161516.1 gb:NM_016408.1 NM_016408 218315_s_at Consensus includes gb:AL117643.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434M245 (from clone DKFZp434M245). /FEA=mRNA /DB_XREF=gi:5912 233 /UG=Hs.5288 Homo sapiens mRNA; cDNA DKFZp434M245 (from clone AL117643 DKFZp434M245) 213198_at Consensus includes gb:AF033199.1 /DEF=Homo sapiens C2H2 zinc finger protein pseudogene, mRNA sequence. /FEA=mRNA /DB_XREF=gi:3252 864 /UG=Hs.8198 zinc finger protein 204 AF033199 214823_at

			gb:NM_014845.1 /DEF=Homo sapiens KIAA0274 gene product (KIAA0274), mRNA. /FEA=mRNA /GEN=KIAA0274 /PROD=KIAA0274 gene product /DB_XREF=gi:7662 033 /UG=Hs.10037 KIAA0274 gene	
			KIAA0274 gene product /FL=gb:D87464.1	
203656_at		NM_014845	gb:NM_014845.1	
203910_at	÷	NM_004815	gb:NM_004815.1 /DEF=Homo sapiens PTPL1- associated RhoGAP 1 (PARG1), mRNA. /FEA=mRNA /GEN=PARG1 /PROD=PTPL1- associated RhoGAP 1 /DB_XREF=gi:4758 881 /UG=Hs.70983 PTPL1-associated RhoGAP 1 /FL=gb:U90920.1 gb:NM_004815.1	
213139_at	SNAI2	AI572079	snail 2	 Hs.93005
			likely ortholog of mouse embryonic	
213113_s_at	EEG1	AI630178	epithelial gene 1	 Hs.274453

Figure /a Co	Jiit u.			·	
220755_s_at		NM_016947	gb:NM_016947.1 /DEF=Homo sapiens G8 protein (G8), mRNA. /FEA=mRNA /GEN=G8 /PROD=G8 protein /DB_XREF=gi:8393 383 /UG=Hs.109798 G8 protein /FL=gb:NM_016947 .1		
220917_s_at		NM_025132	gb:NM_025132.1 /DEF=Homo sapiens KIAA1638 protein (KIAA1638), mRNA. /FEA=mRNA /GEN=KIAA1638 /PROD=hypothetica I protein FLJ23127 /DB_XREF=gi:1338 6465 /UG=Hs.288821 KIAA1638 protein /FL=gb:NM_025132 .1		
220936_s_at		NM_018267	gb:NM_018267.1 /DEF=Homo sapiens hypothetical protein FLJ10903 (FLJ10903), mRNA. /FEA=mRNA /GEN=FLJ10903 /PROD=hypothetica I protein FLJ10903 /DB_XREF=gi:8922 757 /UG=Hs.36727 hypothetical protein FLJ10903 /FL=gb:NM_018267		

Figure /a Co	one a.			
203753_at		NM_003199	gb:NM_003199.1 /DEF=Homo sapiens transcription factor 4 (TCF4), mRNA. /FEA=mRNA /GEN=TCF4 /PROD=transcriptio n factor 4, isoform b /DB_XREF=gi:4507 398 /UG=Hs.326198 transcription factor 4 /FL=gb:M74719.1 gb:NM 003199.1	
205679_x_at		NM_013227	gb:NM_013227.1 /DEF=Homo sapiens aggrecan 1 (chondroitin sulfate proteoglycan 1, large aggregating proteoglycan, antigen identified by monoclonal antibody A0122) (AGC1), transcript variant 2, mRNA. /FEA=mRNA /GEN=AGC1 /PROD=aggrecan 1, isoform 2 precursor /DB_XREF=gi:6995 993 /UG=Hs.2159 aggrecan 1 (chondroitin sulfate proteoglycan 1, large aggregating proteoglycan, antigen identified by monoclonal antibody A0122) /FL=gb:NM_013227 1	

			Consensus includes	
212485_at		AB011125	gb:AU146596 /FEA=EST /DB_XREF=gi:1100 8117 /DB_XREF=est:AU 146596 /CLONE=HEMBB10 00938 /UG=Hs.105749 KIAA0553 protein	
 205499_at		NM_014467	gb:NM_014467.1 /DEF=Homo sapiens sushi- repeat protein (SRPUL), mRNA. /FEA=mRNA /GEN=SRPUL /PROD=sushi- repeat protein /DB_XREF=gi:7657 618 /UG=Hs.126782 sushi-repeat protein /FL=gb:AF060567.1 gb:NM_014467.1	
212488_at	COL5A1	AI983428	collagen, type V, alpha 1	Hs.146428

			- L-NIM 000000 4		
			gb:NM_006200.1 /DEF=Homo		
			sapiens proprotein		
			convertase		
			subtilisinkexin type		
			5 (PCSK5),		
			mRNA.		
		:	/FEA=mRNA		
			/GEN=PCSK5		
			/PROD=proprotein		
			convertase		
			subtilisinkexin type		
			5 VDE VDEE::1122		
			/DB_XREF=gi:1132 1618		
			/UG=Hs.94376		
			proprotein		
			convertase		
			subtilisinkexin type		
			5		
			/FL=gb:NM_006200		
205559_s_at		NM_006200	.1 gb:U56387.2	·	
			-b-NIM 047076 4		
			gb:NM_017976.1 /DEF=Homo		
			sapiens		
			hypothetical protein		
			FLJ10038		
			(FLJ10038),		
			mRNA.		
			/FEA=mRNA		
			/GEN=FLJ10038		
			/PROD=hypothetica		
			protein FLJ10038		
	1		/DB_XREF=gi:8922 197		
			/UG=Hs.181202		
			hypothetical protein		
			FLJ10038		
	1		/FL=gb:NM_017976		
205510_s_at	ī	1		I	1

Figure /a Co	iitu.				
218507 at		NM 013332	gb:NM_013332.1 /DEF=Homo sapiens hypoxia- inducible protein 2 (HIG2), mRNA. /FEA=mRNA /GEN=HIG2 /PROD=hypoxia- inducible protein 2 /DB_XREF=gi:7019 408 /UG=Hs.61762 hypoxia-inducible protein 2 /FL=gb:BC001863.1 gb:AF144755.1 gb:NM_013332.1		
206307 s at		NM 004472	gb:NM_004472.1 /DEF=Homo sapiens forkhead box D1 (FOXD1), mRNA. /FEA=mRNA /GEN=FOXD1 /PROD=forkhead box D1 /DB_XREF=gi:4758 391 /UG=Hs.96028 forkhead box D1 /FL=gb:U59832.1 gb:NM 004472.1		

Figure 7a Co	Jitt G.		,	
218465_at		NM_018126	gb:NM_018126.1 /DEF=Homo sapiens hypothetical protein FLJ10525 (FLJ10525), mRNA. /FEA=mRNA /GEN=FLJ10525 /PROD=hypothetica I protein FLJ10525 /DB_XREF=gi:8922 490 /UG=Hs.31082 hypothetical protein FLJ10525 /FL=gb:BC000948.1 gb:NM_018126.1	
212414_s_at		D50918	Consensus includes gb:D50918.1 //DEF=Human mRNA for KIAA0128 gene, partial cds. //FEA=mRNA //GEN=KIAA0128 //DB_XREF=gi:1469 178 //UG=Hs.90998 KIAA0128 protein; septin 2	
220046_s_at		NM_020307	gb:NM_020307.1 /DEF=Homo sapiens cyclin L ania-6a (LOC57018), mRNA. /FEA=mRNA /GEN=LOC57018 /PROD=cyclin L ania-6a /DB_XREF=gi:9945 319 /UG=Hs.4859 cyclin L ania-6a /FL=gb:AF180920.1 gb:NM_020307.1	

1 iguic 7a oc	 		
220137_at	NM_019086	gb:NM_019086.1 /DEF=Homo sapiens hypothetical protein FLJ20674 (FLJ20674), mRNA. /FEA=mRNA /GEN=FLJ20674 /PROD=hypothetica I protein FLJ20674 /DB_XREF=gi:9506 690 /UG=Hs.152519 hypothetical protein FLJ20674 /FL=gb:NM_019086 .1	
212723 at	AK021780	Consensus includes gb:AK021780.1 /DEF=Homo sapiens cDNA FLJ11718 fis, clone HEMBA1005252, highly similar to Homo sapiens mRNA for KIAA0585 protein. /FEA=mRNA /DB_XREF=gi:1043 3034 /UG=Hs.72660 phosphatidylserine receptor	

Figure 7a CC	inta.			
205110_s_at		NM_004114	gb:NM_004114.1 /DEF=Homo sapiens fibroblast growth factor 13 (FGF13), mRNA. /FEA=mRNA /GEN=FGF13 /PROD=fibroblast growth factor 13 /DB_XREF=gi:4758 365 /UG=Hs.6540 fibroblast growth factor 13 /FL=gb:U66198.1 gb:AF100143.1 gb:NM_004114.1	
212787_at	ZAP3	AI952986	ZAP3 protein	Hs.159471
			gb:NM_004434.1 /DEF=Homo sapiens echinoderm microtubule- associated protein- like (EMAPL), mRNA. /FEA=mRNA /GEN=EMAPL /PROD=echinoder m microtubule- associated protein- like /DB_XREF=gi:4758 267 /UG=Hs.12451 echinoderm microtubule- associated protein- like /FL=gb:U97018.1	
204797_s_at		NM_004434	gb:NM_004434.1	

Figure 7a Cont'd. gb:NM_003829.1 /DEF=Homo sapiens multiple PDZ domain protein (MPDZ), mRNA. /FEA=mRNA /GEN=MPDZ /PROD=multiple PDZ domain protein /DB_XREF=gi:4505 230 /UG=Hs.169378 multiple PDZ domain protein /FL=gb:AF093419.1 205079_s_at NM_003829 gb:NM_003829.1 gb:NM_001584.1 /DEF=Homo sapiens chromosome 11 open reading frame 8 (C110RF8), mRNA. /FEA=mRNA /GEN=C11ORF8 /PROD=chromoso me 11 open reading frame 8 /DB_XREF=gi:4502 484 /UG=Hs.46638 chromosome 11 open reading frame 8

/FL=gb:U57911.1

gb:NM_001584.1

NM 001584

205413_at

Figure 7a Co	Jita.			
205351_at		NM_000821	gb:NM_000821.1 /DEF=Homo sapiens gamma- glutamyl carboxylase (GGCX), mRNA. /FEA=mRNA /GEN=GGCX /PROD=gamma- glutamyl carboxylase /DB_XREF=gi:4503 984 /UG=Hs.77719 gamma-glutamyl carboxylase /FL=gb:L17128.1 gb:M81592.1 gb:NM_000821.1	
			CD59 antigen p18-	
			20 (antigen identified by	
			monoclonal	
			antibodies 16.3A5,	
			EJ16, EJ30, EL32	
212463_at	CD59	BE379006	and G344)	 Hs.42346
212489_at	COL5A1	A1983428	collagen, type V, alpha 1	Hs.146428
	COLSAT		Consensus includes gb:AB002354.2 /DEF=Homo sapiens mRNA for KIAA0356 protein, partial cds. /FEA=mRNA /GEN=KIAA0356 /PROD=KIAA0356 protein /DB_XREF=gi:6634 022 /UG=Hs.32312 KIAA0356 gene	113.140420
212717_at	<u> </u>	AJ002220	product	<u> </u>

		gb:NM_004411.1 /DEF=Homo sapiens dynein, cytoplasmic, intermediate polypeptide 1 (DNCI1), mRNA. /FEA=mRNA /GEN=DNCI1 /PROD=dynein, cytoplasmic, intermediate polypeptide 1 /DB_XREF=gi:4758 177 /UG=Hs.65248 dynein, cytoplasmic, intermediate	
		cytoplasmic,	
		polypeptide 1 /FL=gb:AF063228.1	
205348_s_at	NM_004411	gb:NM_004411.1	

	Figure 7b: Severe	OA stage-st	Figure 7b: Severe OA stage-specific markers (Affymetrix data)		
Gene name	Common name	Genbank	Description	GefSeq	UniGene
			gb:NM_002593.2 /DEF=Homo sapiens procollagen C-endopeptidase enhancer (PCOLCE), mRNA. /FEA=mRNA		
			enhancer /DB_XREF=gi:7262388 /UG=Hs.202097 procollagen		
202465 at		 NM 002593			
			mRNA /FEA=mRNA /GEN=CTPS /PROD=CTP synthase		
202613_at		NM 001905	/DB_XREF=gi:4503132 /UG=Hs.251871 CTP synthase /FL=gb:NM 001905.1		
			ab:BC001808.1 /DEF=Homo sapiens nucleoside diphosphate	:	
			kinase type 6 (inhibitor of p53-induced apoptosis-alpha),		
			clone MGC:1889, mRNA, complete cds. /FEA=mRNA		
			/PROD=nucleoside diphosphate kinase type 6 (inhibitorof p53-	···-	
			induced apoptosis-alpha) /DB_XREF=gi:12804744		
			/UG=Hs.152717 nucleoside diphosphate kinase type 6		
	1		(inhibitor of p53-induced apoptosis-alpha) /FL=gb:BC001808.1		
205851_at		BC001808	gb:BC001850.1 gb:U90449.1 gb:AF051941.1 gb:NM_005793.1		
214005_at	FHL2	BE326952	four and a half LIM domains 2		Hs.8302
			gb:NM_002496.1 /DEF=Homo sapiens NADH dehydrogenase		
			(ubiquinone) Fe-S protein 8 (23kD) (NADH-coenzyme Q		
			reductase) (NDUFS8), mRNA. /FEA=mRNA /GEN=NDUFS8		
			/PROD=NADH dehydrogenase (ubiquinone) Fe-S protein		
			8(23kD) (NADH-coenzyme Q reductase)		
		,	(23kD)		
203190_at		NM_002496	reductase) /FL=gb:U65579.1 gb:NM_002496.1		
		ń.	gb:AF060511.1 /DEF=Homo sapiens clone 016b10 My016		
			protein mRNA, complete cds. /FEA=mRNA /PROD=My016		
			protein /DB_XREF=gi:12001971 /UG=Hs.181634 Homo		
			sapiens cDNA: FLJ23602 fis, clone LNG15735		
		AF060511	/FL=gb:AF060511.1		
34037 at	CCIM1	090268	cerebral cavernous malformations 1	NM_004912	Hs.93810

riguie / D Colif d	Journa.			
			gb:NM_014875.1 /DEF=Homo sapiens KIAA0042 gene product (KIAA0042), mRNA, /FEA=mRNA /GEN=KIAA0042	
206364		MM 044875	/PROD=KIAA0042 gene product /DB_XREF=gi:7661877 /UG=Hs.3104 KIAA0042 gene product /FL=gb:D26361.1	
200304 at		٦,	gp://www.ol.46/0.1	
			gb:NM_005589.1 /DEF=Homo sapiens methylmalonate-	
			semialdehyde dehydrogenase (MMSDH), mRNA. /FEA=mRNA	
	- , _		/GEN=MMSDH /PROD=methylmalonate-semialdehyde	
			dehydrogenase /DB_XREF=gi:11095440 /UG=Hs.293970	
			methylmalonate-semialdehyde dehydrogenase	
			/FL=gb:NM 005589.1 gb:BC004909.1 gb:M93405.1	
204290 s at	<u>Z</u>	NM_005589	gb:AF148505.1 gb:AF159889.1	
			gb:NM_001902.1 /DEF=Homo sapiens cystathionase	
			(cystathionine gamma-lyase) (CTH), mRNA. /FEA=mRNA	
			/GEN=CTH /PROD=cystathionase (cystathionine gamma-lyase)	
			/DB_XREF=gi:4503124 /UG=Hs.19904 cystathionase	
206085_s_at	N	NM_001902	(cystathionine gamma-lyase) /FL=gb:NM_001902.1	
			gb:NM_006887.1 /DEF=Homo sapiens butyrate response	
			factor 2 (EGF-response factor 2) (BRF2), mRNA.	
			/FEA=mRNA /GEN=BRF2 /PROD=butyrate response factor 2	
			(EGF-response factor2) /DB_XREF=gi:5901899 /UG=Hs.78909	
			butyrate response factor 2 (EGF-response factor 2)	
201369_s_at	<u>Z</u>	NM_006887	/FL=gb:BC005010.1 gb:NM_006887.1	
			gb:D38616.1 /DEF=Human mRNA for phosphorylase kinase	
			alpha subunit, complete cds. /FEA=mRNA	
			/PROD=phosphorylase kinase alpha subunit	
			/DB_XREF=gi:1304117 /UG=Hs.54941 phosphorylase kinase,	
209439_s_at		D38616	alpha 2 (liver) /FL=gb:D38616.1 gb:NM_000292.1	
			gb:NM_004113.2 /DEF=Homo sapiens fibroblast growth factor	
			12B (FGF12B), mRNA. /FEA=mRNA /GEN=FGF12B	
			/PROD=fibroblast growth factor 12B /DB_XREF=gi:5729823	
			/UG=Hs.326401 fibroblast growth factor 12B /FL=gb:U76381.2	
207501_s_at	2	NM_004113	gb:NM_004113.2	
			gb:U90552.1 /DEF=Human butyrophilin (BTF5) mRNA,	
			COMPRETE COS. (TEXT-INVIVA GEN-BITS) (TROCK-BURNING)	
	-	1	/DB_XREF=gr:2062/05 /UG=Hs.284283 butyrophilin, subtamily	
209770_at	ר ו	U90552	3, member A1 /FL=gb:U90552.1	

Ligure	rigure / b Cont a.			
209209_s_at	at MIG2	AW469573	mitogen inducible 2	Hs.75260
			gb:NM_017566.1 /DEF=Homo sapiens hypothetical protein DKFZp434G0522 (DKFZp434G0522), mRNA. /FEA=mRNA	
			/GEN=DKFZp434G0522 /PROD=hypothetical protein	
			DKFZp434G0522 /DB_XREF=gi:8922135 /UG=Hs.67991	
221219_s_at	200711	NM 01/566	/566 hypothetical protein DKFZp434G0522 /FL=gb:NM 01/566.1	0.00040
217620_s_at_	PIK3CB	AA805318	phosphoinositide-3-kinase, catalytic, beta polypeptide	HS.239818
			gb:NM_014763.1 /DEF=Homo sapiens mitochondrial ribosomal	
			//PROD=mitochondrial ribosomal protein L19	
			/DB_XREF=gi:7661911 /UG=Hs.75574 mitochondrial ribosomal	
203465_at		NM_014763	4763 protein L19 /FL=gb:D14660.1 gb:NM 014763.1	
			gb:NM_014060.1 /DEF=Homo sapiens MCT-1 protein (MCT-	
			1), mRNA. /FEA=mRNA /GEN=MCT-1 /PROD=MCT-1 protein	35
			/DB_XREF=gi:7662501 /UG=Hs.102696 MCT-1 protein	
218163_at		NM_014060	4060 /FL=gb:BC001013.1 gb:AB034206.1 gb:NM_014060.1	
			gb:U25147.1 /DEF=Human citrate transporter protein mRNA,	
			nuclear gene encoding mitochondrial protein, complete cds.	
			/FEA=mRNA /PROD=citrate transporter protein	
			/DB_XREF=gi:950003 /UG=Hs.111024 solute carrier family 25	
			(mitochondrial carrier, citrate transporter), member 1	
210010_s_at		U25147	/FL=gb:U25147.1	
			gb:NM_003188.1 /DEF=Homo sapiens mitogen-activated	
		14. 150 <u></u>	protein kinase kinase 7 (MAP3K7), mRNA.	
			/FEA=mRNA /GEN=MAP3K7 /PROD=mitogen-activated protein	
			kinase kinase kinase7 /DB_XREF=gi:4507360 /UG=Hs.7510	
			mitogen-activated protein kinase kinase kinase 7	
206854_s_at		NM_003188	NM_003188 /FL=gb:AB009356.1 gb:NM_003188.1	
			Consensus includes gb:D63480.1 /DEF=Human mRNA for	
			KIAA0146 gene, partial cds. /FEA=mRNA /GEN=KIAA0146	
212523_s_at		D63480	/DB_XREF=gi:1469873 /UG=Hs.278634 KIAA0146 protein	

Consensus includes gb:AK022014 / DEFE+Homo sapiens conversions includes gb:AK022014 / DEFE+Homo sapiens breast cancer nuclear receptor-binding auxiliary protein (BRX) mRNA / FER=mRNA / LD11925 fis, clone HEMB1000831, weakly similar to Homo sapiens breast cancer nuclear receptor-binding auxiliary protein (BRX) mRNA / LD11925 fis, clone HEMB1000831, weakly similar to Homo sapiens breast cancer nuclear receptor-binding auxiliary protein (BRX) mRNA / EEF=mRNA / GEN=wY047 protein (BRX) mRNA / EEF=mRNA / GEN=wY047 protein (BRX) mRNA / FER=mRNA / GEN=wY047 protein (WY047), mRNA / FER=mRNA / GEN=wY047 / PROD=MY047 protein / LDB_XREF=gi.7662509 / LG=Hs.1000 leptin receptor overlapping transcript-like 1 / FLEpbE0000642.1	Figure	Figure /b Cont'd.			
Bb:NM_015344.1 / DEF=Homo sapiens MY047 protein (MY047), mRNA. / FEA=mRNA / GEN=MY047 / PROD=MY047 protein / DB_XREF=gi:7662509 / UG=Hs.11000 leptin receptor overlapping transcript-like 1 / FL=gb:BC000642.1	222023_at		AK022014	Consensus includes gb:AK022014.1 /DEF=Homo sapiens cDNA FLJ11952 fis, clone HEMBB1000831, weakly similar to Homo sapiens breast cancer nuclear receptor-binding auxiliary protein (BRX) mRNA. /FEA=mRNA. /DB_XREF=gi:10433327 /UG=Hs.306619 Homo sapiens cDNA FLJ11952 fis, clone HEMBB1000831, weakly similar to Homo sapiens breast cancer nuclear receptor-binding auxiliary protein (BRX) mRNA.	
Consensus includes gb:Al806174 /FEA=EST	202594_at		ı – – – – – – – – – – – – – – – – – – –	gb:NM_015344.1 /DEF=Homo sapiens MY047 protein (MY047), mRNA. /FEA=mRNA /GEN=MY047 /PROD=MY047 protein /DB_XREF=gi:7662509 /UG=Hs.11000 leptin receptor overlapping transcript-like 1 /FL=gb:BC000642.1 gb:AF063605.1 gb:AF161461.1 gb:NM_015344.1	
Qb:NM_016603.1 /DEF=Homo sapiens GAP-like protein (LOC51306), mRNA. /FEA=mRNA /GEN=LOC51306 /PROD=GAP-like protein /DB_XREF=gi:7706136 /UG=Hs.82035 potential nuclear protein C5ORF5; GAP-like notein /FL=gb:AF251038.1 gb:AF157316.1 gb:NM_016603.1 gb:BC001903.1 /DEF=Homo sapiens, Similar to interleukin 1 receptor, beta, clone MGC:2210, mRNA, complete cds. /FEA=mRNA /PROD=Similar to interleukin 10 receptor, beta /FL=gb:BC001903.1 gb:NM_000628.1 receptor, beta /FL=gb:BC001903.1 gb:NM_000628.1 gb:NM_006604.1 /DEF=Homo sapiens ret finger protein-like gi:DNA_006604.1 /DEF=Homo sapiens ret finger protein-like 3 /PB_XREF=gi:5730012 /UG=Hs.167751 /UG=Hs.167751			U19969	Consensus includes gb:Al806174 /FEA=EST /DB_XREF=gi:5392740 /DB_XREF=est:wf06h03.x1 /CLONE=IMAGE:2349845 /UG=Hs.232068 transcription factor 8 (represses interleukin 2 expression)	
gb:BC001903.1 /DEF=Homo sapiens, Similar to interleukin 1 receptor, beta, clone MGC:2210, mRNA, complete cds. //FEA=mRNA /PROD=Similar to interleukin 10 receptor, beta /DB_XREF=gi:12804902 /UG=Hs.173936 interleukin 10 receptor, beta /FL=gb:BC001903.1 gb:NM_000628.1 receptor, beta /FL=gb:BC001903.1 gb:NM_000628.1 potein MGC3298 gb:NM_006604.1 /DEF=Homo sapiens ret finger protein-like (RFPL3), mRNA. /FEA=mRNA /GEN=RFPL3 /PROD=ret finger protein-like 3 /DB_XREF=gi:5730012 /UG=Hs.167751 ret finger protein-like 3 /FL=gb:NM_006604.1			:	gb:NM_016603.1 /DEF=Homo sapiens GAP-like protein (LOC51306), mRNA. /FEA=mRNA /GEN=LOC51306 /PROD=GAP-like protein /DB_XREF=gi:7706136 /UG=Hs.82035 potential nuclear protein C5ORF5; GAP-like protein /FL=gb:AF251038.1 gb:AF157316.1 gb:NM_016603.1	
at MGC3298 N36926 hypothetical protein MGC3298 gb:NM_006604.1 /DEF=Homo sapiens ret finger protein-like (RFPL3), mRNA. /FEA=mRNA /GEN=RFPL3 /PROD=ret finger protein-like 3 /DB_XREF=gi:5730012 /UG=Hs.167751 NM_006604 ret finger protein-like 3 /FL=gb:NM_006604.1	209575_at		BC001903	gb:BC001903.1 /DEF=Homo sapiens, Similar to interleukin 10 receptor, beta, clone MGC:2210, mRNA, complete cds. /FEA=mRNA /PROD=Similar to interleukin 10 receptor, beta /DB_XREF=gi:12804902 /UG=Hs.173936 interleukin 10 receptor, beta /FL=gb:BC001903.1 gb:NM_000628.1	
gb:NM_006604.1 /DEF=Homo sapiens ret finger protein-like (RFPL3), mRNA. /FEA=mRNA /GEN=RFPL3 /PROD=ret finger protein-like 3 /DB_XREF=gi:5730012 /UG=Hs.167751 NM_006604 ret finger protein-like 3 /FL=gb:NM_006604.1	#		N36926	hypothetical protein MGC3298	Hs.380173
	207936_x_at		NM_006604	nger protein-like //PROD=ret /UG=Hs.167751	

						Hs.153498
	gb:BC003564.1 /DEF=Homo sapiens, ATPase, H+ transporting, lysosomal (vacuolar proton pump), member J, clone MGC:1970, mRNA, complete cds. /FEA=mRNA / PROD=ATPase, H+ transporting, lysosomal (vacuolarproton pump), member J /DB_XREF=gi:13097719 /UG=Hs.90336 ATPase, H+ transporting, lysosomal (vacuolar proton pump), member J /FL=gb:BC003564.1 gb:AF038954.1 gb:NM_004888.1	gb:M25915.1 /DEF=Human complement cytolysis inhibitor (CLI) mRNA, complete cds. /FEA=mRNA /DB_XREF=gi:180619 /UG=Hs.75106 clusterin (complement lysis inhibitor, SP-40,40, sulfated glycoprotein 2, testosteronerepressed prostate message 2, apolipoprotein J) /FL=gb:J02908.1 gb:M25915.1 gb:M64722.1 gb:NM_001831.1	gb:J04977.1 /DEF=Human Ku autoimmune antigen gene, complete cds. /FEA=mRNA /GEN=G22P1 /DB_XREF=gi:186791 /UG=Hs.84981 X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining; Ku autoantigen, 80kD) /FL=gb:NM 021141.2 gb:J04977.1 gb:M30938.1	gb:AF126181.1 /DEF=Homo sapiens breast cancer-associated gene 1 protein (BCG1) mRNA, complete cds. /FEA=mRNA /GEN=BCG1 /PROD=breast cancer-associated gene 1 protein /DB_XREF=gi:4732088 /UG=Hs.4943 hepatocellular carcinoma associated protein; breast cancer associated gene 1 /FL=gb:NM_006787.1 gb:BC000304.1 gb:U92544.1 gb:AF128527.1 gb:AF128528.1	gb:BC002486.1 /DEF=Homo sapiens, C-terminal binding protein 2, clone MGC:1563, mRNA, complete cds. /FEA=mRNA /PROD=C-terminal binding protein 2 /DB_XREF=gi:12803334 /UG=Hs.171391 C-terminal binding protein 2 /FL=qb:BC002486.1	chromosome 18 open reading frame 1
	BC003564	M25915	J04977	AF126181	BC002486	AI349506
rigure / o conta.						C18orf1
Ligure	208737_at	208792 s at	208643 s at	208682 s at	210554 s at	

г								
					Hs.155174			
								-
	gb:AF080157.1 /DEF=Homo sapiens IkB kinase-a (IKK-alpha) mRNA, complete cds. /FEA=mRNA /GEN=IKK-alpha /PROD=IkB kinase-a /DB_XREF=gi:4185272 /UG=Hs.198998 conserved helix-loop-helix ubiquitous kinase /FL=gb:U22512.1 gb:AF012890.1 gb:AF009225.1 gb:AF080157.1	gb:BC006456.1 /DEF=Homo sapiens, clone MGC:1426, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:1426) /DB_XREF=gi:13623660 /FL=gb:BC006456.1	gb:AB002382.1 /DEF=Human mRNA for KIAA0384 gene, complete cds. /FEA=mRNA /GEN=KIAA0384 /DB_XREF=gi:2224708 /UG=Hs.166011 catenin (cadherin-associated protein), delta 1 /FL=gb:AB002382.1	gb:D83077.1 /DEF=Homo sapiens mRNA for TPRD, complete cds. /FEA=mRNA /PROD=TPRD //DB_XREF=gi:1304131 /UG=Hs.118174 tetratricopeptide repeat domain 3 /FL=qb:D83077.1	CDC5 cell division cycle 5-like (S. pombe)	gb:BC001167.1 /DEF=Homo sapiens, retinoid X receptor, beta, clone MGC:1831, mRNA, complete cds. /FEA=mRNA /PROD=retinoid X receptor, beta /DB_XREF=gi:12654658 /UG=Hs.79372 retinoid X receptor, beta /FL=gb:NM_021976.1 gb:BC001167.1 gb:M84820.1	Consensus includes gb:AK001135.1 /DEF=Homo sapiens cDNA FLJ10273 fis, clone HEMBB1001137, highly similar to Homo sapiens mRNA for putative phospholipase. //FEA=mRNA /DB_XREF=gi:7022202 /UG=Hs.300208 Sec23-interacting protein p125 /FL=gb:BC002540.1 gb:AB019435.1 gb:NM_007190.1	gb:BC004875.1 /DEF=Homo sapiens, Similar to RIKEN cDNA 2310034L04 gene, clone MGC:11061, mRNA, complete cds. /FEA=mRNA /PROD=Similar to RIKEN cDNA 2310034L04 gene /DB_XREF=gi:13436109 /UG=Hs.66309 Homo sapiens, Similar to RIKEN cDNA 2310034L04 gene, clone MGC:11061, mRNA, complete cds /FL=gb:BC004875.1
	AF080157	BC006456	AB002382	74 D83077	AW268817	BC001167	AK001135	78700Ja
galo i a coma.					CDCSL			
. 5 :56: .	209666_s_at	211068_x_at	211240_x_at	210645 s at	s at	209148_at	209175_at	2005 12

rigure / b Conta	Conta.			
			gb:AB030710.1 /DEF=Homo sapiens FLC3A mRNA for MAP1	
			light chain 3 related protein, complete cds. /FEA=mRNA	
			/GEN=FLC3A /PROD=MAP1 light chain 3 related protein	
			/DB_XREF=gi:12641848 /UG=Hs.6518 ganglioside expression	
			factor 2 /FL=gb:AB030710.1 gb:AF087848.1 gb:AF077046.1	
209046 s at		AB030710	gb:NM_007285.1	
			gb:AB040120.1 /DEF=Homo sapiens mRNA for BCG induced	
			integral membrane protein BIGMo-103, complete cds.	
			/FEA=mRNA /GEN=BIGMo-103 /PROD=BCG induced integral	
			membrane protein BIGMo-103 /DB_XREF=gi:12657580	
			/UG=Hs.284205 up-regulated by BCG-CWS	
209267 s at		AB040120	/FL=gb:AB040120.1	
			gb:AB000889.1 /DEF=Homo sapiens mRNA for phosphatidic	
			acid phosphatase 2b, complete cds. /FEA=mRNA	
			/PROD=phosphatidic acid phosphatase 2b	
			/DB XREF=qi:2467299 /UG=Hs.331371 phosphatidic acid	-
			phosphatase type 2B /FL=gb:U79294.1 gb:AB000889.1	
209355 s at		AB000889	db:AF017786.1	
1			ab:NM 017626.1 /DEF=Homo sapiens hypothetical protein	
			FLJ20027 (FLJ20027), mRNA. /FEA=mRNA /GEN=FLJ20027	
			/PROD=hypothetical protein FLJ20027 /DB XREF=qi:8923029	
			// IG=Hs 7960 Dna.1 (Hsp40) homolog subfamily B member	
202867 s at		NM 017626	12 /FI =ab:NM 017626 1	4
		'n	At-Nilly 004072 4 (DEE-Home conjugated	
			gb:NM_0048/3.1 /DEF=Homo sapiens bCLZ-associated	
			athanogene o (bAco), mkina. /rea-mkina /cen-bAco	
			/PROD=BCL2-associated atnanogene 5	
			/DB_XREF=gi:6631076 /UG=Hs.5443 BCL2-associated	
202985_s_at		NM_004873	athanogene 5 /FL=gb:AF095195.2 gb:NM_004873.1	
			db:NM 014814.1 /DEF=Homo sapiens KIAA0107 gene	
			product (KIAA0107), mRNA. /FEA=mRNA /GEN=KIAA0107	
			/PROD=KIAA0107 gene product /DB_XREF=gi:7661913	
			/UG=Hs.23488 KIAA0107 gene product /FL=gb:BC000630.1	
202753 at		NM 014814		
s at	MYCBP	AL525412	c-mvc binding protein	Hs.78221
203401 c at K	s at KIAAAA9	41123527	KIAAAAQ aana product	Hs 151791
202421 2 at 111	70000	140041	Nixwoosz gene product	

			gb:NM_005125.1 /DEF=Homo sapiens copper chaperone for	
			Superoxide distillatese (CCS), Illativa, if EA-Illativa (GEN=CCS /PROD=copper chaperone for superoxide	
			dismutase /DB_XREF=gi:4826664 /UG=Hs.5002 copper	
			chaperone for superoxide dismutase /FL=gb:AF002210.1	
203522_at		NM_005125	gb:NM 005125.1	
			gb:NM_004381.1 /DEF=Homo sapiens cAMP responsive	
			element binding protein-like 1 (CREBL1), mRNA.	
			/FEA=mRNA /GEN=CREBL1 /PROD=cAMP responsive	
			element binding protein-like 1 /DB_XREF=gi:4758057	
			/UG=Hs 42853 cAMP responsive element binding protein-like	
203168_at		NM_004381	1 /FL=gb:U31903.1 gb:NM_004381.1	
ä	CPT2	AW157077	carnitine palmitoyltransferase II	Hs.274336
			gb:AF047598.1 /DEF=Homo sapiens origin recognition	
		_	complex subunit 4 (ORC4L) mRNA, complete cds.	
			/FEA=mRNA /GEN=ORC4L /PROD=origin recognition complex	
			subunit 4 /DB_XREF=gi:2906225 /UG=Hs.55055 origin	
			recognition complex, subunit 4 (yeast homolog)-like	
			/FL=ab;BC005388.1 ab;AF022108.1 ab;AF047598.1	
203351 s at		AF047598	ab:NM 002552.1 ab:AF132596.1	
			qb:NM_013285.1 /DEF=Homo sapiens nucleolar GTPase	
			(HUMAUANTIG), mRNA. /FEA=mRNA /GEN=HUMAUANTIG	
			/PROD=nucleolar GTPase /DB_XREF=gi:7019418	
			/UG=Hs.75528 nucleolar GTPase /FL=gb:BC000107.1	
201948 at		NM 013285	gb:L05425.1 gb:NM 013285.1	
			Consensus includes gb:AL529409 /FEA=EST	
			/DB_XREF=gi:12792902	
			/CLONE=CS0DD006YM17 (3 prime) /UG=Hs.13313 cAMP	
			responsive element binding protein-like 2 /FL=gb:AF039081.1	
201989_s_at		NM_001310		
			gb:NM_021078.1 /DEF=Homo sapiens GCN5 (general control	
			of amino-acid synthesis, yeast, homolog)-like 2 (GCN5L2),	
			mRNA. /FEA=mRNA /GEN=GCN5L2 /PROD=GCN5 (general	
			control of amino-acid synthesis, yeast, homolog)-like 2	
			/DB_XREF=gi:10835100 /UG=Hs.101067 GCN5 (general	
			control of amino-acid synthesis, yeast, homolog)-like 2	
202182_at		NM_021078	021078 /FL=gb:NM_021078.1	

201842 s at IFFEMP1	MP1	A 826799	FGE-containing fibrulin-like extrace ular matrix protein 1	Hs 76224
20 1072 3 at Li L	- IAII	0501030	EGI -CONTAILING IDAILI-IIVG CYNACCIINI II IIIN DICCIII I	13.1066.1
			gb:NM_002094.1 /DEF=Homo sapiens G1 to S phase transition 1 (GSPT1)_mRNA_/FEA=mRNA_/GEN=GSPT1	
			/PROD=G1 to S phase transition 1 /DB XREF=qi:4504166	
			/UG=Hs.2707 G1 to S phase transition 1	
201912_s_at		NM_002094		
	•			
			triphosphate receptor, type 2 (ITPR2), mRNA. /FEA=mRNA	
			/GEN=ITPR2 /PROD=inositol 1,4,5-triphosphate receptor, type	
			2 /DB_XREF=gi:4504792 /UG=Hs.238272 inositol 1,4,5-	
			triphosphate receptor, type 2 /FL=gb:D26350.1	·
202662_s_at		NM_002223	NM_002223 gb:NM_002223.1	
			gb:NM_021090.1 /DEF=Homo sapiens myotubularin related	
			protein 3 (MTMR3), mRNA. /FEA=mRNA /GEN=MTMR3	
			/PROD=myotubularin related protein 3	
			/DB XREF=gi:10835108 /UG=Hs.63302 myotubularin related	
			protein 3 /FL=gb:NM_021090.1 gb:AB002369.1	
202197_at		NM_021090	NM_021090 gb:AF233438.1	
202341_s_at TRIM2	M2	AA149745	tripartite motif-containing 2	Hs.12372
			db:NM 004922.1 /DEF=Homo sapiens SEC24 (S. cerevisiae)	
			related gene family, member C (SEC24C), mRNA.	
			/FEA=mRNA /GEN=SEC24C /PROD=SEC24 (S. cerevisiae)	
			related gene family,member C /DB_XREF=gi:4758633	
-			/UG=Hs.81964 SEC24 (S. cerevisiae) related gene family,	
202361 at		NM 004922		
i	E		gb:NM_006002.1 /DEF=Homo sapiens ubiquitin carboxyl-	
			terminal esterase L3 (ubiquitin thiolesterase) (UCHL3),	
			mRNA. /FEA=mRNA /GEN=UCHL3 /PROD=ubiquitin carboxyl-	
			terminal esterase L3(ubiquitin thiolesterase)	
			//DB_XREF=gi:5174740 /UG=Hs.77917 ubiquitin carboxyl-	
			terminal esterase L3 (ubiquitin thiolesterase)	
204616_at		NM_006002	/FL=gb:M30496.1 gb:NM_006002.1	

aingi -	igale / D collica.			
204897_at		NM_000958	Consensus includes gb:AA897516 /FEA=EST /DB_XREF=gi:3034136 /DB_XREF=est:aj62c04.s1 /CLONE=IMAGE:1394886 /UG=Hs.199248 prostaglandin E receptor 4 (subtype EP4) /FL=gb:D28472.1 gb:L25124.1 gb:NM_000958.1 gb:L28175.1	
			gb:NM_000019.1 /DEF=Homo sapiens acetyl-Coenzyme A acetyltransferase 1 (acetoacetyl Coenzyme A thiolase) (ACAT1), nuclear gene encoding mitochondrial protein, mRNA. /FEA=mRNA /GEN=ACAT1 /PROD=acetyl-Coenzyme	
205412_at		NM_000019	A acetyltransferase 1 precursor /DB_XREF=gi:455/236 /UG=Hs.37 acetyl-Coenzyme A acetyltransferase 1 (acetoacetyl Coenzyme A thiolase) /FL=gb:NM_000019.1	
206227_at		NM_003613	/UG=Hs.151407 cartilage intermediate layer protein, nucleotide pyrophosphohydrolase /FL=gb:AF035408.1 33613 gb:NM_003613.1	
205908 s at		NM_005014	gb:NM_005014.1 /DEF=Homo sapiens osteomodulin (OMD), mRNA. /FEA=mRNA /GEN=OMD /PROD=osteomodulin /DB_XREF=gi:4826875 /UG=Hs.94070 osteomodulin /FL=gb:AB000114.1 gb:NM_005014.1	
			gb:NM_005807.1 /DEF=Homo sapiens proteoglycan 4, (megakaryocyte stimulating factor, articular superficial zone protein) (PRG4), mRNA. /FEA=mRNA /GEN=PRG4 /PROD=megakaryocyte stimulating factor	
206007 at		NM 005807	/UB_AREF=9I:0031924 /UG=Rs.216791 proteogrycan 4, (megakaryocyte stimulating factor, articular superficial zone protein) /FL=qb:U70136.1 qb:NM 005807.1	
ä	ZFP95	BF196931	zinc finger protein 95 homolog (mouse)	Hs.110839
204012_s_at KIAA0547		AL529189	KIAA0547 gene product	Hs.200596

Figure / b Conta	D Cont a.		
			gb:NM_006715.1 /DEF=Homo sapiens mannosidase, alpha,
-			class 2C, member 1 (MAN2C1), mRNA. /FEA=mRNA
			/GEN=MAN2C1 /PROD=mannosidase, alpha 6A8
			/DB_XREF=gi:6631092 /UG=Hs.26232 mannosidase, alpha,
			class 2C, member 1 /FL=gb:U37248.1 gb:AF044414.2
203668_at		NM_006715	gb:NM_006715.1
			gb:NM_014924.1 /DEF=Homo sapiens KIAA0831 protein
			(KIAA0831), mRNA. /FEA=mRNA /GEN=KIAA0831
			/PROD=KIAA0831 protein /DB_XREF=gi:7662325
			/UG=Hs.103000 KIAA0831 protein /FL=gb:AB020638.1
204568_at		NM_014924	gb:NM_014924.1
			gb:NM_014920.1 /DEF=Homo sapiens MAK-related kinase
-			(KIAA0936), mRNA. /FEA=mRNA /GEN=KIAA0936
			/PROD=KIAA0936 protein /DB_XREF=gi:7662387
			/UG=Hs.108850 MAK-related kinase /FL=gb:AF152469.1
			gb:AB023153.1 gb:AF225919.1 gb:NM_014920.1
204569 at		NM_014920	gb:NM 016513.1
			gb:NM_012395.1 /DEF=Homo sapiens PFTAIRE protein
			kinase 1 (PFTK1), mRNA. /FEA=mRNA /GEN=PFTK1
			/PROD=PFTAIRE protein kinase 1 /DB_XREF=gi:6912583
204604_at		NM_012395	gb:NM_012395.1
_			gb:NM_004477.1 /DEF=Homo sapiens FSHD region gene 1
			(FRG1), mRNA. /FEA=mRNA /GEN=FRG1 /PROD=FSHD
-			region gene 1 /DB_XREF=gi:4758403 /UG=Hs.203772 FSHD
204145 at		NM 004477	
			gb:NM_002800.1 /DEF=Homo sapiens proteasome (prosome,
			macropain) subunit, beta type, 9 (large multifunctional
			protease 2) (PSMB9), mRNA. /FEA=mRNA /GEN=PSMB9
			/PROD=proteasome (prosome, macropain) subunit, betatype,
			9 (large multifunctional protease 2) /DB_XREF=gi:4506204
			/UG=Hs.9280 proteasome (prosome, macropain) subunit, beta
11			type, 9 (large multifunctional protease 2) /FL=gb:U01025.1
204279_at		NM_002800	gb:NM_002800.1

Figure	Figure / b Conta.		
			gb:NM_016627.1 /DEF=Homo sapiens hypothetical protein
			(LOC51321), mRNA. /FEA=mRNA /GEN=LOC51321
			/PROD=hypothetical protein /DB_XREF=gi:7706167
			/UG=Hs.268122 hypothetical protein /FL=gb:AF208856.1
218167_at		NM_016627	gb:NM_016627.1
			gb:NM_018180.1 /DEF=Homo sapiens hypothetical protein
			FLJ10889 (FLJ10889), mRNA. /FEA=mRNA /GEN=FLJ10889
•			/PROD=hypothetical protein FLJ10694 /DB_XREF=gi:9506626
•			/UG=Hs.171835 hypothetical protein FLJ10889
218198_at		NM_018180	
			gb:NM_014175.1 /DEF=Homo sapiens HSPC145 protein
			(HSPC145), mRNA. /FEA=mRNA /GEN=HSPC145
			/PROD=HSPC145 protein /DB_XREF=gi:7661805
			/UG=Hs.18349 HSPC145 protein /FL=gb.AL136665.1
218027_at		NM_014175	
			gb:NM_003730.2 /DEF=Homo sapiens ribonuclease 6
			precursor (RNASE6PL), mRNA. /FEA=mRNA
			/GEN=RNASE6PL /PROD=ribonuclease 6 precursor
			/DB_XREF=gi:5231227 /UG=Hs.8297 ribonuclease 6 precursor
			/FL=gb:BC001660.1 gb:BC001819.1 gb:U85625.2
217983_s_at		NM_003730	_
			gb:NM_024664.1 /DEF=Homo sapiens hypothetical protein
			FLJ11838 (FLJ11838), mRNA. /FEA=mRNA /GEN=FLJ11838
			/PROD=hypothetical protein FLJ11838 /DB_XREF=gi:13375918
			/UG=Hs.72531 hypothetical protein FLJ11838
218341_at		NM_024664	/FL=gb:NM_024664.1
			gb:AF092128.1 /DEF=Homo sapiens putative transmembrane
			protein E3-16 mRNA, complete cds. /FEA=mRNA
			/PROD=putative transmembrane protein E3-16
			/DB_XREF=gi:5138905 /UG=Hs.239625 integral membrane
			protein 2B /FL=gb:NM_021999.1 gb:AF136973.1
217732 s at		AF092128	gb:BC000554.1 gb:AF092128.1 gb:AF152462.1 gb:AF246221.1

/ Ligure /	rigure / b Conta.		
			Consensus includes gb.AL049988.1 /DEF=Homo sapiens
			mRNA; cDNA UKFZp564F212 (from clone UKFZp564F212).
		-	/FEA=mKNA /DB_XKEF=gl:4884z39 /UG=HS.309304 Homo
216614_at		AL049988	DKFZp564F212)
			Consensus includes gb:AF131850.1 /DEF=Homo sapiens
			clone 24988 mRNA sequence. /FEA=mRNA
			/DB_XREF=gi:4406694 /UG=Hs.286027 etoposide-induced
216396_s_at		AF131850	mRNA
			H. sapiens pseudogene for mitochondrial ATP synthase c subunit
217368_at		60669X	(P2 form).
			gb:NM_014161.1 /DEF=Homo sapiens HSPC071 protein
			(HSPC071), mRNA. /FEA=mRNA /GEN=HSPC071
			/PROD=HSPC071 protein /DB_XREF=gi:7661777
			/UG=Hs.23038 HSPC071 protein /FL=gb:AL136633.1
217907_at		NM_014161	gb:BC001623.1 gb:AF161556.1 gb:NM 014161.1
			gb:NM_005770.1 /DEF=Homo sapiens small EDRK-rich factor
			2 (SERF2), mRNA. /FEA=mRNA /GEN=SERF2 /PROD=small
			EDRK-rich factor 2 /DB_XREF=gi:5032084 /UG=Hs.323806
			small EDRK-rich factor 2 /FL=gb:AF320073.1 gb:AF073298.1
217756_x_at		NM_005770	gb:NM_005770.1
			gb:NM_019082.1 /DEF=Homo sapiens putative nucleolar RNA
			helicase (NOH61), mRNA. /FEA=mRNA /GEN=NOH61
			/PROD=putative nucleolar RNA helicase
			/DB_XREF=gi:9506930 /UG=Hs.10098 putative nucleolar RNA
			helicase /FL=gb:AF247666.1 gb:AL136700.1 gb:BC001235.1
217754_at		NM_019082	
			gb:NM_016275.1 /DEF=Homo sapiens selenoprotein T
			(LOC51714), mRNA. /FEA=mRNA /GEN=LOC51714
			/PROD=selenoprotein T /DB_XREF=gi:7706470 /UG=Hs.8148
			selenoprotein T /FL=gb:AF131856.1 gb:AF195141.1
217811_at		NM_016275	_
			Consensus includes gb:X03348.1 /DEF=Human mRNA for
_			beta-glucocorticoid receptor (clone OB10). /FEA=mRNA
			/PROD=beta-glucocorticoid receptor /DB_XREF=gi:31681
			/UG=Hs.75772 nuclear receptor subfamily 3, group C,
216321_s_at		X03348	member 1

Figure	Figure / b Conta.	BE972394	zinc finger protein 131 (clone pHZ-10)	Hs 78743
75 1045 2 al	ZIVF 131	٦	ZINC IIIIgel protein 131 (clone priz-10)	13.10
			gb:NM_030912.1 /DEF=Homo sapiens tripartite motif protein TRIM8 (TRIM8), mRNA. /FEA=mRNA /GEN=TRIM8 /PROD=tripartite motif protein TRIM8 /DB_XREF=gi:13569865	
221012_s_at		NM_030912	/FL=gb:NM_030912.1	
			gb.BC006244.1 /DEF=Homo sapiens, HSPC142 protein, clone	
			MGC:11295, mRNA, complete cds. /FEA=mRNA	
224744 s at		BC006244	//PKOD=HSPC142 protein //DB_XKEF=gi:13623286 //Fi =ab:RC006344 1	
ทู่ส	HRMT1L1	AL570294	HMT1 hnRNP methyltransferase-like 1 (S. cerevisiae)	Hs.235887
			sema domain, immunoglobulin domain (lg), transmembrane	
46665_at	SEMA4C	A1949392	domain (TM) and short cytoplasmic domain, (semaphorin) 4C	Hs.7188
64488_at		AW003091	Homo sapiens FKSG27 (FKSG27) mRNA, complete cds	Hs.6217
47530_at	HSPC219	AA748492	hypothetical protein HSPC219	Hs.9196
			ESTs, Moderately similar to neuronal thread protein [Homo	112.000.004
222370_x_at		N5//81	sapiens [H.sapiens	HS.209364
			gb:NM_025032.1 /DEF=Homo sapiens hypothetical protein	
			/PROD=hypothetical protein FLJ21272 /DB XREF=qi:13376557	
			/UG=Hs.287653 hypothetical protein FLJ21272	
220467_at		NM_025032		
			gb:NM_016594.1 /DEF=Homo sapiens FK506 binding protein	
			precursor (LUC51303), mRNA. /FEA=mRNA /GEN=LUC51303	
			//PKOD=FK506 binging protein precursor	
			/DB_XREF=gi://06130 /UG=Hs.24048 FK506 binding protein	
219117_s_at		NM_016594	precursor /FL=gb:AF2380/9.1 gb:NM_016594.1	
			gb.BC000977.1 /DEF=Homo sapiens, aminolevulinate, delta-,	
			dehydratase, clone MGC:5057, mRNA, complete cds.	
			/FEA=mRNA /PROD=aminolevulinate, delta-, dehydratase	
			//DB_XREF=gi:12654312 /UG=Hs.1227 aminolevulinate, delta-,	
			dehydratase /FL=gb:BC000977.1 gb:M13928.1	
218487_at		BC000977	gb:NM_000031.1	
			gb:NM_018266.1 /DEF=Homo sapiens hypothetical protein FLJ10902 (FLJ10902), mRNA. /FEA=mRNA /GEN=FLJ10902	
			/PROD=hypothetical protein FLJ10902 /DB_XREF=gi:8922755	
70000		22020	/UG=Hs.247112 hypothetical protein FLJ10902	
2 100 12 S at		5]	ITE-90. NINI O 10200. I	

Figure	rigure / b conta.			
			gb:NM_013396.1 /DEF=Homo sapiens ubiquitin specific	
			/PROD=ubiquitin specific protease 25 /DB_XREF=gi:7019564	
220419 s at		NM 013396	/UG=Hs.186961 ubiquitin specific protease 25	
·		۱.	gb:NM 024091.1 /DEF=Homo sapiens hypothetical protein	
			MGC5297 (MGC5297), mRNA. /FEA=mRNA /GEN=MGC5297	
			/PROD=hypothetical protein MGC5297	
			/DB_XREF=gi:13129089 /UG=Hs.23856 hypothetical protein	
219200_at		NM_024091	MGC5297 /FL=gb:BC001295.1 gb:NM_024091.1	
			gb:NM_024546.1 /DEF=Homo sapiens hypothetical protein	
			FLJ13449 (FLJ13449), mRNA. /FEA=mRNA /GEN=FLJ13449	
			/PROD=hypothetical protein FLJ13449 /DB_XREF=gi:13375708	
			/UG=Hs.10711 hypothetical protein FLJ13449	
219303_at		NM_024546		
			Consensus includes gb:AB002365.1 /DEF=Human mRNA for	
			KIAA0367 gene, partial cds. /FEA=mRNA /GEN=kIAA0367	
212805 at		AB002365	/DB_XREF=gi:2224674 /UG=Hs.23311 KIAA0367 protein	
			Consensus includes gb:NM_005830.1 /DEF=Homo sapiens	
			imogen 38 (IMOGN38), mRNA. /FEA=CDS /GEN=IMOGN38	
			/PROD=imogen 38 /DB_XREF=gi:5031786 /UG=Hs.154655	
212603_at		NM_005830	imogen 38 /FL=gb:NM_005830.1	
			Consensus includes gb:AA811192 /FEA=EST	
			/DB_XREF=gi:2880803 /DB_XREF=est:ob72b08.s1	
212846_at		D80001	/CLONE=IMAGE:1336887 /UG=Hs.152629 KIAA0179 protein	
212538_at	zizimin1	AL576253		Hs.8021
			Consensus includes gb:D86985.2 /DEF=Homo sapiens mRNA	
			for KIAA0232 protein, partial cds. /FEA=mRNA	
			/GEN=KIAA0232 /PROD=KIAA0232 protein	
			/DB_XREF=gi:6634002 /UG=Hs.79276 KIAA0232 gene	
ä		D86985	product	
at		BF224151	pleckstrin homology domain interacting protein	Hs.367694
213010_at	PRKCDBP	AI088622	protein kinase C, delta binding protein	Hs.356013

⊢ıgure	Figure / b Cont a.			
			Consensus includes gb:U58515.1 /DEF=Human chitinase	·
213060_s_at		U58515	/UG=Hs.154138 chitinase 3-like 2	
			Consensus includes gb:AB033025.1 /DEF=Homo sapiens	
			mRNA for KIAA1199 protein, partial cds. /FEA=mRNA	
			/GEN=KIAA1199 /PROD=KIAA1199 protein	
212942_s_at		AB033025	/DB_XREF=gi:6330400 /UG=Hs.50081 KIAA1199 protein	
at		AA284075		Hs.117977
212992_at	LOC113146	A1935123	hypothetical protein BC011859 Hs.57	Hs.57548
	RDC1	AI817041		Hs.23016
			Consensus includes gb:AL109804 /DEF=Human DNA	
			sequence from clone RP3-1009E24 on chromosonile 20	-
			Contains a novel gene encoding two isotorms similar to	
			mouse sialoadhesin (a macrophage sialic acid binding	•
			receptor), a novel gene similar to KIAA0417, the CENPB	-
			gene (centromere protein /FEA=mRNA_8	
			/DB_XREF=gi:11121192 /UG=Hs.85004 centromere protein B	
212437_at		AL109804	(80KD)	
			gb:AB050468.1 /DEF=Homo sapiens mRNA for membrane	
			glycoprotein LIG-1, complete cds. /FEA=mRNA /GEN=lig-1	
			/PROD=membrane_glycoprotein_LIG-1_/DB_XREF=gi:13537354	
211596_s_at		AB050468	/FL=gb:AB050468.1	
			gb:AL583909.1 /DEF=Homo sapiens mRNA; cDNA	
			DKFZp761J197 (from clone DKFZp761J197); complete cds.	
			/FEA=mRNA /GEN=DKFZp761J197 /PROD=hypothetical	
			protein /DB_XREF=gi:13093772 /UG=Hs.301696 hypothetical	
211433_x_at		AL583909	protein FLJ11560 /FL=gb:AL583909.1	
			gb:BC005974.1 /DEF=Homo sapiens, vesicle-associated	
			membrane protein 4, clone MGC:14658, mRNA, complete	
			cds. /FEA=mRNA /PROD=vesicle-associated membrane	
211760_s_at		BC005974		
212243_at	GRINL1A	AI632774	glutamate receptor, ionotropic, N-methyl D-aspartate-like 1A	Hs.6283
			Consensus includes gb:AB002330.1 /DEF=Human mRNA for	
			KIAA0332 gene, partial cds. /FEA=mRNA /GEN=KIAA0332	
212061 at		AB002330	/DB_XREF=gi:2224604 /UG=Hs.7976 KIAA0332 protein	
		1000000		

rigure	rigure / b Cont a.				
100000	0 1 1	000011	serine (or cysteine) proteinase inhibitor, clade E (nexin,		27828
212190 at	SERPINEZ	AL341302	plasminogen activator innibitor type 1), member 2		Hs 389013
2 13239 A at 2	LINE Z/ 3	00122103			110 75540
214/83_s_at	NXA11	BG1//920	annexin A11		HS./3210
214967 at		AU146983	ESTs, Weakly similar to hypothetical protein FLJ20234 [Homo sapiens] [H.sapiens]		Hs.262212
	MYL4; GT1;		Human MLC1emb gene for embryonic myosin alkaline light chain,		
216054 x at PRO1957	֧֖֖֖֖֖֖֖֖֖֖֖֖֖֖֖֖֖֖֖֖֖֖֖֖֖֖֖֖֖֖֖֖֖֖֝֡֝֝	X58851	promoter and exon 1.	NM_002476	
216035 x at TCF7L2		AV721430	transcription factor 7-like 2 (T-cell specific, HMG-box)		Hs.348412
			Consensus includes gb:AF057354.1 /DEF=Homo sapiens		
			myotubularin-related protein 1a mRNA, partial cds.		
			/FEA=mRNA /PROD=myotubularin-related protein 1a		
			/DB_XREF=gi:5138901 /UG=Hs.23200 myotubularin related		
216095_x_at		AF057354	protein 1		
			Consensus includes gb:AK002166.1 /DEF=Homo sapiens		
			cDNA FLJ11304 fis, clone PLACE1009997, weakly similar to		
			Rattus norvegicus A-kinase anchoring protein AKAP 220		
			mrna. /FEA=mrna /DB_XREF=gi:7023877 /UG=Hs.232076		
215336_at		AK002166	A kinase (PRKA) anchor protein 11		
			Consensus includes gb:X08020.1 /DEF=Human mRNA for		
			glutathione S-transferase subunit 4 (EC 2.5.1.18).		
			//FEA=mRNA /DB_XREF=gi:31923 /UG=Hs.301961 glutathione		
215333_x_at		X08020	S-transferase M4		
			Consensus includes gb:AK021879.1 /DEF=Homo sapiens		
			CDNA FLJ11817 fis, clone HEMBA1006421. /FEA=mRNA		
			/DB_XREF=gi:10433165 /UG=Hs.293919 Homo sapiens cDNA		
215898_at		AK021879	FLJ11817 fis, clone HEMBA1006421		
214298_x_at	deS-9	6-Sep AL568374	septin 6		Hs.90998
213283_s_at	SALL2	BG285616	sal-like 2 (Drosophila)		Hs.79971
			Consensus includes gb:Al934125 /FEA=EST		
			/DB_XREF=gi:5672995		
213154_s_at		AB014599	/CLONE=IMAGE:2453//4 /UG=HS:1/411 KIAAU699 protein		

250			Consensus includes ab.Al 031177 /DFF=Hilman DNA	
			sequence from clone 889N15 on chromosome Xq22.1-22.3.	
			Contains part of the gene for a novel protein similar to X.	
			laevis Cortical Thymocyte Marker CTX, the possibly	
			alternatively spliced gene for 26S Proteasome subunit p28	
			(Ankyrin repea /FEA=mRNA_3 /DB_XREF=gi:4071056	
			/UG=Hs.8763 Human DNA sequence from clone 889N15 on	
			chromosome Xq22.1-22.3. Contains part of the gene for a	
			novel protein similar to X. laevis Cortical Thymocyte Marker	
			CTX, the possibly alternatively spliced gene for 26S	-
213115_at		AL031177	Proteasome subunit p28 (Ankyrin repeat protei	
213186_at	KIAA0675	BG502305	BG502305 KIAA0675 gene product	Hs.165662
214080_x_at	PRKCSH	AI815793	protein kinase C substrate 80K-H	Hs.1432
213846 at	COX7C	AA382702	cytochrome c oxidase subunit VIIc	Hs.3462
213489_at	MAPRE2	BE671156	microtubule-associated protein, RP/EB family, member 2	Hs.78335
213535_s_at	UBE2I	AA910614	ubiquitin-conjugating enzyme E2I (UBC9 homolog, yeast)	Hs.84285
213103_at	STARD13	AA128023	START domain containing 13	Hs.13649
			gb:NM_002070.1 /DEF=Homo sapiens guanine nucleotide	
			binding protein (G protein), alpha inhibiting activity	
			polypeptide 2 (GNAI2), mRNA. /FEA=mRNA /GEN=GNAI2	
			/PROD=guanine nucleotide binding protein (G protein),alpha	
			inhibiting activity polypeptide 2 /DB_XREF=gi:4504040	
•			/UG=Hs.77269 guanine nucleotide binding protein (G protein),	
			alpha inhibiting activity polypeptide 2 /FL=gb:J03004.1	
201040_at		NM_002070	NM_002070 gb:NM_002070.1	
			gb:NM_002266.1 /DEF=Homo sapiens karyopherin alpha 2	
	,		(RAG cohort 1, importin alpha 1) (KPNA2), mRNA.	
			/FEA=mRNA /GEN=KPNA2 /PROD=karyopherin alpha 2	
			/DB_XREF=gi:4504896 /UG=Hs.159557 karyopherin alpha 2	
			(RAG cohort 1, importin alpha 1) /FL=gb:NM_002266.1	-
201088_at		NM_002266	NM_002266 gb:U09559.1_gb:U28386.1	

The sections

	.53		LENGTH OCCEAN A POPPELLIANT AND --	-----------	---	---	---
			go. Min Judos 10.1 /DET-FIDITIO Sapieris solute carrier ramilly 2				
			(facilitated glucose transporter), member 1 (SLC2A1), mRNA.				
-			/FEA=mRNA /GEN=SLC2A1 /PROD=solute carrier family 2				
			(facilitated glucosetransporter), member 1				
			/DB_XREF=gi:5730050 /UG=Hs.169902 solute carrier family 2				
			(facilitated glucose transporter), member 1 /FL=gb:K03195.1				
201250_s_at		NM_006516					
			gb:NM_000269.1 /DEF=Homo sapiens non-metastatic cells 1,				
	ı	•	protein (NM23A) expressed in (NME1), mRNA. /FEA=mRNA				
			/GEN=NME1 /PROD=non-metastatic cells 1 protein		٠		
			/DB_XREF=gi:4557796 /UG=Hs.118638 non-metastatic cells				
	grante de la constitución de la	A Capter	1, protein (NM23A) expressed in /FL=gb:BC000293.1				
201577_at		NM_000269	gb:NM_000269.1				
			gb:NM_004279.1 /DEF=Homo sapiens peptidase				
			(mitochondrial processing) beta (PMPCB), mRNA.				
			/FEA=mRNA /GEN=PMPCB /PROD=peptidase (mitochondrial				
			processing) beta /DB_XREF=gi:4758733 /UG=Hs.184211				
			peptidase (mitochondrial processing) beta /FL=gb:AF054182.1				
201682_at		NM_004279					
			gb:NM_004766.1 /DEF=Homo sapiens coatomer protein				
		,	complex, subunit beta 2 (beta prime) (COPB2), mRNA.				
			/FEA=mRNA /GEN=COPB2 /PROD=coatomer protein				
			complex, subunit beta 2 (betaprime) /DB_XREF=gi:4758031	•			
٠			/UG=Hs.75724 coatomer protein complex, subunit beta 2	•			
201098_at		NM_004766	$\overline{}$				
			gb:NM_000986.1 /DEF=Homo sapiens ribosomal protein L24				
,	,		(RPL24), mRNA. /FEA=mRNA /GEN=RPL24		*		
			/PROD=ribosomal protein L24 /DB_XREF=gi:4506618				
			/UG=Hs.184582 ribosomal protein L24 /FL=gb:BC000690.1				
200013_at		NM_000986	NM_000986 gb:M94314.1 gb:NM_000986.1				

200	gale in colleg.				
	-		gb:NM_006825.1 /DEF=Homo sapiens transmembrane protein (63kD), endoplasmic reticulumGolgi intermediate compartment		
			(P63), mRNA. /FEA=mRNA /GEN=P63		
			/PROD=transmembrane_protein (63KD),		
		,	IDB XREF=qi:5803112 /UG=Hs.74368 transmembrane protein		
			(63kD), endoplasmic reticulumGolgi intermediate compartment		
200999 s at		NM_006825	/FL=gb:NM_006825.1		
			gb:D13988.1 /DEF=Human rab GDI mRNA, complete cds.		,
			/FEA=mRNA /PROD=human rab GDI /DB_XREF=gi:285974		
		-	/UG=Hs.56845 GDP dissociation inhibitor 2		
200008 s at		D13988	/FL=gb:BC005145.1 gb:D13988.1 gb:NM_001494.2		
			gb:NM_003169.1 /DEF=Homo sapiens suppressor of Ty	- -	
			(S.cerevisiae) 5 homolog (SUPT5H), mRNA. /FEA=mRNA		
			/GEN=SUPT5H /PROD=suppressor of Ty (S.cerevisiae) 5		
			homolog /DB_XREF=gi:4507312 /UG=Hs.70186 suppressor of		
	•		Ty (S.cerevisiae) 5 homolog /FL=gb:U56402.1 gb:AB000516.1		
201480 s at		NM_003169			
				-	
			arginineserine-rich (transformer 2 Drosophila homolog) 10,		
			clone MGC:8454, mRNA, complete cds. /FEA=mRNA		
			/PROD=splicing factor, arginineserine-rich(transformer 2		
		_	Drosophila homolog) 10 /DB_XREF=gi:12653362		-
			/UG=Hs.30035 splicing factor, arginineserine-rich (transformer		•
			2 Drosophila homolog) 10 /FL=gb:BC000160.1		
200892 s_at		BC000451	gb:BC000451.1 gb:U61267.1 gb:U68063.1 gb:NM_004593.1		
			neural precursor cell expressed, developmentally down-regulated		100 45505
200778_s_at	NEDD5	AI191427	S Control of the second		US. 133393
			gb:NM_004494.1 /DEF=Homo sapiens nepatorina-derived		
			growth factor (nigh-mobility group protein 1-like) (nucr.),		
			mRNA, /FEA=mRNA /GEN=HDGF /PROD=hepatoma-derived		
			growth factor (high-mobilitygroup protein 1-like)		
			/DB_XREF=gi:4758515 /UG=Hs.89525 hepatoma-derived		
	-		growth factor (high-mobility group protein 1-like)		
200896 x at	-	NM_004494			
	L	00000	SWI/SNF related, matrix associated, actin dependent regulator of		Hs 123090
212152_x_at SMARCF1	SMARCF1	AI6/9080	chromatin, subtamily 1, member 1		10:12:00:00

_
gb:NM_001274.1 /DEF=Homo sapiens CHK1 (checkpoint, S.pombe) homolog (CHEK1), mRNA. /FEA=mRNA //GEN=CHEK1 /PROD=CHK1 (checkpoint, S.pombe) homolog //DB_XREF=gi:4502802 /UG=Hs.20295 CHK1 (checkpoint, S.pombe) homolog /FL=gb:AF016582.1 gb:NM_001274.1
gb:NM_006530.1 /DEF=Homo sapiens glioma-amplified sequence-41 (GAS41), mRNA. /FEA=mRNA /GEN=GAS41 /PROD=glioma-amplified sequence-41 /DB_XREF=gi:5729837 /UG=Hs.4029 glioma-amplified sequence-41
gb:AF136970.1 /DEF=Homo sapiens sarcosine oxidase mRNA, complete cds. /FEA=mRNA /PROD=sarcosine oxidase /DB_XREF=gi:12239317 /UG=Hs.271167 L-pipecolic acid oxidase /FL=gb:AF136970.1
gb:AB015228.1 /DEF=Homo sapiens mRNA for RALDH2-T, complete cds. /FEA=mRNA /GEN=RALDH2 /PROD=RALDH2-T / DB_XREF=gi:3970845 /UG=Hs.95197 aldehyde dehydrogenase 1 family, member A2 /FL=gb:NM_003888.1 gb:AB015226.1 gb:AB015227.1 gb:AB015228.1
AV689564 SKI-interacting protein
766 fragile X mental retardation, autosomal homolog
HIV-1 inducer of short transcripts binding protein; lymphoma Al568395 related factor
gb:M95178.1 /DEF=Human non-muscle alpha-actinin mRNA, complete cds. /FEA=mRNA /GEN=ACTN1 /PROD=alpha-actinin /DB_XREF=gi:178051 /UG=Hs.119000 actinin, alpha /FL=gb:M95178.1
gb:NM_001644.2 /DEF=Homo sapiens apolipoprotein B mRNA editing enzyme, catalytic polypeptide 1 (APOBEC1), transcript variant 1, mRNA. /FEA=mRNA /GEN=APOBEC1 /PROD=apolipoprotein B mRNA editing enzyme, catalyticpolypeptide 1, isoform 1 /DB_XREF=gi:5921993 /UG=Hs.560 apolipoprotein B mRNA editing enzyme, catalytic
001644 gb:NM 005889.1 gb:L26234.1

2 1981	C IS COLICE.			
204230_s_at		NM_020309	gb:NM_020309.1 /DEF=Homo sapiens brain-specific Nadependent inorganic phosphate cotransporter (BNPI), mRNA. //FEA=mRNA /GEN=BNPI /PROD=brain-specific Na-dependent inorganic phosphatecotransporter /DB_XREF=gi:9945321 //UG=Hs.6535 brain-specific Na-dependent inorganic phosphate cotransporter /FL=gb:AB032436.1 gb:NM_020309.1	
207995_s_at		NM_014257	gb:NM_014257.1 /DEF=Homo sapiens CD209 antigen-like (CD209L), mRNA. /FEA=mRNA /GEN=CD209L	
205207_at		009000 NM	gb:NM_000600.1 /DEF=Homo sapiens interleukin 6 (interferon, beta 2) (IL6), mRNA. /FEA=mRNA /GEN=IL6 /PROD=interleukin 6 (interferon, beta 2) /DB_XREF=gi:10834983 /UG=Hs.93913 interleukin 6 (interferon, beta 2) /FL=gb:NM_000600.1 gb:M14584.1 gb:M18403.1 gb:M29150.1 gb:M54894.1	
206614 at		NM 000557	gb:NM_000557.2 /DEF=Homo sapiens growth differentiation factor 5 (cartilage-derived morphogenetic protein-1) (GDF5), mRNA. /FEA=mRNA /GEN=GDF5 /PROD=growth differentiation factor 5 preproprotein /DB_XREF=gi:5123452 /UG=Hs.1573 growth differentiation factor 5 (cartilage-derived morphogenetic protein-1) /FL=gb:NM_000557.2 gb:U13660.1	
215378_at		AU148255	ESTs	Hs.287627
217831 s at		NM_016143	gb:NM_016143.1 /DEF=Homo sapiens p47 (LOC51674), mRNA. /FEA=mRNA /GEN=LOC51674 /PROD=p47 /DB_XREF=gi:7706394 /UG=Hs.12865 p47 /FL=gb:BC002801.1 gb:AF078856.1 gb:NM_016143.1	
			gb:U74324.1 /DEF=Human guanine nucleotide exchange factor mss4 mRNA, complete cds. /FEA=mRNA /PROD=guanine nucleotide exchange factor mss4 /DB_XREF=gi:1658190 /UG=Hs.90875 RAB interacting factor	
204477_at		U74324	/FL=gb:U74324.1 gb:NM_002871.1	

riguie /	riguie / D colita.	3	
219412_at		7822337	gb:NM_022337.1 /DEF=Homo sapiens RAB38, member RAS oncogene family (RAB38), mRNA. /FEA=mRNA /GEN=RAB38 /PROD=RAB38, member RAS oncogene family /DB_XREF=gi:11641236 /UG=Hs.108923 RAB38, member RAS oncogene family /FL=gb:AF235022.1 gb:NM_022337.1
219222_at		NM_022128	gb:NM_022128.1 /DEF=Homo sapiens ribokinase (RBSK), mRNA. /FEA=mRNA /GEN=RBSK /PROD=ribokinase /DB_XREF=gi:11545854 /UG=Hs.11916 ribokinase /FL=gb:NM_022128.1
208961_s_at		AB017493	gb:AB017493.1 /DEF=Homo sapiens mRNA for DNA-binding zinc finger(GBF), complete cds. /FEA=mRNA /PROD=DNA-binding zinc finger(GBF) /DB_XREF=gi:3582142 /UG=Hs.285313 core promoter element binding protein /FL=gb:BC000311.1 gb:BC004301.1 gb:AF001461.1 gb:AB017493.1 gb:NM_001300.2
219743 at		NM_012259	gb:NM_012259.1 /DEF=Homo sapiens hairyenhancer-of-split related with YRPW motif 2 (HEY2), mRNA. /FEA=mRNA /GEN=HEY2 /PROD=hairyenhancer-of-split related with YRPW motif2 /DB_XREF=gi:6912413 /UG=Hs.144287 hairyenhancer-of-split related with YRPW motif 2 /FL=gb:AF311884.1 gb:AF173901.1 gb:NM_012259.1 gb:AF232238.1 gb:AF237949.1 gb:AB044755.1
219054_at		NM_024563	gb:NM_024563.1 /DEF=Homo sapiens hypothetical protein FLJ14054 (FLJ14054), mRNA. /FEA=mRNA /GEN=FLJ14054 /PROD=hypothetical protein FLJ14054 /DB_XREF=gi:13375730 /UG=Hs.13528 hypothetical protein FLJ14054 NM_024563 /FL=gb:NM_024563.1
205716_at		NM_018843	gb:NM_018843.1 /DEF=Homo sapiens mitochondrial carrier family protein (LOC55972), mRNA. /FEA=mRNA /GEN=LOC55972 /PROD=mitochondrial carrier family protein /IDB_XREF=gi:10047121 /UG=Hs.172294 mitochondrial carrier family protein /FL=gb:NM_018843.1 gb:AF125531.1

200				
213647_at		D42046	Consensus includes gb:D42046.1 /DEF=Human mRNA for KIAA0083 gene, partial cds. /FEA=mRNA /GEN=KIAA0083 /DB_XREF=gi:1531547 /UG=Hs.194665 DNA2 (DNA replication helicase, yeast, homolog)-like	
218892_at		NM_024542	gb:NM_024542.1 /DEF=Homo sapiens hypothetical protein FLJ11790 (FLJ11790), mRNA. /FEA=mRNA /GEN=FLJ11790 /PROD=hypothetical protein FLJ11790 /DB_XREF=gi:13375702 /UG=Hs.9658 hypothetical protein FLJ11790 NM_024542 /FL=gb:NM_024542.1	
205848_at		NM_005256	gb:NM_005256.1 /DEF=Homo sapiens growth arrest-specific 2 (GAS2), mRNA. /FEA=mRNA /GEN=GAS2 /PROD=growth arrest-specific 2 /DB_XREF=gi:4885252 /UG=Hs.129818 growth arrest-specific 2 /FL=gb:U95032.1 gb:NM_005256.1	
215867 × at		AL050025	Consensus includes gb:AL050025.1 /DEF=Homo sapiens mRNA; cDNA DKFZp564D066 (from clone DKFZp564D066); partial cds. /FEA=mRNA /GEN=DKFZp564D066 /PROD=hypothetical protein /DB_XREF=gi:4884095 /UG=Hs.5344 adaptor-related protein complex 1, gamma 1 subunit	
64474 g at	FLJ22127	AA203219	tical protein FLJ22127	Hs.59457
57588 at	SLC24A3	R62432	solute carrier family 24 (sodium/potassium/calcium exchanger), member 3	Hs.12321
			gb:NM_014121.1 /DEF=Homo sapiens PRO0233 protein (PRO0233), mRNA. /FEA=mRNA /GEN=PRO0233 /PROD=PRO0233 protein /DB_XREF=gi:7662535	
207464_at		NM_014121	/UG=HS.Z/8933 PROUZ33 protein /rL=gb.ArU9U9U3.1 gb:NM_014121.1	
216286_at		AV760769	AV760769 MDS Homo sapiens cDNA clone MDSBSE09 5', mRNA sequence.	

_				_				_	_		_				_					_								_				 _
								Hs.167741																								
								NM_006994					·																			
db:NM 004353.1 /DEF=Homo sapiens serine (or cysteine)	proteinase inhibitor, clade H (heat shock protein 47),	member 1 (SERPINH1), mRNA. /FEA=mRNA	//GEN=SERPINH1 /PROD=serine (or cysteine) proteinase	inhibitor, cladeH (heat shock protein 47), member 1	/DB_XREF=gi:4757923 /UG=Hs.241579 serine (or cysteine)	proteinase inhibitor, clade H (heat shock protein 47),		butyrophilin, subfamily 3, member A2	gb:NM_023003.1 /DEF=Homo sapiens transmembrane 6	superfamily member 1 (TM6SF1), mRNA. /FEA=mRNA	//GEN=TM6SF1 /PROD=transmembrane 6 superfamily	member 1 /DB_XREF=gi:13194198 /UG=Hs.133865	transmembrane 6 superfamily member 1 /FL=gb:AF255922.1	023003 gb:NM_023003.1	gb:NM_003811.1 /DEF=Homo sapiens tumor necrosis factor	(ligand) superfamily, member 9 (TNFSF9), mRNA.	//FEA=mRNA /GEN=TNFSF9 /PROD=tumor necrosis factor	(ligand) superfamily,member 9 /DB_XREF=gi:4507608	/UG=Hs.1524 tumor necrosis factor (ligand) superfamily,		gb:NM_024653.1 /DEF=Homo sapiens hypothetical protein	FLJ13902 (FLJ13902), mRNA. /FEA=mRNA /GEN=FLJ13902	//PROD=hypothetical protein FLJ13902 /DB_XREF=gi:13375900	//UG=Hs.58127 hypothetical protein FLJ13902		Consensus includes gb:AJ290445.1 /DEF=Homo sapiens	mRNA for KIAA0524SARM protein. /FEA=mRNA	//GEN=KIAA0524SARM /PROD=KIAA0524SARM protein	/DB_XREF=gi:7711001 /UG=Hs.128759 KIAA0524 protein	gb:NM_012463.1 /DEF=Homo sapiens TJ6 protein (TJ6),	mRNA. /FEA=mRNA /GEN=TJ6 /PROD=TJ6 protein	/FL=gb:AF112972.1 gb:NM_012463.1
	- 14						NM_004353	U90548						NM_023003						NM_003811					NM_024653				AJ290445			NM_012463
								BTN3A2																								
							207714_s_at	38241_at						219892_at						206907_at					218378_s_at				213257_at			205704_s_at

rigure	rigure / b cont a.			
			gb:NM_017767.1 /DEF=Homo sapiens hypothetical protein	
			FLJ20327 (FLJ20327), mRNA. /FEA=mRNA /GEN=FLJ20327	
			/PROD=hypothetical protein FLJ20327 /DB_XREF=gi:8923304	
		•		
219215_s_at		NM_017767	/FL=gb:BC001688.1 gb:NM_017767.1	
		····	gb:NM_016332.1 /DEF=Homo sapiens selenoprotein X, 1	
			(SEPX1), mRNA. /FEA=mRNA /GEN=SEPX1	
			/PROD=selenoprotein X, 1 /DB_XREF=gi:7706510	
		-	/UG=Hs.279623 selenoprotein X, 1 /FL=gb:AF187272.1	
217977_at		NM_016332		
			Consensus includes gb:AL359599.1 /DEF=Homo sapiens	
			mRNA; cDNA DKFZp547C126 (from clone DKFZp547C126).	
			/FEA=mRNA /DB_XREF=gi:8655666 /UG=Hs.283850 Homo	
			sapiens mRNA; cDNA DKFZp547C126 (from clone	
215828_at		AL359599	DKFZp547C126)	
			ESTs, Weakly similar to postmeiotic segregation increased 2-like	
215302_at		AU150691	8 [Homo sapiens] [H.sapiens]	Hs.387966
222322_at		AI791860	ESTs	Hs.335818
			Homo sapiens cDNA FLJ34103 fis, clone FCBBF3007859,	
214318_s_at		W58342	moderately similar to Human putative protein B2 mRNA	Hs.406809
			gb:NM_016558.1 /DEF=Homo sapiens SCAN domain-	
			containing 1 (SCAND1), mRNA. /FEA=mRNA /GEN=SCAND1	
		· · · <u>-</u>	/PROD=SCAN domain-containing 1 /DB_XREF=gi:7706088	
			/UG=Hs.274411 SCAN domain-containing 1	
218206 x at		NM_016558	/FL=gb:BC000785.1 gb:AF204271.1 gb:NM_016558.1	
			gb:L20686.1 /DEF=Homo sapiens guanine nucleotide	
			releasing factor (SOS2) mRNA, complete cds. /FEA=mRNA	
			/GEN=SOS2 /PROD=guanine nucleotide releasing factor	
211665_s_at		L20686	/DB_XREF=gi:1220367 /FL=gb:L20686.1	
			gb:NM_020231.1 /DEF=Homo sapiens x 010 protein	
			(MDS010), mRNA. /FEA=mRNA /GEN=MDS010 /PROD=x	
듦		NM_020231		
212621_at	KIAA0286	AW205215	KIAA0286 protein	Hs.331567

216715_at		AL080315	Consensus includes gb:AL080315 /DEF=Human DNA sequence from clone RP1-6P5 on chromosome 6 Contains a pseudogene similar to EEF1D (eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)), a pseudogene similar to ribosomal protein L21, ESTs, STSs and GSSs /FEA=CDS_1 /DB_XREF=gi:7838240 /UG=Hs.306507 Human DNA sequence from clone RP1-6P5 on chromosome 6 Contains a pseudogene similar to EEF1D (eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)), a pseudogene similar to ribosomal protein L21, ESTs, STSs and GSSs	
			gb:NM_018192.1 /DEF=Homo sapiens hypothetical protein FLJ10718 (FLJ10718), mRNA. /FEA=mRNA /GEN=FLJ10718	
			/PROD=hypothetical protein FLJ10718 /DB_XREF=gi:8922618	
t j	70771.0	NM_018192	/FL=gb:NM_018192.1	He 348412
212759 s at		AI769310	transcription factor 7-like 2 (1-cell specific, nivig-box)	Hs. 129700
at	CBS	BE613178	ie-beta-synthase	Hs.84152
			gb:NM_004343.2 /DEF=Homo sapiens calreticulin (CALR), mRNA_ /FEA=mRNA_/GEN=CALR_/PROD=calreticulin	
			precursor /DB_XREF=gi:5921996 /UG=Hs.16488 calreticulin /FL=gb:BC002500.1 gb:M84739.1 gb:M32294.1	
200935_at		NM_004343)4343 gb:NM_004343.2	
			gb:NM_024669.1 /DEF=Homo sapiens hypothetical protein FLJ11795 (FLJ11795), mRNA. /FEA=mRNA /GEN=FLJ11795	
			/PROD=hypothetical protein FLJ11795 /DB_XREF=gi:13375927	
220112_at		NM_024669	/PL=gb:NM_024669.1	

aingi i	igaic in contra.			
			gb:NM_002252.1 /DEF=Homo sapiens potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3	
			(KCNS3), mRNA. /FEA=mRNA /GEN=KCNS3	
			//PROD=potassium voitage-gated channel,delayed-rectiller, subfamily S, member 3 /DB XREF=gi:4504862	
			/UG=Hs.47584 potassium voltage-gated channel, delayed-	
			rectifier, subfamily S, member 3 /FL=gb:BC004148.1	
205968_at		NM_002252	gb:BC004987.1 gb:AF043472.1 gb:NM 002252.1	
			dJ406P24.1 (Thioredoxin-like pseudogene); Human DNA	
			sequence from clone RP3-406P24 on chromosome 6 Contains a	
			thioredoxin-like pseudogene, 2 CpG islands, ESTs, STSs and	
216532_x_at dJ406P24.1	dJ406P24.1	AL138831	GSSs, complete sequence.	
			Consensus includes gb:AK023959.1 /DEF=Homo sapiens	
			cDNA FLJ13897 fis, clone THYRO1001706. /FEA=mRNA	
			/DB_XREF=gi:10436079 /UG=Hs.301488 Homo sapiens cDNA	
215436_at		AK023959	FLJ13897 fis, clone THYRO1001706	
			gb:NM_017805.1 /DEF=Homo sapiens hypothetical protein	
			FLJ20401 (FLJ20401), mRNA. /FEA=mRNA /GEN=FLJ20401	
			/PROD=hypothetical protein FLJ20401 /DB_XREF=gi:8923375	
			/UG=Hs.233955 hypothetical protein FLJ20401	
220027_s_at		NM_017805	_	
			Consensus includes gb:AA805753 /FEA=EST	
			/DB_XREF=gi:2874503	
			/CLONE=IMAGE:1186398 /UG=Hs.1526 ATPase, Ca++	
212362_at		AK000300	transporting, cardiac muscle, slow twitch 2	
			gb:NM_017726.1 /DEF=Homo sapiens hypothetical protein	
			FLJ20251 (FLJ20251), mRNA. /FEA=mRNA /GEN=FLJ20251	
			/PROD=hypothetical protein FLJ20251 /DB_XREF=gi:8923225	
			/UG=Hs.192927 hypothetical protein FLJ20251	
220082_at		NM_017726	/FL=gb:NM_017726.1	
			gb:BC001771.1 /DEF=Homo sapiens, general transcription	
			factor IIF, polypeptide 2 (30kD subunit), clone MGC:1502,	
			mRNA, complete cds. /FEA=mRNA /PROD=general	
			transcription factor IIF, polypeptide 2(30kD subunit)	
			/DB_XREF=gi:12804688 /UG=Hs.58593 general transcription	
200505		DC004774	factor IIF, polypeptide 2 (30kD subunit) /FL=gb:BC001771.1	
209090 at		פרחחוניו	gu.nivi_004 120.	

-									-	_
		_	Hs.269852							Hs.365523
								NM_000800; NM_033136; NM_033137		
	gb:NM_005711.1 /DEF=Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), mRNA. /FEA=mRNA /GEN=EDIL3 /PROD=EGF-like repeats and discoidin I-like	domains 3 /DB_AREF=91:003 1000 /OG=RS.129704 EGF-like repeats and discoidin I-like domains 3 /FL=gb:U70312.1 db:NM 005711.1	ESTs, Weakly similar to hypothetical protein FLJ11267 [Homo sapiens] [H.sapiens]	gb:NM_000314.1 /DEF=Homo sapiens phosphatase and tensin homolog (mutated in multiple advanced cancers 1) (PTEN), mRNA. /FEA=mRNA /GEN=PTEN	/PROD=phosphatase and tensin homolog (mutated inmultiple advanced cancers 1) /DB_XREF=gi:4506248 /UG=Hs.10712 phosphatase and tensin homolog (mutated in multiple advanced cancers 1) /FL=gb:U92436.1 gb:U93051.1	gb:U9618U.1 gb:NM_000314.1	gb:NM_022346.1 /DEF=Homo sapiens chromosome condensation protein G (HCAP-G), mRNA. /FEA=mRNA //GEN=HCAP-G /PROD=chromosome condensation protein G //DB_XREF=gi:11641252 /UG=Hs.193602 chromosome condensation protein G /FL=gb:AF235023.1 gb:NM_022346.1 gb:AF331796.1 gb:BC000827.1 gb:AB013299.1	Protein sequence is in conflict with the conceptual translation; H.sapiens FGF gene, exon 3.	gb:NM_017794.1 /DEF=Homo sapiens hypothetical protein FLJ20375 (FLJ20375), mRNA. /FEA=mRNA /GEN=FLJ20375 /PROD=hypothetical protein FLJ20375 /DB_XREF=gi:8923357 /UG=Hs.274251 hypothetical protein FLJ20375 /IREP-BC0012461 ab:NM_017794.1	protein kinase, cAMP-dependent, regulatory, type II, alpha
		NM 005711	N35922		•	NIVI_000314	NM_022346	X59065	MN 017794	BF246917
rigure / b Conta.								FGF1; AFGF; ECGF; FGFA; ECGFA; ECGFB; HBGF1; ECGF- beta: FGF-aloha		PRKAR2A
Figure		207379 at	217586 x at			204054_at	218662_s_at	205117 at	3	213052_at

	300000000000000000000000000000000000000			
			gb:D49958.1 /DEF=Homo sapiens mRNA for membrane	
			glycoprotein M6, complete cds. /FEA=mRNA	
			/PROD=membrane glycoprotein M6 /DB_XREF=gi:1663516	
209470_s_at		D49958	/UG=Hs.75819 glycoprotein M6A /FL=gb:D49958.1	
			Consensus includes gb.BC002374.1 /DEF=Homo sapiens,	
			karyopherin alpha 1 (importin alpha 5), clone MGC:8554,	
			mRNA, complete cds. /FEA=mRNA /PROD=karyopherin alpha	
			1 (importin alpha 5) /DB_XREF=gi:12803140 /UG=Hs.169149	
			karyopherin alpha 1 (importin alpha 5) /FL=gb:BC002374.1	
202057_at		NM_002264		
201259_s_at SYPI	SYPL	AI768845		Hs.80919
209494 s at	ZNF278	AI807017	zinc finger protein 278	Hs.27801
			Consensus includes gb:AK000002.1 /DEF=Homo sapiens	
			mRNA for FLJ00002 protein, partial cds. /FEA=mRNA	
			/GEN=FLJ00002 /PROD=FLJ00002 protein	
			/DB_XREF=gi:7209304 /UG=Hs.55879 hypothetical protein	
213485_s_at		AK000002	MGC2487	
			Consensus includes gb:AW168948 /FEA=EST	
			/DB_XREF=gi:6400473 /DB_XREF=est:xj15f07.x1	
			/CLONE=IMAGE:2657317 /UG=Hs.286148 stromal antigen 1	
202293_at		NM_005862		
			Consensus includes gb:AK023260.1 /DEF=Homo sapiens	
			cDNA FLJ13198 fis, clone NT2RP3004454, highly similar to	
			Homo sapiens mRNA for KIAA0448 protein. /FEA=mRNA	
			/DB_XREF=gi:10435114 /UG=Hs.169939 heparan sulfate 2-O-	
			sulfotransferase /FL=gb:NM_012262.2 gb:AB007917.1	
203283_s_at		NM_012262	gb:AB024568.1	
			gb:BC004892.1 /DEF=Homo sapiens, reticulocalbin 2, EF-	
			hand calcium binding domain, clone MGC:1650, mRNA,	
			complete cds. /FEA=mRNA /PROD=reticulocalbin 2, EF-hand	
			calcium bindingdomain /DB_XREF=gi:13436151 /UG=Hs.79088	
			reticulocalbin 2, EF-hand calcium binding domain	
201485_s_at		BC004892	/FL=gb:BC004892.1 gb:NM_002902.1	

/ ainfil	riguie / D Colita.			
			gb:M62896.1 /DEF=Human lipocortin (LIP) 2 pseudogene	
			mKNA, complete cds-like region. /FEA=mKNA	
			/DB_XREF=gi:187146 /UG=Hs.234757 Human lipocortin (LiP)	
210876 at		M62896	2 pseudogene mRNA, complete cds-like region	·
		2000	Consensus includes ab: AE218012 1 /DEF=Homo saniens	
			Alono DD3705 iinkowie mDNA /FEA-mDNA	
			COLOR	
(AE248042	FINOD-UNINOWII	
18 S C47777		AF210012	nypotnetical protein FLU13438	
			gb:NM_004949.1 /DEF=Homo sapiens desmocollin 2 (DSC2),	٠
			transcript variant Dsc2b, mRNA. /FEA=mRNA /GEN=DSC2	-
			/PROD=desmocollin 2, isoform Dsc2b preproprotein	
			/DB_XREF=gi:13435365 /UG=Hs.239727 desmocollin 2	
204751 x at		NM_004949	/FL=gb:NM_004949.1	
	:		Consensus includes gb:AK026720.1 /DEF=Homo sapiens	
			CDNA: FLJ23067 fis, clone LNG04993. /FEA=mRNA	
			/DB_XREF=gi:10439638 /UG=Hs.117167 Homo sapiens	
214719 at		AK026720	cDNA: FLJ23067 fis, clone LNG04993	
			gb:NM_024584.1 /DEF=Homo sapiens hypothetical protein	
			FLJ13646 (FLJ13646), mRNA. /FEA=mRNA /GEN=FLJ13646	
			/PROD=hypothetical protein FLJ13646 /DB_XREF=gi:13375767	
			/UG=Hs.21081 hypothetical protein FLJ13646	
220321_s_at		NM_024584	/FL=gb:NM_024584.1	
			ESTs, Weakly similar to neuronal thread protein [Homo sapiens]	
222280_at		BG491393		Hs.183110
			gb:U25804.1 /DEF=Human Ich-2 cysteine protease mRNA,	
			complete cds. /FEA=mRNA /PROD=lch-2	
			/DB_XREF=gi:886049 /UG=Hs.74122 caspase 4, apoptosis-	
			related cysteine protease /FL=gb:U28976.1 gb:U28977.1	
209310_s_at		U25804	gb:U28978.1 gb:NM_001225.1 gb:U25804.1 gb:U28014.1	
			gb:NM_019112.1 /DEF=Homo sapiens ATP-binding cassette,	
			sub-family A (ABC1), member 7 (ABCA7), mRNA.	
			/FEA=mRNA /GEN=ABCA7 /PROD=ATP-binding cassette, sub	
			family A (ABC1),member 7 /DB_XREF=gi:9506364	
			/UG=Hs.134514 ATP-binding cassette, sub-family A (ABC1),	
			member 7 /FL=gb:AF328787.1 gb:AF250238.1	
219577_s_at		NM_019112	gb:NM_019112.1	

2 2	.garo 12 ocura:			
213143 at		AE007149	Consensus includes gb:BE856707 /FEA=EST /DB_XREF=gi:10370006 /DB_XREF=est:7f66f02.x1 /CLONE=IMAGE:3299643 /UG=Hs.12520 Homo sapiens clone 23568, 23621, 23795, 23873 and 23874 mRNA sequences	
			gb:NM_004643.1 /DEF=Homo sapiens poly(A)-binding protein, nuclear 1 (PABPN1), mRNA /FEA=mRNA /GEN=PABPN1	
			/PROD=poly(A)-binding protein, nuclear 1 /DB XREF=ai:4758875 /UG=Hs.117176 polv(A)-binding	
201545_s_at		NM_004643	protein, nuclear 1 /FL=gb:NM_004643.1	
			gb:D13889.1 /DEF=Human mRNA for Id-1H, complete cds.	
			// EA=mkivA /GEN=id-1n /FkOD=id-1n /DD_AKET=gi.464161 /UG=Hs.75424 inhibitor of DNA binding 1, dominant negative	
			helix-loop-helix protein /FL=gb:BC000613.1 gb:NM_002165.1	
208937_s_at		D13889	gb:D13889.1	
			Consensus includes gb:AA700167 /FEA=EST	
			/DB_XREF=gi:2703130 /DB_XREF=est:zj36h12.s1	
212780 at		1 13857	/OLOINE= WIMGE:492423	
203531 at	CULS	BF435809	cullin 5	Hs.101299
C			gb:NM 024102.1 /DEF=Homo sapiens hypothetical protein	
			MGC2722 (MGC2722), mRNA. /FEA=mRNA /GEN=MGC2722	
			/PROD=hypothetical protein MGC2722	
			/DB_XREF=gi:13129109 /UG=Hs.11039 hypothetical protein	
201421_s_at		NM_024102	MGC2722 /FL=gb:BC001679.1 gb:NM_024102.1	
[213959_s_at	KIAA1005	BF515597	KIAA1005 protein	Hs.12328
			gb:NM_001745.1 /DEF=Homo sapiens calcium modulating	
			ligand (CAMLG), mRNA. /FEA=mRNA /GEN=CAMLG	
			/PROD=calcium modulating ligand /DB_XREF=gi:4502558	
			/UG=Hs.13572 calcium modulating ligand	
203538_at		NM_001745	/FL=gb:NM_001745.1_gb:U18242.1	
55616_at	MGC9753	AI703342	hypothetical gene MGC9753	Hs.91668
			gb:U03644.1 /DEF=Human recepin mRNA, complete cds.	
			/FEA=mRNA /GEN=recepin /PROD=recepin	
			/DB_XREF=gi:476104 /UG=Hs.89421 CBF1 interacting	
200674		1100644	corepressor /FL=gb:AF098297.1 gb:NM_004882.1	
2095/1_at		003044	[gb:O03844.1	

Figure	Figure /b Cont'd.			
218721 s at		NM 017847	gb:NM_017847.1 /DEF=Homo sapiens hypothetical protein FLJ20505 (FLJ20505), mRNA. /FEA=mRNA /GEN=FLJ20505 /PROD=hypothetical protein FLJ20505 /DB_XREF=gi:8923461 /UG=Hs.69388 hypothetical protein FLJ20505 /IDB_XREF=gi:8923461 /IDE=qb:BC003397.1 qb:NM 017847.1	
at t		- AL049265	Consensus includes gb:AW242916 /FEA=EST /DB_XREF=gi:6576686 /DB_XREF=est:xn27f03.x1 /CLONE=IMAGE:2694941 /UG=Hs.71968 Homo sapiens mRNA; cDNA DKFZp564F053 (from clone DKFZp564F053)	
218708 at		NM_013248	gb:NM_013248.1 /DEF=Homo sapiens NTF2-related export protein 1 (NXT1), mRNA. /FEA=mRNA /GEN=NXT1 /PROD=NTF2-related export protein 1 /DB_XREF=gi:7019470 /UG=Hs.24563 NTF2-related export protein 1 /FL=gb:BC000759.1 gb:BC002687.1 gb:BC003029.1 gb:BC003410.1 gb:AF156957.1 gb:NM_013248.1	
213531_s_at	RAB3GAP	A1040009	RAB3 GTPase-ACTIVATING PROTEIN	Hs.227881
	TLE1	AI951720	transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila)	Hs.28935
200666_s_at		NM_006145	gb:NM_006145.1 /DEF=Homo sapiens heat shock 40kD protein 1 (HSPF1), mRNA. /FEA=mRNA /GEN=HSPF1 /PROD=heat shock 40kD protein 1 /DB_XREF=gi:5453689 /UG=Hs.82646 DnaJ (Hsp40) homolog, subfamily B, member 1 /FL=gb:BC002352.1 gb:NM_006145.1 gb:D49547.1	
200517 c at		A B 0 2 0 9 8 2	gb:AB020982.1 /DEF=Homo sapiens ASH2L mRNA, complete cds, similar to Drosophila ash2 sequence. /FEA=mRNA /GEN=ASH2L /DB_XREF=gi:4417209 /UG=Hs.6856 ash2 (absent, small, or homeotic, Drosophila, homolog)-like /FL=gb:AF056718.1 gb:AB020982.1 gb:NM_004674.1	
ੂਲ [AL578583	Homo sapiens, clone MGC:32686 IMAGE:4051739, mRNA, complete cds	Hs.44205

					· · · · · · · · · · · · · · · · · · ·	
	Hs.8102					
gb:BC002387.1 /DEF=Homo sapiens, nucleosome assembly protein 1-like 1, clone MGC:8688, mRNA, complete cds. //FEA=mRNA /PROD=nucleosome assembly protein 1-like 1 //DB_XREF=gi:12803166 /UG=Hs.179662 nucleosome assembly protein 1-like 1 //FL=gb:BC002387.1 gb:AL162068.1	ribosomal protein S20	gb:U56725.1 /DEF=Human heat shock protein mRNA, complete cds. /FEA=mRNA /PROD=heat shock protein //DB_XREF=gi:4204879 /UG=Hs.75452 heat shock 70kD protein 2 /FL=gb:U56725.1	gb:AB036737.1 /DEF=Homo sapiens mRNA for RERE, complete cds. /FEA=mRNA /PROD=RERE //DB_XREF=gi:8096339 /UG=Hs.194369 arginine-glutamic acid dipeptide (RE) repeats /FL=gb:AF118275.1 gb:NM_012102.1 gb:AB036737.1	gb:M32721.1 /DEF=Human poly(ADP-ribose) polymerase mRNA, complete cds. /FEA=mRNA /GEN=PPOL /DB_XREF=gi:190266 /UG=Hs.177766 ADP-ribosyltransferase (NAD+; poly (ADP-ribose) polymerase) /FL=gb:NM_001618.2 gb:M18112.1 gb:M32721.1 gb:J03473.1	gb:NM_007178.1 /DEF=Homo sapiens unr-interacting protein (UNRIP), mRNA. /FEA=mRNA /GEN=UNRIP /PROD=unr-interacting protein /DB_XREF=gi:6005931 /UG=Hs.3727 unr-interacting protein /FL=gb:BC000162.1 gb:AB024327.1 gb:NM_007178.1 gb:AL136691.1 gb:AF161496.1	gb:NM_005730.1 /DEF=Homo sapiens conserved gene amplified in osteosarcoma (OS4), mRNA. /FEA=mRNA /GEN=OS4 /PROD=conserved gene amplified in osteosarcoma /DB_XREF=gi:5031964 /UG=Hs.180669 conserved gene amplified in osteosarcoma /FL=gb:U81556.1 ob:NM_005730 1
BC002387	AL576654	U56725	AB036737	M32721	NM_007178	00573G
	RPS20					
208753 s at	ြဟ	211538 s at	200940_s_at	208644 at	200870_at	203445 s. at

rigure	rigure / D Contra.			
			gb:NM_005703.2 /DEF=Homo sapiens upstream regulatory	
			/GEN=UREB1 /PROD=upstream regulatory element binding	
208598 s at		NM 005703	protein 1 /DB_XREF=gi:6692990 /UG=Hs.3383 upstream	
,			gb:NM_017925.1 /DEF=Homo sapiens hypothetical protein	
			FLJ20686 (FLJ20686), mRNA. /FEA=mRNA /GEN=FLJ20686	
			/PROD=hypothetical protein FLJ20686 /DB_XREF=gi:8923616	
			/UG=Hs.271480 hypothetical protein FLJ20686	
205684_s_at		NM_017925	/FL=gb:NM_017925.1	
			gb:NM_025126.1 /DEF=Homo sapiens hypothetical protein	
			/PROD=hypothetical protein FLJ21786 /DB XREF=qi:13376704	
			/UG=Hs.316809 hypothetical protein FLJ21786	
219035_s_at		NM_025126	NM_025126 /FL=gb:NM_025126.1	
			ESTs, Weakly similar to RNA binding motif protein 12; putative	
51228_at		N36928	brain nuclearly-targeted protein [Homo sapiens] [H.sapiens]	Hs.33540
213491_x_at	RPN2	AL514285		Hs.75722
			gb:NM_024756.1 /DEF=Homo sapiens hypothetical protein	
			FLJ13465 (FLJ13465), mRNA. /FEA=mRNA /GEN=FLJ13465	
			/PROD=hypothetical protein FLJ13465 /DB_XREF=gi:13376090	
219091_s_at		NM_024756		
			gb:NM_001392.1 /DEF=Homo sapiens dystrobrevin, alpha	
			(DTNA), mRNA /FEA=mRNA /GEN=DTNA	
			/PROD=dystrobrevin, alpha /DB_XREF=gi:4503410	
			/UG=Hs.54435 dystrobrevin, alpha·/FL=gb:BC005300.1	
205741_s_at		NM_001392	gb:NM_001392.1	ļ
			gb:NM_004446.1 /DEF=Homo sapiens glutamyl-prolyl-tRNA synthetase (FPRS)_mRNA_/FEA=mRNA_/GEN=EPRS	
			//PROD=alutamyl-prolyl tRNA synthetase	
200843_s_at		NM_004446	synthetase /FL=gb:NM_004446.1	

Figure /b Contid	o Conta.		
			gb:NM_018128.1 /DEF=Homo sapiens hypothetical protein
			FLJ10534 (FLJ10534), mKNA. /FEA=mKNA /GEN=FLJ10534
			/PROD=hypothetical protein FLJ10534 /DB_XREF=gi:8922495
			/UG=Hs.204501 hypothetical protein FLJ10534
218156_s_at		NM_018128	_
			Consensus includes gb:AL050069.1 /DEF=Homo sapiens
			mRNA; cDNA DKFZp566A0946 (from clone
			DKFZp566A0946); partial cds. /FEA=mRNA
			/GEN=DKFZp566A0946 /PROD=hypothetical protein
			/DB XREF=gi:4884299 /UG=Hs.78006 DKFZP566A0946
214844 s at		AL050069	protein
			gb:NM_022157.1 /DEF=Homo sapiens Rag C protein
			(GTR2), mRNA. /FEA=mRNA /GEN=GTR2 /PROD=Rag C
			protein /DB_XREF=gi:11995471 /UG=Hs.110950 Rag C
218088_s_at		NM_022157	
			gb:AF332197.1 /DEF=Homo sapiens adult SIX2 (SIX2)
			mRNA, complete cds. /FEA=mRNA /GEN=SIX2 /PROD=SIX2
			/DB_XREF=gi:13242164 /UG=Hs.101937 sine oculis
			homeobox (Drosophila) homolog 2 /FL=gb:AF332197.1
206510 at		AF332197	gb:AF136940.1 gb:NM_016932.1
			gb:M27968.1 /DEF=Human basic fibroblast growth factor
			(FGF) mRNA, complete cds. /FEA=mRNA /GEN=FGF2
			/DB_XREF=gi:182562 /UG=Hs.284244 fibroblast growth factor
204421 s at		M27968	2 (basic) /FL=gb:M27968.1 gb:NM_002006.1
			gb:NM_018457.1 /DEF=Homo sapiens DKFZp564J157 protein
			(DKFZP564J157), mRNA. /FEA=mRNA /GEN=DKFZP564J157
		_	/PROD=DKFZp564J157 protein /DB_XREF=gi:8922156
			/UG=Hs.63042 DKFZp564J157 protein /FL=gb:AF217517.1
217794 at		NM_018457	
			gb:NM_021727.1 /DEF=Homo sapiens fatty acid desaturase
			3 (FADS3), mRNA. /FEA=mRNA /GEN=FADS3 /PROD=fatty
			acid desaturase 3 /DB_XREF=gi:13375615 /UG=Hs.21765
204257_at		NM_021727	[gb:BC004901.1 gb:AF134404.1

/ Ligure /	rigure / b cont a.		
			Consensus includes gb:AK024789.1 /DEF=Homo sapiens
			cDNA: FLJ21136 fis, clone CAS07469. /FEA=mRNA /DR_XREF=ni:10437175_/11G=Hs_206882_Homo_saniens
214715 x at		AK024789	mRNA for FLJ00032 protein, partial cds
			gb:NM_022915.1 /DEF=Homo sapiens hypothetical protein
			FLJ12701 (FLJ12701), mRNA. /FEA=mRNA /GEN=FLJ12701
			/PROD=hypothetical protein FLJ12701 /DB_XREF=gi:12597660
			/UG=Hs.203559 hypothetical protein FLJ12701
218202_x_at		NM_022915	_
			Consensus includes gb:AB023215.1 /DEF=Homo sapiens
			mRNA for KIAA0998 protein, partial cds. /FEA=mRNA
			/GEN=KIAA0998 /PROD=KIAA0998 protein
214672_at		AB023215	/DB_XREF=gi:4589639 /UG=Hs.131525 KIAA0998 protein
			gb:NM_020123.1 /DEF=Homo sapiens endomembrane protein
			emp70 precursor isolog (LOC56889), mRNA. /FEA=mRNA
			/GEN=LOC56889 /PROD=endomembrane protein emp70
			precursor isolog /DB_XREF=gi:10047129 /UG=Hs.8203
			endomembrane protein emp70 precursor isolog
217758_s_at		NM_020123	
			gb:NM_001129.2 /DEF=Homo sapiens AE-binding protein 1
			(AEBP1), mRNA. /FEA=mRNA /GEN=AEBP1
			/PROD=adipocyte enhancer binding protein 1 precursor
			/DB_XREF=gi:4755145 /UG=Hs.118397 AE-binding protein 1
201792_at		NM_001129	NM_001129 /FL=gb:D86479.1 gb:AF053944.1 gb:NM_001129.2
			gb:NM_014183.1 /DEF=Homo sapiens HSPC162 protein
			(HSPC162), mRNA. /FEA=mRNA /GEN=HSPC162
			/PROD=HSPC162 protein /DB_XREF=gi:7661821
			/UG=Hs.100002 HSPC162 protein /FL=gb:BC002481.1
			gb:AY026513.1 gb:AF161511.1 gb:NM_014183.1
217917_s_at		NM_014183	gb:AF165516.1
	-		gb:D13891.1 /DEF=Human mRNA for Id-2H, complete cds.
			/FEA=mRNA /GEN=Id-2H /PROD=Id-2H /DB_XREF=gi:464183
			/UG=Hs.180919 inhibitor of DNA binding 2, dominant
,			negative helix-loop-helix protein /FL=gb:M97796.1
201566_x_at		D13891	gb:NM_002166.1_gb:D13891.1

306.	galora conta.				
			r similar to PAX8_HUMAN Paired box protein Pax-8	NM_003466; NM_013951; NM_013952;	_
121_at	PAX8	66969X			Hs.400990
		MM 2080	gb:NM_018060.1 /DEF=Homo sapiens hypothetical protein FLJ10326 (FLJ10326), mRNA. /FEA=mRNA /GEN=FLJ10326 /PROD=hypothetical protein FLJ10326 /DB_XREF=gi:8922355 /UG=Hs.262823 hypothetical protein FLJ10326		
206257 at		NM 015603	gb:NM_015603.1 /DEF=Homo sapiens DKFZP586M1019 protein (DKFZP586M1019), mRNA. /FEA=mRNA /GEN=DKFZP586M1019 /PROD=DKFZP586M1019 protein /DB_XREF=gi:7661689 /UG=Hs.227782 DKFZP586M1019 protein /FL=ab:BC002787.1 ab:AL050284.1 ab:NM 015603.1		
205907 s at	OMD	AI765819	osteomodulin		Hs.94070
207979 s at		NM_004931	gb:NM_004931.1 /DEF=Homo sapiens CD8 antigen, beta polypeptide 1 (p37) (CD8B1), mRNA. /FEA=mRNA /GEN=CD8B1 /PROD=CD8 antigen, beta polypeptide 1 (p37) /DB_XREF=gi:4826666 /UG=Hs.2299 CD8 antigen, beta polypeptide 1 (p37) /FL=gb:NM_004931.1		
218401_s_at		NM_012482	gb:NM_012482.1 /DEF=Homo sapiens zinc finger protein 281 (ZNF281), mRNA. /FEA=mRNA /GEN=ZNF281 /PROD=zinc finger protein 281 /DB_XREF=gi:6912751 /UG=Hs.59757 zinc finger protein 281 /FL=gb:AF125158.1 gb:NM_012482.1		
218383 at		NM 017815	gb:NM_017815.1 /DEF=Homo sapiens hypothetical protein FLJ20424 (FLJ20424), mRNA. /FEA=mRNA /GEN=FLJ20424 /PROD=hypothetical protein FLJ20424 /DB_XREF=gi:8923395 /UG=Hs.8886 hypothetical protein FLJ20424 //MG=Hs.8886 hypothetical protein FLJ20424 //MG=Hs.8886 hypothetical protein FLJ20424 //MG=Hs.8886 hypothetical protein FLJ20424 //MG=Hs.8886 hypothetical protein FLJ20424 //MG=Hs.8886 hypothetical protein FLJ20424 //MG=MG=MG=MG=MG=MG=MG=MG=MG=MG=MG=MG=MG=M		
		NM 021106	gb:NM_021106.1 /DEF=Homo sapiens regulator of G-protein signalling 3 (RGS3), mRNA. /FEA=mRNA /GEN=RGS3 /PROD=regulator of G-protein signalling 3 /DB_XREF=gi:10864074 /UG=Hs.82294 regulator of G-protein signalling 3 /FL=gb:NM_021106.1 gb:U27655.1		

	COLLA.		
			gb:NM_019843.2 /DEF=Homo sapiens eIF4E-transporter (4E- T) mRNA /FEA=mRNA /GEN=4E-T /PROD=eIF4E-
210626		040040	transporter /DB_XREF=gi:10947034 /UG=Hs.12720 eIF4E-
2 10020 at		NIVI 0 18043	de.NM 004402 1 (DEE-Domo conjone deafness autocomol
			_
			/PROD=deafness, autosomal dominant 5 protein
			/DB_XREF=gi:4758153 /UG=Hs.13530 deafness, autosomal
			dominant 5 /FL=gb:AF073308.1 gb:NM_004403.1
203695_s_at		NM_004403	gb:AF007790.2
			gb:NM_003922.1 /DEF=Homo sapiens hect (homologous to
			the E6-AP (UBE3A) carboxyl terminus) domain and RCC1
			(CHC1)-like domain (RLD) 1 (HERC1), mRNA. /FEA=mRNA
			/GEN=HERC1 /PROD=guanine nucleotide exchange factor
			p532 /DB_XREF=gi:4557025 /UG=Hs.76127 hect (homologous
			to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1
			(CHC1)-like domain (RLD) 1 /FL=gb:U50078.1
218306_s_at	_	NM_003922	
			gb:NM_000050.1 /DEF=Homo sapiens argininosuccinate
			synthetase (ASS), mRNA. /FEA=mRNA /GEN=ASS
			/PROD=argininosuccinate synthetase /DB_XREF=gi:4557336
			/UG=Hs.160786 argininosuccinate synthetase
207076_s_at	_	NM_0000050	/FL=gb:NM_000050.1
			Consensus includes gb:NM_003944.1 /DEF=Homo sapiens
			selenium binding protein 1 (SELENBP1), mRNA. /FEA=CDS
			/GEN=SELENBP1 /PROD=selenium binding protein 1
			/DB_XREF=gi:4506872 /UG=Hs.288973 selenium binding
214433_s_at		NM_003944	protein 1 /FL=gb:U29091.1 gb:NM_003944.1
			gb:AF281030.1 /DEF=Homo sapiens Tara mRNA, complete
			cds. /FEA=mRNA /PROD=Tara /DB_XREF=gi:12006357
			/UG=Hs.40342 putative nuclear protein /FL=gb:AF281030.1
210276_s_at	/	AF281030	gb:BC003618.1
			gb:NM_004798.1 /DEF=Homo sapiens kinesin family member
			3B (KIF3B), mRNA. /FEA=mRNA /GEN=KIF3B
			/PROD=kinesin family member 3B /DB_XREF=gi:4758645
			/UG=Hs.168212 kinesin family member 3B
203943_at		NM_004798	/FL=gb:AB002357.1 gb:NM_004798.1

_									r —	
	gb:NM_000247.1 /DEF=Homo sapiens MHC class I polypeptide-related sequence A (MICA), mRNA. /FEA=mRNA //GEN=MICA /PROD=MHC class I chain-related gene A	protein 7Db_AREr=gl.4337730 70G-ns.90396 MnC class i polypeptide-related sequence A /FL=gb:NM_000247.1 gb:L14848.1	Consensus includes gb:AA912711 /FEA=EST /DB_XREF=gi:3052103 /DB_XREF=est:ol30f08.s1 /CLONE=IMAGE:1524999 /UG=Hs.26395 erythrocyte membrane protein band 4.1-like 1	gb:NM_012090.1 /DEF=Homo sapiens actin binding protein; macrophin (microfilament and actin filament cross-linker protein) (ACF7) mRNA /FFA=mRNA /GEN=ACF7	/PROD=actin binding protein; macrophin (microfilamentand actin filament cross-linker protein) /DB_XREF=gi:10048480 /UG=Hs.108258 actin binding protein; macrophin		gb:NM_017635.1 /DEF=Homo sapiens hypothetical protein FLJ20039 (FLJ20039), mRNA. /FEA=mRNA /GEN=FLJ20039 /PROD=hypothetical protein FLJ20039 /DB_XREF=gi:8923045 /UG=Hs.267448 hypothetical protein FLJ20039 /	· · · · · · · · · · · · · · · · · · ·	gb:NM_001689.1 /DEF=Homo sapiens ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3 (ATP5G3), mRNA. /FEA=mRNA /GEN=ATP5G3 /PROD=ATP synthase, H+ transporting, mitochondrial F0complex, subunit c (subunit 9) isoform 3	
		NM_000247	AB002336			NM 012090	NM_017635	NM 018235	il e	NM_001689
iguia i a conta.										
21081		205904_at	212336_at			207358 x at	218242 s at	217752 s at	ц П	207508_at

Figure ,	Figure /b Contd.		
220202 s at		NM 018835	gb:NM_018835.1 /DEF=Homo sapiens membrane-associated nucleic acid binding protein (MNAB), mRNA. /FEA=mRNA /GEN=MNAB /PROD=membrane-associated nucleic acid bindingprotein /DB_XREF=gi:9256536 /UG=Hs.112227 membrane-associated nucleic acid binding protein NR 018835 /FL=qb:NM 018835.1
		D83768	Consensus includes gb:D83768.1 /DEF=Human clone N9S Rep-8 mRNA, partial cds. /FEA=mRNA /GEN=Rep-8 /DB_XREF=gi:1913786 /UG=Hs.153678 reproduction 8
209471 <u>_s_</u> at		L00634	gb:L00634.1 /DEF=Human farnesyl-protein transferase alpha-subunit mRNA, complete cds. /FEA=mRNA /PROD=farnesyl-protein transferase alpha-subunit /DB_XREF=gi:292030 /UG=Hs.138381 farnesyltransferase, CAAX box, alpha/FL=gb:L00634.1 gb:L10413.1 gb:NM_002027.1
212263_at		AF142419	Consensus includes gb:Al114716 /FEA=EST /DB_XREF=gi:6360061 /DB_XREF=est:HA1315 /UG=Hs.15020 homolog of mouse quaking QKI (KH domain RNA binding protein) /FL=gb:AF142419.1 gb:AF142422.1
202477_s_at		659900 WN	gb:NM_006659.1 /DEF=Homo sapiens gamma-tubulin complex protein 2 (GCP2), mRNA. /FEA=mRNA /GEN=GCP2 /PROD=gamma-tubulin complex protein 2 /DB_XREF=gi:5729839 /UG=Hs.13386 gamma-tubulin complex protein 2 /FL=gb:BC005011.1 gb:AF042379.1 gb:NM_006659.1
221534_at		AF073483	gb:AF073483.1 /DEF=Homo sapiens p5326 mRNA, complete cds. /FEA=mRNA /PROD=p5326 /DB_XREF=gi:12002057 /UG=Hs.93678 Homo sapiens, clone IMAGE:3640823, mRNA, partial cds /FL=gb:AF073483.1
202863 <u>a</u> t		NM_003113	gb:NM_003113.1 /DEF=Homo sapiens nuclear antigen Sp100 (SP100), mRNA. /FEA=mRNA /GEN=SP100 /PROD=nuclear antigen Sp100 /DB_XREF=gi:4507164 /UG=Hs.77617 nuclear antigen Sp100 /FL=gb:M60618.1 gb:NM_003113.1

Figure 7b Cont'd	ont'd.		
		gb:NM_018113.1 /DEF=Homo sapiens hypothetical protein	
		FLJ10494 (FLJ10494), mRNA. /FEA=mRNA /GEN=FLJ10494	
		/PROD=hypothetical protein FLJ10494 /DB_XREF=gi:8922462	
220036 s at	NM 018113	/UG=HS.Z/Z838 nypotnetical protein FLJ10494 3 /FL=ab:NM 018113.1	,
ြဟ	BESE	H3 histone, family 3A	Hs.367720
		mRNA for laminin alpha 3 chain. /FEA=mRNA	
		//DB_XREF=gi:9716101 /UG=Hs.83450 laminin, alpha 3	
216250_s_at	X77598	(nicein (150kD), kalinin (165kD), BM600 (150kD), epilegrin)	
		gb:BC002515.1 /DEF=Homo sapiens, antiquitin 1, clone	
		MGC:1569, mRNA, complete cds. /FEA=mRNA	
		/PROD=antiquitin 1 /DB_XREF=gi:12803386 /UG=Hs.74294	
		aldehyde dehydrogenase 7 family, member A1	
208950_s_at	BC002515		
		gb:NM_012288.1 /DEF=Homo sapiens TRAM-like protein	
		(KIAA0057), mRNA. /FEA=mRNA /GEN=KIAA0057	
		/PROD=TRAM-like protein /DB_XREF=gi:6912449	
		/UG=Hs.153954 TRAM-like protein /FL=gb:D31762.1	
202369_s_at	NM_012288		
		gb:NM_007006.1 /DEF=Homo sapiens cleavage and	
		polyadenylation specific factor 5, 25 kD subunit (CPSF5),	
		mRNA. /FEA=mRNA /GEN=CPSF5 /PROD=cleavage and	
		polyadenylation specific factor 5,25 kD subunit	-
	-	//DB_XREF=gi:5901925 /UG=Hs.9605 cleavage and	
		polyadenylation specific factor 5, 25 kD subunit	
202697_at	NM_007006		
		gb:NM_001012.1 /DEF=Homo sapiens ribosomal protein S8	
		(RPS8), mRNA. /FEA=mRNA /GEN=RPS8 /PROD=ribosomal	
		protein S8 /DB_XREF=gi:4506742 /UG=Hs.151604 ribosomal	
200858_s_at	NM_001012		
		gb:NM_016109.1 /DEF=Homo sapiens PPAR(gamma)	
		angiopoietin related protein (PGAR), mRNA. /FEA=mRNA	•
		/GEN=PGAR /PROD=PPAR(gamma) angiopoietin related	
	_	protein /DB_XREF=gi:7705828 /UG=Hs.9613 PPAR(gamma)	
		angiopoietin related protein /FL=gb:AF153606.1	
221009_s_at	NIM 0161	10109 gb:NM_016109.1	

			gb:NM_014308.1 /DEF=Homo sapiens phosphoinositide-3-kinase, regulatory subunit, polypeptide p101 (P101-PI3K), mRNA. /FEA=mRNA /GEN=P101-PI3K	
			/PROD=phosphoinositide-3-kinase, regulatory	
			subunit,polypeptide p101/105_AREF=gl:/03/432 /UG=Hs.278901 phosphoinositide-3-kinase, regulatory subunit,	
220566_at		NM_014308	polypeptide p101 /FL=gb:AF128881.1 gb:NM_014308.1	
			gb:NM_025029.1 /DEF=Homo sapiens hypothetical protein FLJ14346 (FLJ14346), mRNA. /FEA=mRNA /GEN=FLJ14346	
		-	/PROD=hypothetical protein FLJ14346 /DB_XREF=gi:13376551	
220720 x at		NM 025029	/UG=Hs.287640 hypothetical protein FLJ14346 /FL=ab:NM 025029.1	
:		'.	gb:NM 024033.1 /DEF=Homo sapiens hypothetical protein	
			MGC5242 (MGC5242), mRNA. /FEA=mRNA /GEN=MGC5242	
			/PROD=hypothetical protein MGC5242	
			/DB_XREF=gi:13162284 /UG=Hs.77365 hypothetical protein	
220949_s_at		NM_024033 I	MGC5242 /FL=gb:BC000168.2 gb:NM 024033.1	
212246_at	SDNSF	BE880828	neural stem cell derived neuronal survival protein	HS.847/5
			gb:NM_018165.1 /DEF=Homo sapiens hypothetical protein	
		_	FLJ10645 (FLJ10645), mRNA. /FEA=mRNA /GEN=FLJ10645	
			/PROD=hypothetical protein FLJ10645 /DB_XREF=gi:8922564	
			/UG=Hs.44143 polybromo 1 /FL=gb:AF177387.1	
220355_s_at		NM_018165	gb:NM_018165.1	
			gb:NM_031298.1 /DEF=Homo sapiens hypothetical protein	
			MGC2963 (MGC2963), mRNA. /FEA=mRNA /GEN=MGC2963	
2242EE 0 2+		NIM 031208	/PROD=hypothetical protein MicC2963	
o		1 1		
			mRNA_/FEA=mRNA /GEN=UBB /PROD=ubiquitin B	
			/DB_XREF=gi:11024713 /UG=Hs.183842 ubiquitin B	
200633 at		NM_018955	/FL=gb:NM_018955.1_gb:BC000379.1	
			gb:NM_024305.1 /DEF=Homo sapiens hypothetical protein	
			MGC4278 (MGC4278), mRNA. /FEA=mRNA /GEN=MGC42/8	
			/PROD=hypothetical protein MGC42/8	
		NIM COA3OE	/DB_XREF=gi:13236535 /UG=Hs.318/8U nypotnetical protein	
750327 at		- II	וווסטאביים זו ב-מטינים מביים מביים מביים מביים מביים מביים מביים מביים מביים מביים מביים מביים מביים מביים מבי	

Lidare	ridare / b Courd.		
			Consensus includes gb:AF070613.1 /DEF=Homo sapiens
			24585 mRNA sequence. /FEA=mKNA
			/DB_XREF=gi:3387995 /UG=Hs.131814 tankyrase, TRF1-
		0000	interacting ankyrin-related ADP-ribose polymerase
202561_at	V V V V V	AFU/U013	/FL=gD:AFU82556.1 gD:NW U03/4/.1
s at	FUXU1A	AW11/498	
			Consensus includes gb:D86957.1 /DEF=Human mRNA for
			KIAA0202 gene, partial cds. /FEA=mRNA /GEN=KIAA0202
			/DB_XREF=gi:1503987 /UG=Hs.80712 KIAA0202 protein
208999_at		D86957	/FL=gb:BC001329.1
			Consensus includes gb:AK021514.1 /DEF=Homo sapiens
			CDNA FLJ11452 fis, clone HEMBA1001435. /FEA=mRNA
			/DB XREF=qi:10432710 /UG=Hs.148598 Homo sapiens cDNA
215978 x at		AK021514	FLJ11452 fis, clone HEMBA1001435
			gb:NM_016391.1 /DEF=Homo sapiens hypothetical protein
			(HSPC111), mRNA. /FEA=mRNA /GEN=HSPC111
			/PROD=hypothetical protein /DB_XREF=gi:7705450
			/UG=Hs.279918 hypothetical protein /FL=gb:AF151875.1
203023 at		NM 016391	gb:AF161460.1 gb:AF151019.1 gb:NM 016391.1
1			ESTs, Weakly similar to hypothetical protein FLJ22184 [Homo
212509_s_at		BF968134	sapiens] [H.sapiens] Hs.356623
			gb:NM_014734.1 /DEF=Homo sapiens KIAA0247 gene
			product (KIAA0247), mRNA. /FEA=mRNA /GEN=KIAA0247
		_	/PROD=KIAA0247 gene product /DB_XREF=gi:7662019
			/UG=Hs.82426 KIAA0247 gene product /FL=gb:D87434.1
202181_at		NM 014734	gb:NM_014734.1
			gb:NM 000101.1 /DEF=Homo sapiens cytochrome b-245,
			alpha polypeptide (CYBA), mRNA. /FEA=mRNA /GEN=CYBA
			/PROD=flavocytochrome b-558 alpha polypeptide
			/DB_XREF=gi:4557504 /UG=Hs.68877 cytochrome b-245,
203028 s at		NM 000101	alpha polypeptide /FL=gb:M21186.1 gb:NM_000101.1
			gb:BC000265.1 /DEF=Homo sapiens, clone MGC:3182,
			mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein
			for MGC:3182) /DB_XREF=gi:12653008 /UG=Hs.315417
7000		000000	Homo sapiens, clone MGC:3182, mRNA, complete cds
209435_s_at_		BC0000200	/FL=gp:bCu00zob.

ridare	rigure / b conta.			
200045 at		NM 001090	gb:NM_001090.1 /DEF=Homo_sapiens ATP-binding cassette, sub-family F (GCN20), member 1 (ABCF1), mRNA. /FEA=mRNA /GEN=ABCF1 /PROD=ATP-binding cassette, sub-family F, member 1 /DB_XREF=gi:10947134 /UG=Hs.9573 ATP-binding cassette, sub-family F (GCN20), member 1	
205297_s_at		NM_000626	gb:NM_000626.1 /DEF=Homo sapiens CD79B antigen (immunoglobulin-associated beta) (CD79B), transcript variant 1, mRNA. /FEA=mRNA /GEN=CD79B /PROD=CD79B antigen, isoform 1 precursor /DB_XREF=gi:11038673 /UG=Hs.89575 CD79B antigen (immunoglobulin-associated beta) /FL=gb:NM_000626.1 gb:M80461.1 gb:M89957.1	
222036 s at	at MCM4	A1859865	MCM4 minichromosome maintenance deficient 4 (S. cerevisiae)	Hs.154443
211048_s_at		BC006344	gb:BC006344.1 /DEF=Homo sapiens, protein disulfide isomerase related protein (calcium-binding protein, intestinal-related), clone MGC:13117, mRNA, complete cds. //FEA=mRNA /PROD=protein disulfide isomerase related protein(calcium-binding protein, intestinal-related)	
219696_at		NM_019049	gb:NM_019049.1 /DEF=Homo sapiens hypothetical protein (FLJ20054), mRNA. /FEA=mRNA /GEN=FLJ20054 /PROD=hypothetical protein /DB_XREF=gi:9506654 /UG=Hs.101590 hypothetical protein /FL=gb:NM_019049.1	
202070_s_at		NM_005530	gb:NM_005530.1 /DEF=Homo sapiens isocitrate dehydrogenase 3 (NAD+) alpha (IDH3A), mRNA. //FEA=mRNA /GEN=IDH3A /PROD=isocitrate dehydrogenase 3 (NAD+) alpha /DB_XREF=gi:5031776 /UG=Hs.250616 isocitrate dehydrogenase 3 (NAD+) alpha //FL=gb:NM_005530.1 gb:U07681.1	

209452_s_at AF036	5824	gb:AF035824.1 /DEF=Homo sapiens vesicle soluble NSF attachment protein receptor (VTI1) mRNA, complete cds. //FEA=mRNA /GEN=VTI1 /PROD=vesicle soluble NSF		
s at AFO	5824	/GEN=VTI1 /PROD=vesicle soluble NSF		
s at AF0:	5824			
s at AFO:	5824	anaciment protein receptor / DD_ARET-91.2007.399		
s_at AF0:	5824	/UG=Hs.169206 vesicle-associated soluble NSF attachment		
s at AF03	5824	protein receptor (v-SNARE; homolog of S. cerevisiae VTI1)		
s at NM	5824	/FL=gb:BC003142.1 gb:AF035824.1 gb:AF060902.1	-	
s_at		70.1		
s at	gb:NM_01589	gb:NM_015895.1 /DEF=Homo sapiens geminin (LOC51053),		
s at	mRNA. /FEA	mRNA. /FEA=mRNA /GEN=LOC51053 /PROD=geminin		
s at	//DB_XREF=g	/DB_XREF=gi:7705681 /UG=Hs.234896 geminin		
_	015895 /FL=gb:AF06	015895 /FL=gb:AF067855.1 gb:NM_015895.1	-	
	 ab:BC006466	qb:BC006466.1 /DEF=Homo sapiens, clone MGC:2310,		
	mRNA, comp	mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein	-	
211070_x_at BC00	BC006466 for MGC:231	for MGC:2310) /DB_XREF=gi:13623678 /FL=gb:BC006466.1		
	ESTs, Weakly	ESTs, Weakly similar to cytokine receptor-like factor 2; cytokine		
213434_at H95263		receptor CRL2 precusor [Homo sapiens] [H.sapiens]	Hs.4(Hs.408811
	gb:NM_0046	gb:NM_004640.1 /DEF=Homo sapiens HLA-B associated		
	transcript-1	transcript-1 (D6S81E), mRNA. /FEA=mRNA /GEN=D6S81E		
	/PROD=HLA-	/PROD=HLA-B associated transcript-1 /DB_XREF=gi:4758111		
-	/UG=Hs.5529	/UG=Hs.55296 HLA-B associated transcript-1		
200041_s_at	.004640 /FL=gb:BC00	.004640 /FL=gb:BC004350.1 gb:NM_004640.1		
	gb:NM_0144	gb:NM_014445.1 /DEF=Homo sapiens stress-associated		
	endoplasmic	endoplasmic reticulum protein 1; ribosome associated		
	membrane p	membrane protein 4 (SERP1), mRNA. /FEA=mRNA		
	/GEN=SERP	/GEN=SERP1 /PROD=stress-associated endoplasmic		
	reticulum pro	reticulum protein1; ribosome associated membrane protein 4		
	/DB_XREF=g	/DB_XREF=gi:7657551 /UG=Hs.76698 stress-associated		
	endoplasmic	endoplasmic reticulum protein 1; ribosome associated		
		membrane protein 4 /FL=gb:AL136807.1 gb:AF136975.1		
200971_s_at NM_0	014445 gb:AB022427	gb:AB022427.1 gb:NM 014445.1		

STIPO OF SIDE I				
202125 s at		NM 015049	gb:NM_015049.1 /DEF=Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 3 (ALS2CR3), mRNA. /FEA=mRNA /GEN=ALS2CR3 /PROD=amyotrophic lateral sclerosis 2 (juvenile)chromosome region, candidate 3 /DB_XREF=gi:13027379 /UG=Hs.154248 amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 3 /FL=gb:AB038951.1 gb:NM_015049.1	
<i>#</i>		EC004146	gb:BC004146.1 /DEF=Homo sapiens, proteasome (prosome, macropain) subunit, beta type, 5, clone MGC:2175, mRNA, complete cds. /FEA=mRNA /PROD=proteasome (prosome, macropain) subunit, betatype, 5 /DB_XREF=gi:13278740 /UG=Hs.78596 proteasome (prosome, macropain) subunit, beta type, 5 /FL=gb:BC004146.1 gb:NM_002797.1	
202268_s_at		NM_003905	105.1 /DEF=Homo sapiens amyloid ng protein 1, 59kD (APPBP1), mR AGEN=APPBP1 /PROD=Amyloid k ng protein1 /DB_XREF=gi:4502168 a precursor protein-binding protein 86798.1 gb:BC000480.1 gb:U50939.105.1	
212450_at		D87445	Consensus includes gb:D87445.2 /DEF=Homo sapiens mRNA for KIAA0256 protein, partial cds. /FEA=mRNA /GEN=KIAA0256 /PROD=KIAA0256 protein /DB_XREF=gi:6634006 /UG=Hs.118978 KIAA0256 gene product	
208869 s at		AF087847	gb:AF087847.1 /DEF=Homo sapiens GABA-A receptor- associated protein like 1 (GABARAPL1) mRNA, complete cds. /FEA=mRNA /GEN=GABARAPL1 /PROD=GABA-A receptor-associated protein like 1 /DB_XREF=gi:13375570 /UG=Hs.282654 Homo sapiens mRNA; cDNA DKFZp564N1272 (from clone DKFZp564N1272); complete cds /FL=qb:AL136676.1 gb:AF087847.1	
-	ATP10D	AI478147	Q	Hs.173540

mRNA; cDNA DKFZp564C152 (from clone DKFZp564C152). //FEA=mRNA /GEN=DKFZp564C152 /PROD=hypothetical
AL049980 DKFZP564C152 protein
gb:NM_001889.1 /DEF=Homo sapiens crystallin, zeta
/GEN=CRYZ /PROD=crystallin, zeta (quinone reductase)
/DB_XREF=gi:4503066 /UG=Hs.83114 crystallin, zeta (quinone NM_001889
+-
carboxyglutamic acid) polypeptide 1 (PRRG1), mRNA
/red=mkiva /geiv=rkkg1 /rkOD-ploime-lich gla (G- carboxyglutamic acid)polypeptide 1 /DB XREF=gi:4506134
NM_000950 polypeptide 1 /FL=gb:AF009242.1 gb:NM_000950.1
gb:NM_007262.1 /DEF=Homo sapiens RNA-binding protein requision subjinit (D.I-1) mRNA /FFA=mRNA /GFN=D.I-1
/PROD=RNA-binding protein regulatory subunit
/DB_XREF=gi:6005748 /UG=Hs.10958 RNA-binding protein
0001
NM_UU/262 gb:D6138U.1
gb:M29872.1 /DEF=Human alcohol dehydrogenase class /ADH5) mRNA_complete_cds_/FFA=mRNA_/GFN=ADH5
/DB_XREF=gi:178131 /UG=Hs.78989 alcohol dehydrogenase
M29872 gb:M29872.1 gb:M30471.1
gb:NM_004889.1 /DEF=Homo sapiens ATP synthase, H+
transporting, mitochondrial F0 complex, subunit t, isoform 2
(A)
Synthase, H+ transporting, mitochondrial Fucomplex, suburing icoform 2 /OB YDEE-ai-4757841 / I/2=He 155751 ATD
synthase H+ transporting mitochondrial F0 complex subunit
f, isoform 2 /FL=gb:BC003678.1 gb:AF047436.1
NM_004889 gb:NM_004889.1
N761728 ribonuclease, RNase A family, 4

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213241 at		AF035307	Consensus includes gb:AF035307.1 /DEF=Homo sapiens clone 23785 mRNA sequence. /FEA=mRNA /DB_XREF=gi:2661068 /UG=Hs.184697 Homo sapiens clone 23785 mRNA sequence
			gb:BC000853.1 /DEF=Homo sapiens, Similar to chromosome
			cds. /FEA=mRNA /PROD=Similar to chromosome 2 open
			reading frame 3 /DB_XREF=gi:12654086 /UG=Hs.184175
210175_at		BC000853	chromosome 2 open reading frame 3 /FL=gb:BC000853.1
			Consensus includes gb:AF052128.1 /DEF=Homo sapiens clone 23677 mRNA sequence. /FEA=mRNA
			/DB XREF=gi:3360437 /UG=Hs.1521 immunoglobulin mu
215980_s_at		AF052128	binding protein 2
			Consensus includes gb:AB007930.1 /DEF=Homo sapiens
			mRNA for KIAA0461 perotein, partial cds. /FEA=mRNA
			/GEN=KIAA0461 /PROD=KIAA0461 perotein
212153_at		AB007930	/DB_XREF=gi:3413883 /UG=Hs.107088 KIAA0461 protein
			gb:NM_004629.1 /DEF=Homo sapiens Fanconi anemia,
			complementation group G (FANCG), mRNA. /FEA=mRNA
			/GEN=FANCG /PROD=X-ray repair complementing defective
			repair inChinese hamster cells 9 /DB_XREF=gi:4759335
203564_at		NM_004629	
			gb:NM_020412.1 /DEF=Homo sapiens CHMP1.5 protein
			(CHMP1.5), mRNA. /FEA=mRNA /GEN=CHMP1.5
			/PROD=CHMP1.5 protein /DB_XREF=gi:9966900
			/UG=Hs.42733 CHMP1.5 protein /FL=gb:AF281064.1
218178_s_at		NM_020412	
			gb:AF029729.1 /DEF=Homo sapiens neuralized mRNA,
			complete cds. /FEA=mRNA /PROD=neuralized
			/DB_XREF=gi:4103927 /UG=Hs.172700 neuralized
		000	(Drosophila)-like /FL=gb:U87864.1 gb:AF029729.1
204889_s_at		AF029729	[gb:NM_004210.1

Figure / D Cont a	inta.		
			Consensus includes gb:AB020691.1 /DEF=Homo sapiens
			mRNA for KIAA0884 protein, partial cds. /FEA=mRNA
			/GEN=KIAA0884 /PROD=KIAA0884 protein
215162_at	<u> </u>	AB020691	/DB_XREF=gi:4240256 /UG=Hs.198232 KIAA0884 protein
			gb:NM_004522.1 /DEF=Homo sapiens kinesin family member
			5C (KIF5C), mRNA. /FEA=mRNA /GEN=KIF5C
			/PROD=kinesin family member 5C /DB_XREF=gi:4758649
			/UG=Hs.6641 kinesin family member 5C /FL=gb:AB011103.1
203130_s_at		NM_004522	gb:NM 004522.1
			Consensus includes gb:AK025301.1 /DEF=Homo sapiens
			cDNA: FLJ21648 fis, clone COL08469. /FEA=mRNA
			/DB_XREF=gi:10437789 /UG=Hs.306797 Homo sapiens
216775_at		AK025301	cDNA: FLJ21648 fis, clone COL08469
			gb:NM_001740.2 /DEF=Homo sapiens calbindin 2, (29kD,
			calretinin) (CALB2), transcript variant CALB2, mRNA.
			/FEA=mRNA /GEN=CALB2 /PROD=calbindin 2, full length
			protein isoform /DB_XREF=gi:6031158 /UG=Hs.106857
205428_s_at	_	NM_001740	calbindin 2, (29kD, calretinin) /FL=gb:NM_001740.2
			Consensus includes gb:AL137428.1 /DEF=Homo sapiens
			mRNA; cDNA DKFZp761N1323 (from clone
			DKFZp761N1323). /FEA=mRNA /DB_XREF=gi:6807985
			/UG=Hs.306459 Homo sapiens mRNA; cDNA
216692_at		AL137428	DKFZp761N1323 (from clone DKFZp761N1323)
			Consensus includes gb:AL080112.1 /DEF=Homo sapiens
			mRNA; cDNA DKFZp586H0722 (from clone
			DKFZp586H0722). /FEA=mRNA /DB_XREF=gi:5262539
			/UG=Hs.332731 Homo sapiens mRNA; cDNA
216859_x_at		AL080112	DKFZp586H0722 (from clone DKFZp586H0722)
			gb:NM_004480.1 /DEF=Homo sapiens fucosyltransferase 8
	_		(alpha (1,6) fucosyltransferase) (FUT8), mRNA. /FEA=mRNA
	··-		/GEN=FUT8 /PROD=fucosyltransferase 8 (alpha
			(1,6)fucosyltransferase) /DB_XREF=gi:4758407
			/UG=Hs.118722 fucosyltransferase 8 (alpha (1,6)
203988_s_at		NM_004480	NM_004480 fucosyltransferase) /FL=gb:D89289:1 gb:NM_004480.1

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			gb:BC000351.1 /DEF=Homo sapiens, phosphate	
			complete cds. /FEA=mRNA /PROD=phosphate	
			cytidylyltransferase 2, ethanolamine /DB_XREF=gi:12653166	
			/UG=Hs.226377 phosphate cytidylyltransferase 2,	
11			ethanolamine /FL=gb:BC000351.1 gb:D84307.1	
209577_at		BC000351	gb:NMi 002861.1	
			gb:AFUZ1834.1 /DEF=Homo sapiens tissue ractor patriway	
			Innibitor beta (TPPIbeta) mKNA, complete cds. /PEA=mKNA	
			/GEN=TFPIbeta /PROD=tissue factor pathway inhibitor beta	
			/DB_XREF=gi:4103170 /UG=Hs.170279 tissue factor pathway	_
			inhibitor (lipoprotein-associated coagulation inhibitor)	
210664_s_at		AF021834	/FL=gb:AF021834.1	
			Consensus includes gb:AI701430 /FEA=EST	
			/DB_XREF=gi:4989330 /DB_XREF=est:we29h08.x1	
			/CLONE=IMAGE:2342559 /UG=Hs.199160 myeloidlymphoid or	
			mixed-lineage leukemia (trithorax (Drosophila) homolog)	
212076 at		NM_005933	/FL=gb:L04284.1 gb:NM_005933.1	
			gb:AF074723.1 /DEF=Homo sapiens RNA polymerase	
			transcriptional regulation mediator (MED6) mRNA, complete	
			cds. /FEA=mRNA /GEN=MED6 /PROD=RNA polymerase	
			transcriptional regulationmediator /DB_XREF=gi:3329505	
			/UG=Hs.167738 RNA polymerase II transcriptional regulation	
			mediator (Med6, S. cerevisiae, homolog of)	
210104_at		AF074723	/FL=gb:BC004106.1 gb:AF074723.1	
			gb:NM_004741.1 /DEF=Homo sapiens nucleolar	
			phosphoprotein p130 (P130), mRNA. /FEA=mRNA	
			/GEN=P130 /PROD=nucleolar phosphoprotein p130	
			/DB_XREF=gi:4758859 /UG=Hs.75337 nucleolar	
205895_s_at		NM_004741	phosphoprotein p130 /FL=gb:BC001883.1 gb:NM_004741.1	
			gb:NM 006026.1 /DEF=Homo sapiens H1 histone family,	
			member X (H1FX), mRNA. /FEA=mRNA /GEN=H1FX	
			/PROD=H1 histone family, member X /DB_XREF=gi:5174448	
204805 s at		NM 006026	/FL=gb:BC000426.1 gb:D64142.1 gb:NM_006026.1	
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218849 s at		NM 006663	gb:NM_006663.1 /DEF=Homo sapiens ReIA-associated inhibitor (RAI), mRNA. /FEA=mRNA /GEN=RAI /PROD=ReIA-associated inhibitor /DB_XREF=gi:5730000 /UG=Hs.324051 ReIA-associated inhibitor /FL=gb:AF078037.1 gb:NM_006663.1	
	FLJ20294	AI359466	hypothetical protein FLJ20294	Hs.7995
1	at VDP	BE875592	vesicle docking protein p115	Hs.325948
			gb:NM_007215.1 /DEF=Homo sapiens polymerase (DNA	
			directed), gamma 2, accessory subunit (POLG2), mRNA.	
			/FEA=mRNA /GEN=POLG2 /PROD=polymerase (DNA	
			directed), gamma 2, accessorysubunit /DB_XREF=gi:6005837	
			/UG=Hs.30541 polymerase (DNA directed), gamma 2,	
			accessory subunit /FL=gb:BC000913.1 gb:U94703.1	
205811_at		NM_007215		
			Consensus includes gb:AL512728.1 /DEF=Homo sapiens	
			mRNA; cDNA DKFZp547P082 (from clone DKFZp547P082).	
			/FEA=mRNA /GEN=DKFZp547P082 /PROD=hypothetical	
			protein /DB_XREF=gi:12224871 /UG=Hs.307068 Homo	
			sapiens mRNA; cDNA DKFZp547P082 (from clone	
216813_at		AL512728	DKFZp547P082)	
			gb:NM_030820.1 /DEF=Homo sapiens hypothetical protein	
			DKFZp564B052 (DKFZp564B052), mRNA. /FEA=mRNA	
			/GEN=DKFZp564B052 /PROD=hypothetical protein	
208096 s at		NM 030820	DKFZp564B052 /DB_XREF=gi:13540617 /FL=gb:NM_030820.1	
			gb:NM_017660.1 /DEF=Homo sapiens hypothetical protein	
			FLJ20085 (FLJ20085), mRNA. /FEA=mRNA /GEN=FLJ20085	
			/PROD=hypothetical protein FLJ20085 /DB_XREF=gi:8923093	
			/UG=Hs.118964 hypothetical protein FLJ20085	
218131_s_at		NM_017660 /	FL=gb:NM_017660.1	
214213_x_at I	LMNA	AA063189	amin A/C	Hs.77886
			Consensus includes gb:AF009267.1 /DEF=Homo sapiens	
			clone FBA1 Cri-du-chat region mRNA. /FEA=mRNA	
,		1	/DB_XREF=gi:2331069 /UG=Hs.102238 Homo sapiens clone	
215908_at		AF009267	FBA1 Cri-du-chat region mRNA	

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217482 at		AK021987	Consensus includes gb:AK021987.1 /DEF=Homo sapiens cDNA FLJ11925 fis, clone HEMBB1000354. /FEA=mRNA /DB_XREF=gi:10433296 /UG=Hs.191158 Homo sapiens cDNA FLJ11925 fis, clone HEMBB1000354	
			gb:NM_016581.1 /DEF=Homo sapiens ECSIT (LOC51295), mRNA. /FEA=mRNA /GEN=LOC51295 /PROD=ECSIT	
			/DB_XREF=gi:7706114 /UG=Hs.22199 ECSIT	
218225_at		NM_016581	/FL=gb:BC000193.1 gb:BC005119.1 gb:AF243044.1 gb:NM_016581.1	
			gb:NM_004216.1 /DEF=Homo sapiens death effector domain-	
			containing (DEDD), mRNA. /FEA=mRNA /GEN=DEDD	
			/PRODE-death effector domain-containing //DB XREF=g:4758143 /UG=Hs.169681 death effector domain-	
			containing /FL=gb:AF083236.1 gb:AF043733.1 gb:AF100341.1	
202480_s_at		NM_004216		
			gb:AL136621.1 /DEF=Homo sapiens mRNA; cDNA	
			DKFZp564B162 (from clone DKFZp564B162); complete cds.	-
			/FEA=mRNA /GEN=DKFZp564B162 /PROD=hypothetical	
			protein /DB_XREF=gi:12052767 /UG=Hs.109526 zinc finger	
210281_s_at		AL136621	protein 198 /FL=gb:AL136621.1	
203749_s_at F	RARA	AI806984		Hs.250505
			gb:NM_024903.1 /DEF=Homo sapiens hypothetical protein	
			FLJ14297 (FLJ14297), mRNA. /FEA=mRNA /GEN=FLJ14297	
			/PROD=hypothetical protein FLJ14297 /DB_XREF=gi:13435146	
			/UG=Hs.245043 hypothetical protein FLJ14297	
220159_at		NM_024903		
			gb:NM_025189.1 /DEF=Homo sapiens hypothetical protein	
			FLJ13659 (FLJ13659), mRNA. /FEA=mRNA /GEN=FLJ13659	
			/PROD=hypothetical protein FLJ13659 /DB_XREF=gi:13430887	
			/UG=Hs.301651 hypothetical protein FLJ13659	i e
206829_x_at		NM_025189	/FL=gb:NM_025189.1	:
214417_s_at FETUB	ETUB	N39010	fetuin B	Hs.81073
204466_s_at §	SNCA	BG260394	synuclein, alpha (non A4 component of amyloid precursor)	Hs.76930

D IDDIL				
			gb:NM_012072.2 /DEF=Homo sapiens complement component C1q receptor (C1QR), mRNA. /FEA=mRNA./GEN=C1QR /PROD=complement component C1q receptor/DB_XREF=gi:11496985 /UG=Hs.97199 complement	
202878_s_at		NM_012072	NM_012072 component C1q receptor /FL=gb:NM_012072.2 gb:U94333.1	
			MGC11279 (MGC11279), mRNA. /FEA=mRNA	
			/GEN=MGC11279 /PROD=hypothetical protein MGC11279	
210020		AIM 024328	/DB_XREF=gi:13236572 /UG=Hs.10915 hypothetical protein	·
Z 10950 at		141VI 024320	ab:NM 013375.1 /DEF=Homo sapiens TATA-binding protein-	
			binding protein (ABT1), mRNA. /FEA=mRNA /GEN=ABT1	
			/PROD=TATA-binding protein-binding protein	
			/DB_XREF=gi:7019318 /UG=Hs.109428 TATA-binding protein-	
218405_at		NM_013375	NM_013375 binding protein /FL=gb:AB027258.1 gb:NM_013375.1	
208903_at	RPS28	BF431363	ribosomal protein S28 Hs.153177	153177
			gb:NM_014661.1 /DEF=Homo sapiens KIAA0140 gene	
			product (KIAA0140), mRNA. /FEA=mRNA /GEN=KIAA0140	
			/PROD=KIAA0140 gene product /DB_XREF=gi:7661937	
			/UG=Hs.156016 KIAA0140 gene product /FL=gb:D50930.1	
203206_at		NM_014661	gb:NM_014661.1	
			gb:NM_018044.1 /DEF=Homo sapiens hypothetical protein	
			FLJ10267 (FLJ10267), mRNA. /FEA=mRNA /GEN=FLJ10267	
			/PROD=hypothetical protein FLJ10267 /DB_XREF=gi:8922321	
203802_x_at		NM_018044		
			gb:NM_007015.1 /DEF=Homo sapiens chondromodulin I	
			precursor (CHM-1), mKNA. /FEA=mKNA /GEN=CHM-1	
			TROD-CHOINGIGNORM I precuisor / DB_AACH-91.0301331	
0000		7,000	/UG=HS.9/932 chondromodulin precuisor	
206309_at		SL0/00 MN	/FL=gb:AB006000.1 gb:NM_00/015.1	
			Consensus includes gb:AK022530.1 /DEF=Homo sapiens	
			Homo sapiens mRNA for KIAA0962 protein. /FEA=mRNA	
212908 at		AB023179	/DB_XREF=gi:10433971 /UG=Hs.9059 KIAA0962 protein	
, , , , , , , , , , , , , , , , , , ,	J	2 2		

г								
	-					Hs.405654		Hs.123637
	gb:AB022918.1 /DEF=Homo sapiens mRNA for alpha2,3-sialyltransferase ST3Gal VI, complete cds. /FEA=mRNA /GEN=ST3Gal VI /PROD=alpha2,3-sialyltransferase ST3Gal VI /DB_XREF=gi:4827246 /UG=Hs.34578 alpha2,3-sialyltransferase /FL=gb:AB022918.1			Consensus includes gb:AB020719.1 /DEF=Homo sapiens mRNA for KIAA0912 protein, partial cds. /FEA=mRNA /GEN=KIAA0912 /PROD=KIAA0912 protein /DB_XREF=gi:4240312 /UG=Hs.207802 KIAA0912 protein	gb:U35398.1 /DEF=Human G protein-coupled receptor mRNA, complete cds. /FEA=mRNA /PROD=G protein-coupled receptor /DB_XREF=gi:1015418 /UG=Hs.166607 G protein-coupled receptor 68 /FL=gb:U35398.1 gb:NM_003485.1	ESTs	AU146809 HEMBB1 Homo sapiens cDNA clone HEMBB1001564 3', mRNA sequence.	putative homeodomain transcription factor 1
	AB022918	NM_001400	NM_014271	AB020719	U35398	BE567032	AU146809	AA927671
rigure / b conta.								PHTF1
Ligure	210942_s_at	ja j	220663_at	215170_s_at	211249 at	215167 at	215576 at	215285 s at

Sing 1	. 5 00110				
			gb:BC002807.1 /DEF=Homo sapiens, membrane-spanning 4-domains, subfamily A, member 2, clone MGC:3969, mRNA, complete cds. /FEA=mRNA /PROD=membrane-spanning 4-domains, subfamily A, member2 /DB_XREF=gi:12803920 /UG=Hs.89751 membrane-spanning 4-domains, subfamily A, member 2 (Fc fragment of IgE, high affinity 1, receptor for; beta polyneptide) /FI =ch:NM 021950 1 db:BC002807.1		
210356_x_at		BC002807			
			gb:NM_004055.2 /DEF=Homo sapiens calpain 5 (CAPN5), mRNA. /FEA=mRNA /GEN=CAPN5 /PROD=calpain 5 /DB XREF=qi:6552324 /UG=Hs.6133 calpain 5		
205166_at		NM_004055	004055 /FL=gb:U94346.1 gb:NM_004055.2		
			Consensus includes gb:AB032967.1 /DEF=Homo sapiens		
			//GEN=KIAA1141 /PROD=KIAA1141 protein		
213130 at		AB032967	/DB_XREF=gi:6329951 /UG=Hs.59255 DKFZP434N043 protein		
2028_s_at	E2F1	M96577		NM_005225	Hs.96055
			gb:NM_018087.1 /DEF=Homo sapiens hypothetical protein		
	·		FLJ10407 (FLJ10407), mRNA. /FEA=mRNA /GEN=FLJ1040/		
			/PROD=hypothetical protein FLJ1040/ /UB_XREF=gi:8922408		
218073 s at		NM 018087	/UG=HS:30/38		
ਗੁੱ¦⊲	PCBP2	AW103422	poly(rC) binding protein 2		Hs.63525
			gb:NM_006759.2 /DEF=Homo sapiens UDP-glucose		
	<u> </u>		pyrophosphorylase 2 (UGP2), mRNA. /FEA=mRNA		
			/GEN=UGP2 /PROD=UDP-glucose pyrophosphorylase 2		
205480 s_at		NM_006759	_		
			gb:NM_002415.1 /DEF=Homo sapiens macrophage migration		
			inhibitory factor (glycosylation-inhibiting factor) (MIF), mRNA.		
			inhibitory footor/altocalation inhibiting footor/		
			I/DB XREF=ai-4505184 /UG=Hs.73798 macrophage migration		
			inhibitory factor (glycosylation-inhibiting factor)		
21/8/1_s_at		NM_002415	gb:NM 002415.1		

250				
at		AL523310	microtubule-associated protein 4	Hs.239298
a	GAPD	BE561479	giyceraldehyde-3-phosphate dehydrogenase	Hs.169476
			gb:NM_005114.1 /DEF=Homo sapiens heparan sulfate	
			(glucosamine) 3-O-sultotransterase 1 (HS3S11), mKNA.	
			1 program	
			grucosaminyis-O-suriotransierase i precursor	
			/UB_ARET-gl.4620/03 /UG-HS.40300 Hebalall Sullate	
205466 6 24		MM 005117	(glucosamine) 3-O-suitotransierase /rL=gb.Aru18360.1	
		#1.1.000 MIN		
			go:NIM_U2U156.1 /DEF=Homo sapiens core1 UDF-galactose:N	
			acetylgalactosamine-alpha-R beta 1,3-galactosyltransferase	
			(C1GALT1), mRNA. /FEA=mRNA /GEN=C1GALT1	
			/PROD=core1UDP-galactose:N-acetylgalactosamine-alpha-R	
			beta1,3-galactosyltransferase /DB_XREF=gi:9910143	
			/UG=Hs.46744 core1 UDP-galactose:N-acetylgalactosamine-	
			alpha-R beta 1,3-galactosyltransferase /FL=gb:AF155582.1	
219439 at		NM 020156		
			gb:NM 007375.1 /DEF=Homo sapiens TAR DNA binding	
			protein (TARDBP), mRNA. /FEA=mRNA /GEN=TARDBP	
			/PROD=TAR DNA binding protein /DB_XREF=gi:6678270	
			/UG=Hs.193989 TAR DNA binding protein /FL=gb:AL050265.1	
200020_at		NM_007375	gb:NM_007375.1_gb:U23731.1	
213423_x_at	N33	AI884858	Putative prostate cancer tumor suppressor	Hs.71119
			Consensus includes ab AL031681 /DEF=Human DNA	
			sequence from clone 862K6 on chromosome 20012-13 13	
			Coptains the gene for a protein similar to Drosophila lethal	
			(2) malianant brain timor (1/3)mbt) protein the SERSE cone	
			(3) mangnant brain turnol ((3)mbt) protein, the Strop general to accompanie of the Strop (3) and Str	
			for arginineserine-rich splicing factor 6 (SKPSS), a 4E-BP2	
			(4 /FEA=mKNA_3 /DB_AKEF=gi:10196006 /UG=HS:0691	
208804_s_at		AL031681	splicing factor, arginineserine-rich 6 /FL=gb:U30828.1	
			ob AL136710.1 /DEF=Homo sapiens mRNA: cDNA	
			DKFZp566P0524 (from clone DKFZp566P0524); complete	
			cds. /FEA=mRNA /GEN=DKFZp566P0524 /PROD=hypothetical	
			protein /DB_XREF=gi:12052939 /UG=Hs.75893 ankyrin 3,	
209442 x at		AL136710	node of Ranvier (ankyrin G) /FL=gb:AL136/10.1	

	rigula / D Colli a.				
				NM_002878;	
	_			NM_133627; NM_133628:	
			RADO I-like 3 (3. cereviside)	NM_133629;	
37793_r_at	RAD51L3	AF034956		NM_133630	Hs.125244
			gb:NM_003247.1 /DEF=Homo sapiens thrombospondin 2		-
			(THBSZ), MKNA. /FEA=MKNA /GEN=THBSZ		
			/rrod=unormovspondin z /db_/rrrqus-430/430		
203083 at		NM 003247	18:100020 (iii) Chicago (iii)		
		II .	Concession includes ab. AE244534 1 (IDEE=Homo sanions		
			bydatidiform mole associated and imprinted (HYMAI) mRNA		
			complete sequence. /FEA=mRNA /DB XREF=q::9502099		
215513 at		AF241534	/UG=Hs.196015 hydatidiform mole associated and imprinted		
ш			Cluster Incl. L08835:Homo sapiens DMR-N9, partial cds; and		
			myotonic dystrophy kinase (DM kinase) gene, complete cds		
			/cds=(776,2665) /gb=L08835 /gi=181601 /ug=Hs.898		
37996_s_at		L08835	/len=3407		
			qb:NM 018639.1 /DEF=Homo sapiens CS box-containing WD		
			protein (LOC55884), mRNA. /FEA=mRNA /GEN=LOC55884		
			/PROD=CS box-containing WD protein /DB_XREF=gi:8923880		
			/UG=Hs.136644 CS box-containing WD protein		
201760 s at		NM 018639	/FL=gb:AF229181.1 gb:AF163324.1 gb:NM_018639.1		
213360 s at	WBSCR20C	AA514622	Williams Beuren syndrome chromosome region 20C		Hs.295112
213500 at	COPB2	AI307760	coatomer protein complex, subunit beta 2 (beta prime)		Hs.75724
202199 s_at	SRPK1	AW082913	SFRS protein kinase 1		Hs.75761
			Consensus includes gb:AK023289.1 /DEF=Homo sapiens		
			cDNA FLJ13227 fis, clone OVARC1000071, weakly similar to		
			Homo sapiens NTF2-related export protein NXT1 (NXT1)		
			mRNA. /FEA=mRNA /DB_XREF=gi:10435160 /UG=Hs.25010		
			hypothetical protein P15-2 /FL=gb:AF246127.1		
209628_at		AK023289	gb:NM_018698.1_gb:AF201942.1		
			Consensus includes gb:AK022316.1 /DEF=Homo sapiens		
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		A 17000046	CDNA FLJ12254 fis, clone MAMMA1001465. /FEA=mRNA		
215418 at		AN0223 10	/UB_ARET-9: 10453003 /UG-TS:440// alpita-parviii		

rigare / D Colif a	COIR G.			
			AV761453 MDS Homo sapiens cDNA clone MDSBZA03 5',	
at		AV761453		
222077_s_at RA	RACGAP1	AU153848		Hs.23900
			Consensus includes gb:AW051311 /FEA=EST	
	_		/DB_XREF=gi:5913581 /DB_XREF=est:wy89b01.x1	
			/CLONE=IMAGE:2555689 /UG=Hs.169149 karyopherin alpha	
			1 (importin alpha 5) /FL=gb:BC002374.1 gb:BC003009.1	
202056_at		NM_002264		
			Consensus includes gb:AJ278150.1 /DEF=Homo sapiens	_
			mRNA for putative lipid kinase. /FEA=mRNA /PROD=putative	
			lipid kinase /DB_XREF=gi:8250242 /UG=Hs.260238	
222132_s_at		AJ278150	hypothetical protein FLJ10842	
211940_x_at H3F3A		BE869922		Hs.367720
			gb:NM_003506.1 /DEF=Homo sapiens frizzled (Drosophila)	
			homolog 6 (FZD6), mRNA. /FEA=mRNA /GEN=FZD6	
			/PROD=frizzled 6 /DB_XREF=gi:4503830 /UG=Hs.114218	
			frizzled (Drosophila) homolog 6 /FL=gb:AB012911.1	
203987_at		NM_003506		
			gb:NM_001431.1 /DEF=Homo sapiens erythrocyte membrane	
			protein band 4.1-like 2 (EPB41L2), mRNA. /FEA=mRNA	
			/GEN=EPB41L2 /PROD=erythrocyte membrane protein band	_
			4.1-like 2 /DB_XREF=gi:4503578 /UG=Hs.7857 erythrocyte	-
			membrane protein band 4.1-like 2 /FL=gb:AF027299.1	
201719_s_at		NM_001431	gb:NM_001431.1	
			gb.AF078847.1 /DEF=Homo sapiens basic transcription factor	
			2 mRNA, complete cds. /FEA=mRNA /PROD=basic	
			transcription factor 2 /DB_XREF=gi:5531808 /UG=Hs.191356	
			general transcription factor IIH, polypeptide 2 (44kD subunit)	
221540_x_at		AF078847	/FL=gb:AF078847.1 gb:NM_001515.1	
			gb:NM_024715.1 /DEF=Homo sapiens hypothetical protein	
			FLJ22625 (FLJ22625), mRNA. /FEA=mRNA /GEN=FLJ22625	
			/PROD=hypothetical protein FLJ22625 /DB_XREF=gi:13376016	_
220495_s_at		NM_024715	/FL=gb:NM_024715.1	

	_						
	Hs.247118						
gb:NM_006800.1 /DEF=Homo sapiens male-specific lethal-3 (Drosophila)-like 1 (MSL3L1), mRNA. /FEA=mRNA /GEN=MSL3L1 /PROD=male-specific lethal-3 (Drosophila)-like 1 /DB_XREF=gi:5803103 /UG=Hs.88764 male-specific lethal-3 (Drosophila)-like 1 /FL=gb:AF117065.1 gb:NM_006800.1	phosphatidylinositol glycan, class B	gb:AF081496.1 /DEF=Homo sapiens kinetochore protein BUB3 (BUB3) mRNA, complete cds. /FEA=mRNA /GEN=BUB3 /PROD=kinetochore protein BUB3 /DB_XREF=gi:3639059 /UG=Hs.40323 BUB3 (budding liminhibited by henzimidazoles 3 yeast) homolog	/FL=gb:BC005138.1 gb:AF047472.1 gb:AF053304.1 gb:AF081496.1 gb:NM_004725.1			gb:L40326.1 /DEF=Homo sapiens Hepatitis B virus X-associated protein 1 mRNA, complete cds. /FEA=mRNA /PROD=X-associated protein 1 /DB_XREF=gi:695361 /UG=Hs.108327 damage-specific DNA binding protein 1 (127kD) /FL=gb:U18299.1 gb:U32986.1 gb:NM_001923.2 gb:L40326.1	
008900 MM	AU144243		AF081496	NM 018058	NM 006311	L40326	NM_015251
o o	PIGB						
207551 s at	214152 at		201457 x at		200856 x at		201855_s_at

Sing.	garo is come.			
218057 x at		NM_006067	gb:NM_006067.1 /DEF=Homo sapiens neighbor of COX4 (NOC4), mRNA. /FEA=mRNA /GEN=NOC4 /PROD=neighbor of COX4 /DB_XREF=gi:5174614 /UG=Hs.173162 neighbor of COX4 /FL=gb:BC001472.1 gb:AF005888.1 gb:NM_006067.1	
			gb:NM_000943.1 /DEF=Homo sapiens peptidylprolyl isomerase C (cyclophilin C) (PPIC), mRNA. /FEA=mRNA	
			/GEN=PPIC /PROD=peptidylprolyl isomerase C (cyclophilin C) //IDB XREF=qi:4505990 /UG=Hs.110364 peptidylprolyl	
204518 s at		NM 000943	isomerase Č (cyclophilin C) /FL=gb:BC002678.1 00943 gb:NM 000943.1	
64900 at	FLJ22167	AA401703	in FLJ22167	Hs.287366
			Consensus includes gb:AF070569.1 /DEF=Homo sapiens	
			clone 24659 mRNA sequence. /FEA=mKNA /DB XREF=qi:3387938 /UG=Hs.29206 Homo sapiens clone	
214696_at		AF070569	24659 mRNA sequence	
			Consensus includes gb:AA939270 /FEA=EST /DB_XREF=gi:3099183 /DB_XREF=est:oq31b02.s1 /CLONE=IMAGE:1587915 /UG=Hs.5151 RAN binding protein	•
200993_at		AL137335	7 /FL=gb:AF098799.1 gb:NM_006391.1	
			gb:AL353950.1 /DEF=Homo sapiens mRNA; cDNA DKFZp761L0516 (from clone DKFZp761L0516); complete cds. /FEA=mRNA /GEN=DKFZp761L0516 /PROD=hypothetical protein /DB_XREF=gi:7669991 /UG=Hs.272458 protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha) /FL=gb:J05480.1 gb:L14778.1	
202429 s at		AL353950	gb:NM_000944.1 gb:AL353950.1	
			gb:BC002568.1 /DEF=Homo sapiens, hypothetical protein, complete cds. /FEA=mRNA	
			/PROD=hypothetical protein /DB_XREF=gi:12803484	
200000		8930000	/UG=Hs.4900 hypothetical protein /FL=gb:AF248964.1	
200900_S_dt		0002000	go. B. Coursons. 1 go. Ar 110003. 1	

2 2 2				
218226 s at		NM 004547	gb:NM_004547.2 /DEF=Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4 (15kD, B15) (NDUFB4), mRNA. /FEA=mRNA /GEN=NDUFB4 /PROD=NADH dehydrogenase (ubiquinone) 1 betasubcomplex, 4 (15kD, B15) /DB_XREF=gi:6041668 /UG=Hs.227750 NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4 (15kD, B15) /FL=gb:BC000855.1 gb:AF044957.1 gb:NM_004547.2	
ja te			gb:NM_015511.1 /DEF=Homo sapiens DKFZP564N1363 protein (DKFZP564N1363), mRNA. /FEA=mRNA /GEN=DKFZP564N1363 /PROD=DKFZP564N1363 protein /DB_XREF=gi:7661627 /UG=Hs.11314 DKFZP564N1363 protein /FL=gb:BC001751.1 gb:AF132957.1 gb:AL117419.1 015511 gb:AF113672.1 gb:NM_015511.1	
218873 at		NM 017710	gb:NM_017710.1 /DEF=Homo sapiens hypothetical protein FLJ20203 (FLJ20203), mRNA. /FEA=mRNA /GEN=FLJ20203 /PROD=hypothetical protein FLJ20203 /DB_XREF=gi:8923193 /UG=Hs.20594 hypothetical protein FLJ20203 017710 /FL=qb:NM_017710.1	
204332_s_at		M64073	Consensus includes gb:M64073.1 /DEF=Human glycosylasparaginase mRNA, complete cds. /FEA=CDS /PROD=glycosylasparaginase /DB_XREF=gi:183329 /UG=Hs.207776 aspartylglucosaminidase /FL=gb:M64073.1 gb:NM_000027.1	
212627_s_at 209150_s_at	KIAA0116	AL581473 U94831	KIAA0116 protein gb:U94831.1 /DEF=Homo sapiens multispanning membrane protein mRNA, complete cds. /FEA=mRNA /PROD=multispanning membrane protein /DB_XREF=gi:2276459 /UG=Hs.91586 transmembrane 9 superfamily member 1 /FL=gb:U94831.1 gb:NM_006405.1	HS. 1828//
209657 s. at		M65217	gb:M65217.1 /DEF=Human heat shock factor 2 (HSF2) mRNA, complete cds. /FEA=mRNA /GEN=heat shock factor 2 /PROD=HSF2 /DB_XREF=gi:184404 /UG=Hs.158195 heat shock transcription factor 2 /FL=gb:M65217.1 gb:NM_004506.2	
212440_at	RY1	BG252325	putative nucleic acid binding protein RY-1	Hs.54649

Figure	Figure /b Cont'd.			
			Consensus includes gb:AW139179 /FEA=EST	
			/DB_XREF=gi:6143497 /DB_XREF=est:UI-H-BI1-aet-f-06-0-	
			UI.s1 /CLONE=IMAGE:2720411 /UG=Hs.6048 FEM-1	
			(C.elegans) homolog b /FL=gb:AF178632.1 gb:NM_015322.1	
212373_at		NM_015322	gb:AF204883.1	
			Consensus includes gb:BE999972 /FEA=EST	
			/DB_XREF=gi:10700248 /DB_XREF=est:7h15b02.x1	
			/CLONE=IMAGE:3316011 /UG=Hs.186613 sphingosine-1-	
212322_at		AF144638	phosphate lyase 1 /FL=gb:AF144638.1	
			gb:BC000927.1 /DEF=Homo sapiens, Similar to poly (A)	
			polymerase, clone MGC:5378, mRNA, complete cds.	
			/FEA=mRNA /PROD=Similar to poly (A) polymerase	
			/DB XREF=gi:12654216 /UG=Hs.49007 poly(A) polymerase	
209388_at		BC000927	alpha /FL=gb:BC000927.1	
212594 at	PDCD4	N92498	programmed cell death 4 (neoplastic transformation inhibitor)	Hs.326248
			gb:BC002461.1 /DEF=Homo sapiens, BCL2adenovirus E1B	
			19kD-interacting protein 2, clone MGC:1529, mRNA,	
-			complete cds. /FEA=mRNA /PROD=BCL2adenovirus E1B	
			19kD-interacting protein 2 /DB_XREF=gi:12803290	
			/UG=Hs.155596 BCL2adenovirus E1B 19kD-interacting protein	
209308_s_at		BC002461	2 /FL=gb:BC002461.1	
			gb:BC002755.1 /DEF=Homo sapiens, Similar to MAP kinase-	
			interacting serinethreonine kinase 1, clone MGC:3690,	
			mRNA, complete cds. /FEA=mRNA /PROD=Similar to MAP	
			kinase-interactingserinethreonine kinase 1	
			/DB_XREF=gi:12803828 /UG=Hs.5591 MAP kinase-interacting	
209467 s at		BC002755	serinethreonine kinase 1 /FL=gb:BC002755.1	
1			gb:AF095192.1 /DEF=Homo sapiens BAG-family molecular	
			chaperone regulator-2 mRNA, complete cds. /FEA=mRNA	
			/PROD=BAG-family molecular chaperone regulator-2	
			/DB_XREF=gi:4322819 /UG=Hs.55220 BCL2-associated	
			athanogene 2 /FL=gb:AF095192.1 gb:AL050287.1	
209406_at		AF095192	gb:NM_004282.2	

2 12 12	. D. O. O. I.			
209089 at		BC001267	gb:BC001267.1 /DEF=Homo sapiens, RAB5A, member RAS oncogene family, clone MGC:5048, mRNA, complete cds. /FEA=mRNA /PROD=RAB5A, member RAS oncogene family /DB_XREF=gi:12654846 /UG=Hs.73957 RAB5A, member RAS oncogene family /FL=gb:BC001267.1	
212144 at		AL021707	Consensus includes gb:AL021707 /DEF=Human DNA sequence from clone RP3-508115 on chromosome 22q12-13 Contains the gene for GTPBP1 (GTP binding protein 1), two novel genes KIAA0063 and KIAA0668, a novel gene based on ESTs and cDNA, a pseudogene similar to AOP1 (antioxidant protein 1) /FEA=mRNA_3 /DB XREF=qi:4582132 /UG=Hs:5898 KIAA0668 protein	
	NUDT1	AI935415	nudix (nucleoside diphosphate linked moiety X)-type motif 1	Hs.153357
205961_s_at		NM_004682	gb:NM_004682.1 /DEF=Homo sapiens PC4 and SFRS1 interacting protein 2 (PSIP2), mRNA. /FEA=mRNA /GEN=PSIP2 /PROD=PC4 and SFRS1 interacting protein 2 /DB_XREF=gi:4758869 /UG=Hs.306179 PC4 and SFRS1 004682 interacting protein 2 /FL=gb:AF098483.1 gb:NM_004682.1	
207233_s_at		NM_000248	gb:NM_000248.1 /DEF=Homo sapiens microphthalmia-associated transcription factor (MITF), mRNA. /FEA=mRNA/GEN=MITF /PROD=microphthalmia-associated transcription factor /DB_XREF=gi:4557754 /UG=Hs.166017 microphthalmia-associated transcription factor /FL=gb:NM_000248.1	
214766 s at		AL080144	Consensus includes gb:AL080144.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434N093 (from clone DKFZp434N093); partial cds. /FEA=mRNA /GEN=DKFZp434N093 /PROD=hypothetical protein /DB_XREF=gi:5262592 /UG=Hs.33363 DKFZP434N093 protein	
213285_at		AV691491	ESTs, Weakly similar to MUC2_HUMAN Mucin 2 precursor (Intestinal mucin 2) [H.sapiens]	Hs.391892

2022	3 2 0 0 2 0 3 5			
			gb:NM_003288.1 /DEF=Homo sapiens tumor protein D52-like 2 (TPD52L2), mRNA. /FEA=mRNA /GEN=TPD52L2	
			/PROD=tumor protein D52-like 2 /DB_XREF=gi:4507642 /UG=Hs.154718 tumor protein D52-like 2 /FL=gb:AF004430.1	
201379_s_at		NM_003288	gb:NM_003288.1	
			Consensus includes gb:NM_007054.1 /DEF=Homo sapiens	
			kinesin family member 3A (KIF3A), mRNA. /FEA=CDS	
			/GEN=KIF3A /PROD=kinesin family member 3A	***
		,	/DB_XREF=gi:6857803 /UG=Hs.43670 kinesin family member	
213623_at		NM_007054	3A /FL=gb:AF041853.1 gb:NM_007054.1	
713655 at 1		AA502643	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase	Hs 79474
ď,	1 VV VL	20202070		2.101.1
			gb:AL136939.1 /DEF=Homo sapiens mRNA; cDNA	
			DKTZp300B10Z4 (IIOIII CIOIIE DKTZp300B10Z4), COIIIpiete cds. /FEA=mRNA /GEN=DKFZ0586B1824 /PROD=hvpothetical	
			protein /DB XREF=gi:12053372 /UG=Hs.250175 homolog of	
			yeast long chain polyunsaturated fatty acid elongation	
•			enzyme 2 /FL=gb:NM_021814.1 gb:AL136939.1	
208788 at		AL136939	gb:AF111849.1 gb:AF231981.1	
			gb:NM_015414.1 /DEF=Homo sapiens ribosomal protein L36	
			(RPL36), mRNA. /FEA=mRNA /GEN=RPL36	
			/PROD=ribosomal protein L36 /DB_XREF=gi:7661637	
			/UG=Hs.300759 ribosomal protein L36 /FL=gb:AF077043.1	
219762_s_at		NM_015414	gb:NM_015414.1	
			gb:NM_016576.1 /DEF=Homo sapiens GMPR2 for guanosine	
			monophosphate reductase isolog (LOC51292), mRNA.	
			/FEA=mRNA /GEN=LOC51292 /PROD=GMPR2 for guanosine	
			monophosphate reductaseisolog /DB_XREF=gi:7706108	
			/UG=Hs.234546 GMPR2 for guanosine monophosphate	
-			reductase isolog /FL=gb:AB032903.1 gb:NM_016576.1	
217990_at		NM_016576	gb:AF135159.1	
			gb:BC004424.1 /DEF=Homo sapiens, clone MGC:3538,	
			mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein	
			for MGC:3538) /DB_XREF=gi:13325209 /UG=Hs.250745	
, C		0.000	polymerase (RNA) III (DNA directed) (62kD)	·
2105/3 s at		BC004424	/FL=gb:BC004424.1	

מונים מי שומלים	3 2 5			
			gb:NM_025238.1 /DEF=Homo sapiens BTB (POZ) domain	
			CONTAINING 1 (BIBUT), MKNA, /FEA=MKNA /GEN=BIBUT	
			/PROD=B1B (POZ) domain containing 1	
			/DB_XREF=gi:13376847 /UG=Hs.21332 BTB (POZ) domain	
			containing 1 /FL=gb:AL136853.1 gb:AF257241.1	
217945_at		NM_025238	gb:NM_025238.1_gb:AF355402.1	
			gb:NM_002634.2 /DEF=Homo sapiens prohibitin (PHB),	
			mRNA. /FEA=mRNA /GEN=PHB /PROD=prohibitin	-
-			/DB_XREF=gi:6031190 /UG=Hs.75323 prohibitin	
200659_s_at		NM_002634	/FL=gb:NM_002634.2	
			gb:NM_022073.1 /DEF=Homo sapiens hypothetical protein	
			FLJ21620 (FLJ21620), mRNA. /FEA=mRNA /GEN=FLJ21620	
			/PROD=hypothetical protein FLJ21620 /DB_XREF=gi:11545786	
			/UG=Hs.18878 hypothetical protein FLJ21620	
219232_s_at		NM_022073	322073 /FL=gb:NM_022073.1	
			gb:NM_004670.1 /DEF=Homo sapiens 3-phosphoadenosine 5-	
			phosphosulfate synthase 2 (PAPSS2), mRNA. /FEA=mRNA	
			/GEN=PAPSS2 /PROD=3-prime-phosphoadenosine 5-prime-	
			phosphosulfatesynthase 2 /DB_XREF=gi:4758879	
_			/UG=Hs.274230 3-phosphoadenosine 5-phosphosulfate	
-			synthase 2 /FL=gb:AF150754.2 gb:AF313907.1	
	-		gb:AF091242.1 gb:NM_004670.1 gb:AF074331.1	
203059_s_at		NM_004670	gb:AF173365.1	
			gb:NM_003174.2 /DEF=Homo sapiens supervillin (SVIL),	
			transcript variant 1, mRNA. /FEA=mRNA /GEN=SVIL	
			/PROD=supervillin, isoform 1 /DB_XREF=gi:11496980	
			/UG=Hs.154567 supervillin /FL=gb:NM_003174.2	
202565_s_at		NM_003174	003174 gb:AF051850.1 gb:AF051851.1	
			gb:NM_031283.1 /DEF=Homo sapiens HMG-box transcription	
			factor TCF-3 (TCF-3), mRNA. /FEA=mRNA /GEN=TCF-3	
			/PROD=HMG-box transcription factor TCF-3	
221016_s_at		NM_031283	031283 /DB_XREF=gi:13786122 /FL=gb:NM_031283.1	

			Consensus includes gb:M27487.1 /DEF=Homo sapiens MHC class II DPw3-alpha-1 chain mRNA, complete cds. //FEA=CDS /GEN=HLA-DPA1 /PROD=MHC class II DP3-alpha //DB_XREF=gi:703088 /UG=Hs.914 Human mRNA for SB
211990_at		M27487	classii nistocompatibility antigeri alpria-chairi /rr-gb.twz/46/
			gb:NM_006186.1 /DEF=Homo sapiens nuclear receptor subfamily 4, group A, member 2 (NR4A2), mRNA.
			/FEA=mRNA /GEN=NR4A2 /PROD=nuclear receptor subfamily
			4, group A, member 2 /DB_XREF=gi:5453821 /UG=Hs.82120
204622 x at		NM_006186	nuclear receptor subfamily 4, group A, member z /FL=gb:NM 006186.1
			gb:NM_005544.1 /DEF=Homo sapiens insulin receptor
			/PROD=insulin receptor substrate 1 /DB_XREF=gi:5031804
000		•	/UG=Hs.96063 insulin receptor substrate 1
204000 at		1000044	/FL=gb:\NM 003344.1
			gb:NM_014676.1 /DEF=Homo sapiens pumilio (Drosophila)
			homolog 1 (PUM1), mRNA. /FEA=mRNA /GEN=PUM1
			/PROD=pumilio (Drosophila) homolog 1
			/DB_XREF=gi:13491165 /UG=Hs.153834 pumilio (Drosophila)
201166_s_at		NM_014676	homolog 1 /FL=gb:AF315592.1 gb:NM_0146/6.1
			gb:NM_004585.2 /DEF=Homo sapiens retinoic acid receptor
			responder (tazarotene induced) 3 (RARRES3), mRNA.
			/FEA=mRNA /GEN=RARRES3 /PROD=retinoic acid receptor
			responder (tazaroteneinduced) 3 /DB_XREF=gi:8051633
			/UG=Hs.17466 retinoic acid receptor responder (tazarotene
			induced) 3 /FL=gb:AF060228.1 gb:AF092922.1
204070_at		NM_004585	
			gb:NM_018095.1 /DEF=Homo sapiens hypothetical protein
			FLJ10450 (FLJ10450), mRNA. /FEA=mRNA /GEN=FLJ10450
	-		/PROD=hypothetical protein FLJ10450 /DB_XREF=gi:8922425
			/UG=Hs.267604 hypothetical protein FLJ10450
2185/0_at		NM 018095	/FL=gb:BC002/36.1 gb:NM_018095.1

/ eligure /	rigure / b Cont a.		
			gb:NM_012460.1 /DEF=Homo sapiens translocase of inner
			mitochondrial membrane 9 (yeast) homolog (TIMM9), mRNA.
			/FEA=mRNA /GEN=TIMM9 /PROD=translocase of inner
			mitochondrial membrane 9(yeast) homolog
			/DB_XREF=gi:6912713 /UG=Hs.323914 translocase of inner
			mitochondrial membrane 9 (yeast) homolog
218316_at		NM_012460	012460 /FL=gb:AF150100.1 gb:AF152353.1 gb:NM_012460.1
			gb:NM_018195.1 /DEF=Homo sapiens hypothetical protein
			FLJ10726 (FLJ10726), mRNA. /FEA=mRNA /GEN=FLJ10726
			/PROD=hypothetical protein FLJ10726 /DB_XREF=gi:8922622
218314_s_at		NM_018195	/FL=gb:NM_018195.1
			gb:NM_003618.1 /DEF=Homo sapiens mitogen-activated
			protein kinase kinase kinase 3 (MAP4K3), mRNA.
			/FEA=mRNA /GEN=MAP4K3 /PROD=mitogen-activated protein
			kinase kinasekinase 3 /DB_XREF=gi:4506376
			/UG=Hs.227400 mitogen-activated protein kinase kinase
218311 at		NM 003618	kinase kinase 3 /FL=gb:AF000145.1 gb:NM_003618.1
a.		l	gb:NM_013386.1 /DEF=Homo sapiens hypothetical protein
			(DKFZp586G0123), mRNA. /FEA=mRNA
			/GEN=DKFZp586G0123 /PROD=hypothetical protein
			/DB_XREF=gi:9558726 /UG=Hs.24713 hypothetical protein
204342_at		NM_013386	
			gb:NM_024956.1 /DEF=Homo sapiens hypothetical protein
-			FLJ23375 (FLJ23375), mRNA. /FEA=mRNA /GEN=FLJ23375
			/PROD=hypothetical protein FLJ23375 /DB_XREF=gi:13376442
			/UG=Hs.285996 hypothetical protein FLJ23375
218776 s at		NM_024956	
			gb:NM_000216.1 /DEF=Homo sapiens Kallmann syndrome 1
	-		sequence (KAL1), mRNA. /FEA=mRNA /GEN=KAL1
			/PROD=Kallmann syndrome 1 protein /DB_XREF=gi:4557682
			/UG=Hs.89591 Kallmann syndrome 1 sequence
205206_at		NM_000216	000216 /FL=gb:M97252.1 gb:NM 000216.1

Figure	rigure / b Cont a.			
			gb:NM_000122.1 /DEF=Homo sapiens excision repair cross-	
			complementing rodent repair deficiency, complementation	
-			group 3 (xeroderma pigmentosum group B complementing)	
			(ERCC3), mRNA. /FEA=mRNA /GEN=ERCC3	
			/PROD=excision repair cross-complementing rodentrepair	
			deficiency, complementation group 3 (xerodermapigmentosum	
			group B complementing) /DB_XREF=gi:4557562	
			/UG=Hs.77929 excision repair cross-complementing rodent	
			repair deficiency, complementation group 3 (xeroderma	
-,-			pigmentosum group B complementing) /FL=gb:M31899.1	
202176_at		NM_000122	gb:NM_000122.1	
			gb:NM_022817.1 /DEF=Homo sapiens period (Drosophila)	
			homolog 2 (PER2), transcript variant 1, mRNA. /FEA=mRNA	
			/GEN=PER2 /PROD=period 2, isoform 2	
			/DB_XREF=gi:12707561 /UG=Hs.153405 period (Drosophila)	
205251_at		NM_022817	homolog 2 /FL=gb:NM_022817.1	
			gb:NM_022362.1 /DEF=Homo sapiens MMS19 (MET18 S.	
			cerevisiae)-like (MMS19L), mRNA. /FEA=mRNA	
			/GEN=MMS19L /PROD=MMS19 (MET18 S. cerevisiae)-like	_
			/DB_XREF=gi:13375625 /UG=Hs.288891 MMS19 (MET18 S.	
202167_s_at		NM_022362	cerevisiae)-like /FL=gb:NM_022362.1	
			Consensus includes gb:AL031282 /DEF=Human DNA	
			sequence from clone 283E3 on chromosome 1p36.21-36.33.	
			Contains the alternatively spliced gene for Matrix	
			Metalloproteinase in the Female Reproductive tract MIFR1, -	
			2, MMP2122A, -B and -C, a novel gene, the alternatively	
			spliced CDC2L2 /FEA=mRNA_6 /DB_XREF=gi:3860395	
217122_s_at		AL031282	/UG=Hs.214646 KIAA0447 gene product	
221985_at	FLJ20059	AW006750		Hs.246875
			gb:NM_006360.1 /DEF=Homo sapiens dendritic cell protein	
			(GA17), mRNA. /FEA=mRNA /GEN=GA17 /PROD=dendritic	
			cell protein /DB_XREF=gi:5453653 /UG=Hs.69469 dendritic	
<u> </u>			cell protein /FL=gb:AF277183.1 gb:AF064603.1	
ä		NM_006360	gb:NM_006360.1	
at	NUCKS	AW515443		Hs.118064

aingi i	igale / D Colif a.			
217478 s at		X76775	Consensus includes gb:X76775 /DEF=H.sapiens HLA-DMA gene /FEA=mRNA_1 /DB_XREF=gi:512468 /UG=Hs.77522 major histocompatibility complex, class II, DM alpha	-
			gb:NM_003588.1 /DEF=Homo sapiens cullin 4B (CUL4B), mRNA. /FEA=mRNA /GEN=CUL4B /PROD=cullin 4B /DB XREF=ai:13270466 /UG=Hs.155976 cullin 4B	
202214_s_at		NM_003588	/FL=gb:NM_003588.1 gb:AB014595.1	
			gb:NM_005463.1 /DEF=Homo sapiens heterogeneous nuclear ribonucleoprotein D-like (HNRPDL), mRNA. /FEA=mRNA	
			/GEN=HNRPDL /PROD=heterogeneous nuclear	
			ribonucleoprotein D-like /DB_XREF=gi:4885422	
			/UG=Hs.170311 heterogeneous nuclear ribonucleoprotein D-	
201993_x_at		NM_005463	like /FL=gb:AB017019.1 gb:NM 005463.1	
			Consensus includes gb:S77154.1 /DEF=TINUR= NGFI-Bnur77	
			beta-type transcription factor homolog human, T lymphoid	
	•		CEIL III E, TEEN, III NINA, 2408 III. ITENATIONIA IGENTINON	
	•		/DB_AKEr=gi:913966 /UG=HS.82120 nuclear receptor	
3 s at		S77154	er 2	
63009_at	FLJ10539	AI188402	hypothetical protein FLJ10539	93391
			gb:NM_000285.1 /DEF=Homo sapiens peptidase D (PEPD), mRNA /FEA=mRNA /GEN=PEPD /PROD=Xaa-Pro	
			dipeptidase /DB XREF=qi:4557834 /UG=Hs.73947 peptidase	
202108 at		NM_000285	D /FL=gb:BC004305.1 gb:J04605.1 gb:NM_000285.1	
			gb:BC000651.1 /DEF=Homo sapiens, Similar to solute carrier	
			family 1 (glutamate transporter), member 7, clone	
			MGC:2078, mRNA, complete cds. /FEA=mRNA	
			/PROD=Similar to solute carrier family 1	
			(glutamatetransporter), member / /UB_XREF=gi:12653/30	
			/UG=Hs.307039 Homo sapiens, Similar to solute carrier	
			tamily 1 (glutamate transporter), member 7, clone	
210923_at		BC000651	MGC:2078, mRNA, complete cds /FL=gb:BC000651.1	
			Consensus includes go:Brolling //rEA=ESI	
			/DB_XKEF=gi:11594389 /DB_XKEF=es:UI-H-BI4-apn-c-05-0-	
10000		_	tamily 16 (monocarboxylic acid transporters), member 1	
202234_S_at		I COCOO MINI	003031 //FL=gb:\niv 003031:1 gb:L31001:1	

rigure	rigure / b cont a.			
			gb:NM_006109.1 /DEF=Homo sapiens skb1 (S. pombe)	
			/PROD=skb1 (S. pombe) homolog /DB_XREF=gi:5174682	
217786_at		NM_006109	_	
			gb:BC001434.1 /DEF=Homo sapiens, clone MGC:2477,	
			mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:2477) /DB XREF=qi:12655158 /UG=Hs.9061	
221637_s_at		BC001434	hypothetical protein MGC2477 /FL=gb:BC001434.1	
			gb:NM_005146.1 /DEF=Homo sapiens squamous cell	
			carcinoma antigen recognised by T cells (SART1), mRNA.	
			/FEA=mRNA /GEN=SART1 /PROD=squamous cell carcinoma	
			antigen recognised by Tcells /DB_XREF=gi:10863888	
			/UG=Hs.288319 squamous cell carcinoma antigen recognised	
			by T cells /FL=gb:NM_005146.1 gb:BC001058.1	
200051_at		NM_005146		
			gb:NM_003670.1 /DEF=Homo sapiens basic helix-loop-helix	
			domain containing, class B, 2 (BHLHB2), mRNA.	
			/FEA=mRNA /GEN=BHLHB2 /PROD=differentiated embryo	
			chondrocyte expressed gene1 /DB_XREF=gi:4503298	
			/UG=Hs.171825 basic helix-loop-helix domain containing,	
201170_s_at		NM_0036/0	NM_0036/0 class B, 2 /FL=gb:AB004066.1 gb:NM_0036/0.1	
			gb:NM_005033.1 /DEF=Homo sapiens	
			polymyositisscleroderma autoantigen 1 (75kD) (PMSCL1),	
,			mRNA. /FEA=mRNA /GEN=PMSCL1	
			/PROD=polymyositisscleroderma autoantigen 1 (75kD)	
			/DB_XREF=gi:4826921 /UG=Hs.91728 polymyositisscleroderma	
205061_s_at		NM_005033	autoantigen 1 (75kD) /FL=gb:M58460.1 gb:NM_005033.1	
			Homo sapiens, Similar to putative ion channel protein	
			CATSPER2, clone MGC:33346 IMAGE:4828636, mRNA,	(
217588_at		AW971983	complete cds	Hs.293003

2 0 5 5 -				
212641 at		AL023584	Consensus includes gb:AL023584 /DEF=Human DNA sequence from clone 67K17 on chromosome 6q24.1-24.3. Contains the HIVEP2 (Schnurri-2) gene for HIV type 1 Enhancer-binding Protein 2, and a possible pseudogene in an intron of this gene. Contains STSs and GSSs and an AAAT repeat polymorp /FEA=mRNA /DB_XREF=gi:3790154 /UG=Hs.75063 human immunodeficiency virus type 1 enhancer-binding protein 2 /FL=gb:NM_006734.1	
209970_x_at		M87507	gb:M87507.1 /DEF=Homo sapien interleukin-1 beta convertase (IL1BCE) mRNA, complete cds. /FEA=mRNA /GEN=IL1BCE /PROD=interleukin 1-beta convertase /DB_XREF=gi:435598 /UG=Hs.2490 caspase 1, apoptosis-related cysteine protease (interleukin 1, beta, convertase) /FL=gb:M87507.1	
202273 at		002609 MN	gb:NM_002609.1 /DEF=Homo sapiens platelet-derived growth factor receptor, beta polypeptide (PDGFRB), mRNA, /FEA=mRNA /GEN=PDGFRB /PROD=platelet-derived growth factor receptor, betapolypeptide /DB_XREF=gi:4505682 /UG=Hs.76144 platelet-derived growth factor receptor, beta polypeptide /FL=gb:M21616.1 gb:J03278.1 gb:NM_002609.1	
219459_at	·	NM_018082	gb:NM_018082.1 /DEF=Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA. /FEA=mRNA /GEN=FLJ10388 /PROD=hypothetical protein FLJ10388 /DB_XREF=gi:8922398 /UG=Hs.197642 hypothetical protein FLJ10388 /FL=gb:NM_018082.1	
217671_at		BE466926	ESTs, Weakly similar to 2109260A B cell growth factor [Homo sapiens] [H.sapiens]	Hs.279706
217973_at		NM_016286	gb:NM_016286.1 /DEF=Homo sapiens carbonyl reductase (LOC51181), mRNA. /FEA=mRNA /GEN=LOC51181 /PROD=carbonyl reductase /DB_XREF=gi:7705924 /UG=Hs.9857 carbonyl reductase /FL=gb:BC001470.1 gb:NM_016286.1	

		Consensus includes gb:D38169.1 /DEF=Homo sapiens mRNA		
		for inositol 1,4,5-trisphosphate 3-kinase isoenzyme, partial		
		cds. /FEA=mRNA /PROD=inositol 1,4,5-trisphosphate 3-kinase		
		isoenzyme /DB_XREF=gi:2463541 /UG=Hs.21453 inositol		
213076_at	D38169	1,4,5-trisphosphate 3-kinase C		
		gb:NM_001038.1 /DEF=Homo sapiens sodium channel,		
		nonvoltage-gated 1 alpha (SCNN1A), mRNA. /FEA=mRNA		
		/GEN=SCNN1A /PROD=sodium channel, nonvoltage-gated 1		
		alpha /DB_XREF=gi:4506814 /UG=Hs.2794 sodium channel,		
203453_at	NM_001038			
		gb:NM_004240.1 /DEF=Homo sapiens thyroid hormone		
		receptor interactor 10 (TRIP10), mRNA. /FEA=mRNA		
		/GEN=TRIP10 /PROD=thyroid hormone receptor interactor 10		
		/DB_XREF=gi:11342675 /UG=Hs.73999 thyroid hormone		-
202734_at	NM_004240	004240 receptor interactor 10 /FL=gb:NM_004240.1		
		gb:AF109161.1 /DEF=Homo sapiens p35srj (MRG1) mRNA,		
		complete cds. /FEA=mRNA /GEN=MRG1 /PROD=p35srj		
		/DB_XREF=gi:4193945 /UG=Hs.82071 Cbpp300-interacting		
		transactivator, with GluAsp-rich carboxy-terminal domain, 2		
209357_at	AF109161	/FL=gb:BC004377.1 gb:AF109161.1		
217599_s_at HIC	BE910600	I-mfa domain-containing protein	Hs.1	Hs.132739
		gb:NM_005260.2 /DEF=Homo sapiens growth differentiation		
		factor 9 (GDF9), mRNA. /FEA=CDS /GEN=GDF9		
		/PROD=growth differentiation factor 9 precursor		
	-	/DB_XREF=gi:6715598 /UG=Hs.248113 growth differentiation		-
221314_at	NM_005260	005260 factor 9 /FL=gb:NM 005260.2		
		gb:BC003111.1 /DEF=Homo sapiens, Similar to pre-B-cell		
		leukemia transcription factor 2, clone MGC:2174, mRNA,		
		complete cds. /FEA=mRNA /PROD=Similar to pre-B-cell		
		leukemia transcriptionfactor 2 /DB_XREF=gi:13111886		
		/UG=Hs.93728 pre-B-cell leukemia transcription factor 2		
211097_s_at	BC003111	/FL=gb:BC003111.1	\dashv	

_							
			Hs.99843				
	Consensus includes gb:AL031588 /DEF=Human DNA sequence from clone 1163J1 on chromosome 22q13.2-13.33. Contains the 3 part of a gene for a novel KIAA0279 LIKE EGF-like domain containing protein (similar to mouse Celsr1, rat MEGF2), a novel gene for a protein similar to C. elegans B0 /FEA=mRNA_1 /DB_XREF=gi:4007108 /UG=Hs.250671 hypothetical protein FLJ10140	gb:U32974.1 /DEF=Human IAP-like protein ILP mRNA, complete cds. /FEA=mRNA /PROD=IAP-like protein ILP /DB_XREF=gi:1016687 /UG=Hs.172777 baculoviral IAP repeat-containing 4 /FL=gb:U32974.1 gb:U45880.1 gb:NM_001167.1	DKFZP586N0721 protein	gb:NM_024812.1 /DEF=Homo sapiens hypothetical protein FLJ12015 (FLJ12015), mRNA. /FEA=mRNA /GEN=FLJ12015 /PROD=hypothetical protein FLJ12015 /DB_XREF=gi:13376199 /UG=Hs.169395 hypothetical protein FLJ12015	gb:NM_007144.1 /DEF=Homo sapiens zinc finger protein 144 (Mel-18) (ZNF144), mRNA. /FEA=mRNA /GEN=ZNF144 /PROD=zinc finger protein 144 (Mel-18) /DB_XREF=gi:6005963 /UG=Hs.184669 zinc finger protein 144 (Mel-18) /FL=gb:BC004858.1 gb:D13969.1 gb:NM_007144.1		gb:NM_000201.1 /DEF=Homo sapiens intercellular adhesion molecule 1 (CD54), human rhinovirus receptor (ICAM1), mRNA. /FEA=mRNA /GEN=ICAM1 /PROD=intercellular adhesion molecule 1 precursor /DB_XREF=igi:4557877 /UG=Hs.168383 intercellular adhesion molecule 1 (CD54), human rhinovirus receptor /FL=gb:M24283.1 gb:J03132.1 o000201 lqb:NM_000201.1
	AL031588	U32974	BF971416	NM 024812	ri 19	NM_030817	NM 000201
			DKFZP586N0721				
	213634 s_at	206536_s_at	205396_at	218899 s at	×	221031 s_at	202638 s at

Figure /b Cont'd.			
	gb:NM_019114.1 /DE mRNA. /FEA=mRNA /DB_XREF=gi:950656 NM_019114 /FL=gb:NM_019114.1	gb:NM_019114.1 /DEF=Homo sapiens EHM2 gene (EHM2), mRNA. /FEA=mRNA /GEN=EHM2 /PROD=EHM2 gene /DB_XREF=gi:9506568 /UG=Hs.267997 EHM2 gene /FL=gb:NM_019114.1	
	gb:M1756 with DRv M17565	gb:M17565.1 /DEF=Human MHC class II DQ-beta associated with DRw6, DQw1 protein, complete cds. /FEA=mRNA/GEN=HLA-DQB1 /DB_XREF=gi:188188 /FL=gb:M17565.1	
	015	gb:NM_023015.1 /DEF=Homo sapiens hypothetical protein FLJ21919 (FLJ21919), mRNA. /FEA=mRNA /GEN=FLJ21919 /PROD=hypothetical protein FLJ21919 /DB_XREF=gi:12711679 /UG=Hs.105894 hypothetical protein FLJ21919 /FL=qb:NM 023015.1	
ı – –	gb:NM_0 FLJ12876 /PROD=I /UG=Hs. NM_022754 /FL=gb:N	gb:NM_022754.1 /DEF=Homo sapiens hypothetical protein FLJ12876 (FLJ12876), mRNA. /FEA=mRNA /GEN=FLJ12876 /PROD=hypothetical protein FLJ12876 /DB_XREF=gi:12232420 /UG=Hs.16131 hypothetical protein FLJ12876 /FEGE:NM 022754.1	
	gb:NM_0 (Kruppel- MRNA. / protein 1 leukemia protein 1	gb:NM_006006.1 /DEF=Homo sapiens zinc finger protein 145 (Kruppel-like, expressed in promyelocytic leukemia) (ZNF145), mRNA. /FEA=mRNA /GEN=ZNF145 /PROD=zinc finger protein 145 (Kruppel-like, expressedin promyelocytic leukemia) /DB_XREF=gi:5174752 /UG=Hs.37096 zinc finger protein 145 (Kruppel-like, expressed in promyelocytic leukemia) /FL=gb:NM_006006.1	
	gb:NM_0 FLJ1276i /PROD=I /UG=Hs.X NM_025163 /FL=gb:N	gb:NM_025163.1 /DEF=Homo sapiens hypothetical protein FLJ12768 (FLJ12768), mRNA. /FEA=mRNA /GEN=FLJ12768 /PROD=hypothetical protein FLJ12768 /DB_XREF=gi:13376764 /UG=Hs.289077 hypothetical protein FLJ12768	
	gb:NM_0 voltage-g /FEA=CC gated, ty /UG=Hs./	gb:NM_006514.1 /DEF=Homo sapiens sodium channel, voltage-gated, type X, alpha polypeptide (SCN10A), mRNA. /FEA=CDS /GEN=SCN10A /PROD=sodium channel, voltage-gated, type X, alphapolypeptide /DB_XREF=gi:5730032 /UG=Hs.250443 sodium channel, voltage-gated, type X, alpha polypeptide /FL=gb:AF117907.1 gb:NM_006514.1	

Figure	rigure / b Cont a.		
		:	gb:AF157323.1 /DEF=Homo sapiens p45SKP2-like protein mRNA, complete cds. /FEA=mRNA /PROD=p45SKP2-like
209005_at		AF157323	protein /DB_XREF=gi:7688696 /UG=Hs.5548 f-box and leucine-rich repeat protein 5 /FL=gb:AF199420.1 gb:AF142481.1 gb:AF157323.1
		700700	gb:BC001004.1 /DEF=Homo sapiens, clone MGC:5439, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:5439) /DB_XREF=gi:12654362 /UG=Hs.75871 protein kinase C binding protein 1 /FL=gb:BC001004.1
200049 20049 20049			gb:NM_018846.1 /DEF=Homo sapiens SBBI26 protein (SBBI26), mRNA. /FEA=mRNA /GEN=SBBI26 /PROD=SBBI26 protein /DB_XREF=gi:9055325 /UG=Hs.26481 SBBI26 protein
220239_at		NM_018846	
200802_at		NM_006513	gb:NM_006513.1 /DEF=Homo sapiens seryl-tRNA synthetase (SARS), mRNA. /FEA=mRNA /GEN=SARS /PROD=seryl-tRNA synthetase /DB_XREF=gi:5730028 /UG=Hs.4888 seryl-tRNA synthetase /FL=gb:BC000716.1 gb:NM_006513.1
209165 at		AF083208	gb:AF083208.1 /DEF=Homo sapiens Che-1 mRNA, complete cds. /FEA=mRNA /PROD=Che-1 /DB_XREF=gi:5813798 /UG=Hs.16178 apoptosis antagonizing transcription factor /FL=gb:BC000591.1 gb:AF083208.1 gb:NM_012138.1
200804 at		NM 003217	gb:NM_003217.1 /DEF=Homo sapiens testis enhanced gene transcript (TEGT), mRNA. /FEA=mRNA /GEN=TEGT //PROD=testis enhanced gene transcript //DB_XREF=gi:4507432 /UG=Hs.74637 testis enhanced gene transcript (BAX inhibitor 1) /FL=gb:BC000916.1 ab:AF033095.1 ab:NM 003217.1
[Consensus includes gb:Al186739 /FEA=EST /DB_XREF=gi:3737377 /DB_XREF=est:qe79c01.x1 /CLONE=IMAGE:1745184 /UG=Hs.326416 Homo sapiens mRNA; cDNA DKFZp564H1916 (from clone
213032_at		AL110126	DKFZp564H1916)

Figure	Figure 7b Cont'd.			
			Homo sapiens, Similar to RIKEN cDNA 5530601119 gene, clone	
65630_at		AI742455	MGC:9743 IMAGE:3854028, mRNA, complete cds	Hs.28974
212230_at	RPS20	AL576654	ribosomal protein S20	Hs.8102
			gb:NM_022838.1 /DEF=Homo sapiens hypothetical protein	
			/PROD=hypothetical protein FLJ12969 /DB_XREF=gi:12383085	
			/UG=Hs.119699 hypothetical protein FLJ12969	
219335 at		NM_022838	-	
			gb:BC006230.1 /DEF=Homo sapiens, lysophospholipase-like,	
			clone MGC:10338, mRNA, complete cds. /FEA=mRNA	
			/PROD=lysophospholipase-like /DB_XREF=gi:13623260	
211026_s_at		BC006230	/FL=gb:BC006230.1	
			gb:BC001120.1 /DEF=Homo sapiens, lectin, galactoside-	
			binding, soluble, 3 (galectin 3), clone MGC:2058, mRNA,	
			complete cds. /FEA=mRNA /PROD=lectin, galactoside-binding,	
			soluble, 3(galectin 3) /DB_XREF=gi:12654570 /UG=Hs.621	
			lectin, galactoside-binding, soluble, 3 (galectin 3)	
			/FL=gb:M35368.1 gb:BC001120.1 gb:M57710.1 gb:M36682.1	
208949 s at		BC001120	gb:AB006780.1 gb:NM_002306.1	
201142 at	EIF2S1	AA577698	eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa	Hs.151777
			Consensus includes gb.AB028966.1 /DEF=Homo sapiens	
			mRNA for KIAA1043 protein, partial cds. /FEA=mRNA	
			/GEN=KIAA1043 /PROD=KIAA1043 protein	
215146 s at		AB028966	/DB XREF=gi:5689422 /UG=Hs.11390 KIAA1043 protein	
			gb:U97075.1 /DEF=Homo sapiens FLICE-like inhibitory protein	
			short form mRNA, complete cds. /FEA=mRNA /PROD=FLICE	
			like inhibitory protein short form /DB_XREF=gi:2253680	
			/UG=Hs.195175 CASP8 and FADD-like apoptosis regulator	
210563_x_at		U97075	/FL=gb:U97075.1	
			gb:AF119889.1 /DEF=Homo sapiens PRO2667 mRNA,	
			complete cds. /FEA=mRNA /PROD=PRO2667	
			/DB_XREF=gi:7770214 /UG=Hs.321170 Homo sapiens	
210718_s_at		AF119889	PRO2667 mRNA, complete cds /FL=gb:AF119889.1	
221989 at	RPL10	AW057781	ribosomal protein L10	Hs.77091

Lignie	rigule / D Colita.			
			gb:NM_005715.1 /DEF=Homo sapiens uronyl 2- sulfotransferase (1IST)_mRNA_/FFA=mRNA_/GFN=1JST	
			/PROD=uronyl 2-sulfotransferase /DB_XREF=gi:5032218	
205139 s at		NM 005715	/UG=Hs.134015 uronyl 2-sulfotransferase /FL=gb:AB020316.1	
_	MGC3035	AL040896	hypothetical protein MGC3035	Hs.22412
n			gb:NM_002567.1 /DEF=Homo sapiens prostatic binding	
			protein (PBP), mRNA. /FEA=mRNA /GEN=PBP	
			/PROD=prostatic binding protein /DB_XREF=gi:4505620	
			/UG=Hs.80423 prostatic binding protein /FL=gb:D16111.1	
205353_s_at		NM_002567		
			Consensus includes gb:Z24459 /DEF=H.sapiens MTCP1	
			gene, exons 2A to 7 (and joined mRNA) /FEA=mRNA_4	
			/DB_XREF=gi:2252491 /UG=Hs.3548 mature T-cell	
216862_s_at		Z24459	proliferation 1	
			gb:BC000533.1 /DEF=Homo sapiens, Similar to eukaryotic	
			translation initiation factor 3, subunit 8 (110kD), clone	
			MGC:8693, mRNA, complete cds. /FEA=mRNA	
			/PROD=Similar to eukaryotic translation initiationfactor 3,	
			subunit 8 (110kD) /DB_XREF=gi:12653522 /UG=Hs.4835	
			eukaryotic translation initiation factor 3, subunit 8 (110kD)	
210949_s_at		BC000533	/FL=gb:BC000533.1	
209445_x_at	FLJ10803	AI765280	hypothetical protein FLJ10803	Hs.8173
			Consensus includes gb:AJ130971.1 /DEF=Homo sapiens	
-			4. /FEA=mRNA /PROD=U2 snRNP-specific A protein	
			/DB_XREF=gi:3970726 /UG=Hs.80506 small nuclear	
215722_s_at		AJ130971	ribonucleoprotein polypeptide A	
			gb:BC004973.1 /DEF=Homo sapiens, signal transducer and	
			MGC:3649 mRNA complete cds. /FEA=mRNA /PROD=signal	
			transducer and activator of transcription6, interleukin-4	
			induced /DB_XREF=gi:13436385 /UG=Hs.181015 signal	
			transducer and activator of transcription 6, interleukin-4	***
201331 s at		BC004973	induced /FL=gb:BC004973.1 gb:NM_003153.1 gb:U16031.1	
1				

Lignie	rigule / D Cont a.			
			gb:M27877.1 /DEF=Homo sapiens HPF1 protein, complete	-
			/UG=Hs.305953 zinc finger protein 83 (HPF1)	
221645_s_at		M27877	/FL=gb:M27877.1	
Ť		AA195936	general transcription factor IIA, 2, 12kDa	Hs.76362
at	HNRPC	AA664258	heterogeneous nuclear ribonucleoprotein C (C1/C2)	Hs.182447
			gb:AF041209.1 /DEF=Homo sapiens midline 1 fetal kidney	
			isoform 2 (MID1) mRNA, complete cds. /FEA=mRNA	
			/GEN=MID1 /PROD=midline 1 fetal kidney isoform 2	
			/DB_XREF=gi:3462508 /UG=Hs.27695 midline 1 (OpitzBBB	
210694_s_at		AF041209	syndrome) /FL=gb:AF041209.1	
			gb:BC000389.1 /DEF=Homo sapiens, transmembrane 4	
			superfamily member 7, clone MGC:8437, mRNA, complete	
			cds. /FEA=mRNA /PROD=transmembrane 4 superfamily	
			member 7 /DB_XREF=gi:12653240 /UG=Hs.26518	
			transmembrane 4 superfamily member 7 /FL=gb:BC000389.1	
209263 x at		BC000389	gb:AF022813.1 gb:AF054841.1 gb:NM_003271.1	
-	ET	BE866585	hypothetical protein ET	Hs.73965
-	FLJ35827	AA478965	hypothetical protein FLJ35827	Hs.330379
			gb:NM_004106.1 /DEF=Homo sapiens Fc fragment of IgE,	
			high affinity I, receptor for; gamma polypeptide (FCER1G),	
			mRNA. /FEA=mRNA /GEN=FCER1G /PROD=Fc fragment of	
			IgE, high affinity I, receptorfor, gamma polypeptide precursor	
			/DB_XREF=gi:4758343 /UG=Hs.743 Fc fragment of IgE, high	
			affinity I, receptor for; gamma polypeptide /FL=gb:M33195.1	
204232_at		NM_004106	004106 gb:NM_004106.1	
			gb:BC003689.1 /DEF=Homo sapiens, high-mobility group	
			(nonhistone chromosomal) protein 17, clone MGC:5301,	
			mRNA, complete cds. /FEA=mRNA /PROD=high-mobility	
			group (nonhistone chromosomal)protein 17	
			/DB_XREF=gi:13277559 /UG=Hs.181163 high-mobility group	
((nonhistone chromosomal) protein 17 /FL=gb:BC003689.1	
208668_x_at		BC003689	lgb:M12623.1	

- Ligure	rigure / b Cont a.			
			gb:AF107405.1 /DEF=Homo sapiens pre-mRNA splicing factor (SFRS3) mRNA, complete cds. /FEA=mRNA /GEN=SFRS3 /PROD=pre-mRNA splicing factor	
208673 s at		AF107405	/DB_XREF=gi:5531903 /UG=Hs.167460 splicing factor, arginineserine-rich 3 /FL=gb:BC000914.1 gb:AF107405.1	
			gb:NM_000282.1 /DEF=Homo sapiens propionyl Coenzyme A	
			carboxylase, alpha polypeptide (PCCA), nuclear gene	
			encoding mitochondrial protein, mKNA. /rEA=mKNA //GEN=DCCA /DROD=Pronionyl-Coenzyme A carboxylase	
			alphapolypeptide precursor /DB_XREF=gi:4557832	,
			/UG=Hs.80741 propionyl Coenzyme A carboxylase, alpha	
203860_at		NM_000282	polypeptide /FL=gb:BC000140.1 gb:NM_000282.1	
			gb:NM_000177.1 /DEF=Homo sapiens gelsolin (amyloidosis,	
			Finnish type) (GSN), mRNA. /FEA=mRNA /GEN=GSN	
			/PROD=gelsolin (amyloidosis, Finnish type)	
			/DB_XREF=gi:4504164 /UG=Hs.290070 gelsolin (amyloidosis,	
200696_s_at		NM_000177	Finnish type) /FL=gb:NM_000177.1	
			gb:NM_020310.1 /DEF=Homo sapiens MAX binding protein	
			(MNT), mRNA. /FEA=mRNA /GEN=MNT /PROD=MAX	
			binding protein /DB_XREF=gi:9945317 /UG=Hs.25497 MAX	
204206_at		NM_020310	binding protein /FL=gb:NM_020310.1	
			gb:NM_000609.1 /DEF=Homo sapiens stromal cell-derived	
			factor 1 (SDF1), mRNA. /FEA=mRNA /GEN=SDF1	-
			/PROD=stromal cell-derived factor 1 /DB_XREF=gi:10834987	
			/UG=Hs.237356 stromal cell-derived factor 1	
203666_at		609000 MN	/FL=gb:NM_000609.1_gb:L36033.1_gb:U16752.1	
		- w- w	gb:NM_004553.1 /DEF=Homo sapiens NADH dehydrogenase	
			(ubiquinone) Fe-S protein 6 (13kD) (NADH-coenzyme Q	
			reductase) (NDUFS6), mRNA. /FEA=mRNA /GEN=NDUFS6	
	•		/PROD=NADH dehydrogenase (ubiquinone) Fe-S protein	
			6(13kD) (NADH-coenzyme Q reductase)	
			/DB_XREF=gi:4758791 /UG=Hs.49767 NADH dehydrogenase	
			(ubiquinone) Fe-S protein 6 (13kD) (NADH-coenzyme Q	
203606 at		NM 004553	reductase) /FL=gb:AF044959.1 gb:NM_004553.1	
221824 s at I	s at MGC26766	AA770170	hypothetical protein MGC26766	Hs.395949

Ligare	rigure / b Cont a.			
212640 at		C03C12/\V	ESTs, Weakly similar to T32252 hypothetical protein T15B7.2 -	He 400340
2 12040_at		70071 / 1	Caerior labulus elegans (Celegans)	13.400043
242500 24		VK026208	CONSCINCT MICROACS 90.7NV23250.1 7DLT FIGURE Saprens CDNA: FLJ21645 fis, clone COL08436. /FEA=mRNA	
2 12333 at		UNDEDESO	ab: BC003525.1 /DEF=Homo sapiens. Similar to Max. clone	
			MGC:10775, mRNA, complete cds. /FEA=mRNA	
			/PROD=Similar to Max /DB_XREF=gi:13097617	
209332_s_at		BC003525	/UG=Hs.42712 MAX protein /FL=gb:BC003525.1	
221971_x_at	MRIP2	BE672818	ARF GTPase-activating protein	Hs.356559
			gb:NM_003194.1 /DEF=Homo sapiens TATA box binding	
			protein (TBP), mRNA. /FEA=mRNA /GEN=TBP /PROD=TATA	
			box binding protein /DB_XREF=gi:4507378 /UG=Hs.1100	
			TATA box binding protein /FL=gb:M34960.1 gb:M55654.1	
203135_at		NM_003194		
			gb:AB020980.1 /DEF=Homo sapiens mRNA for putative	
			membrane protein, complete cds. /FEA=mRNA	
			/PROD=membrane protein /DB_XREF=gi:6467174	
			/UG=Hs.93832 putative membrane protein /FL=gb:BC000104.1	-
208716_s_at		AB020980	gb:AB020980.1	
			gb:NM_024624.1 /DEF=Homo sapiens hypothetical protein	
			FLJ22116 (FLJ22116), mRNA. /FEA=mRNA /GEN=FLJ22116	
			/PROD=hypothetical protein FLJ22116 /DB_XREF=gi:13375847	
			/UG=Hs.34497 hypothetical protein FLJ22116	
218781_at		NM_024624	/FL=gb:AL136544.1 gb:NM_024624.1	
			gb:BC003080.1 /DEF=Homo sapiens, Similar to HSPC171	
			protein, clone MGC:770, mRNA, complete cds. /FEA=mRNA	
			/PROD=Similar to HSPC171 protein /DB_XREF=gi:13111781	
221597_s_at		BC003080	/UG=Hs.279593 HSPC171 protein /FL=gb:BC003080.1	
212848_s_at	FLJ14675	BG036668	hypothetical protein FLJ14675	Hs.334790
			gb.AF176704.1 /DEF=Homo sapiens F-box protein FBX9	
			mRNA, complete cds. /FEA=mRNA /PROD=F-box protein	
			FBX9	
[210638_s_at		AF176704	protein 9 /FL=gb:AF176704.1	

355				
202522 at		AI 031591	Consensus includes gb:AL031591 /DEF=Human DNA sequence from clone RP3-353E16 on chromosome 22q11.22-12.3 Contains the 5 part of the MN1 gene for meningioma (disrupted in balanced translocation) 1, the PITPNB gene for phosphatidylinositol transfer protein beta, ESTs, STSs, GSSs and /FEA=mRNA /DB_XREF=gi:6006484 /UG=Hs.7370 phosphotidylinositol transfer protein, beta /FL=gb:D30037.1	
	TNRC15	AL045800	trinucleotide repeat containing 15	Hs.323317
218700 s at		BC002585	gb:BC002585.1 /DEF=Homo sapiens, RAB7, member RAS oncogene family-like 1, clone MGC:1653, mRNA, complete cds. /FEA=mRNA /PROD=RAB7, member RAS oncogene family-like 1 /DB_XREF=gi:12803516 /UG=Hs.115325 RAB7, member RAS oncogene family-like 1 /FL=gb:BC002585.1 gb:NM_003929.1	
201647 s at		NM 005506		
201744_s_at		NM_002345	gb:NM_002345.1 /DEF=Homo sapiens lumican (LUM), mRNA. /FEA=mRNA /GEN=LUM /PROD=lumican /DB_XREF=gi:4505046 /UG=Hs.79914 lumican /FL=gb:NM_002345.1 gb:U18728.1 gb:U21128.1	
201417_at		NM_003107		

Figure	Figure / D Cont a.			200100	0000
160020_at	MMP14	Z48481	matrix metalloproteinase 14 (membrane-inserted)	NM 004995 Hs.2399	Hs.2399
			Consensus includes gb:AK001487.1 /DEF=Homo sapiens cDNA FLJ10625 fis, clone NT2RP2005540, highly similar to Homo sapiens mRNA for KIAA0494 protein. /FEA=mRNA		
201776_s_at		AK001487	product /FL=gb:BC002525.1 gb:AB007963.1 gb:NM_014774.1		
			Consensus includes gb:AL137673.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434H0872 (from clone		
216652 s at		AL137673	DKFZp434H0872).		
			gb:NM_005113.1 /DEF=Homo sapiens golgi autoantigen,		
			goigin subiariliy a, 5 (GOLGA5), rinkiya. /rEA-ilikiya. /GEN=GOLGA5 /PROD=golgi autoantigen, golgin subfamily a,		
			5 /DB_XREF=gi:4826747 /UG=Hs.241572 golgi autoantigen,		
ఠ		NM 005113			11- 46400
ال		AI348935			HS 22450
28/80_s_at	FLJ1035/	K42449	nypotrietical protein r.LJ 10337		13.55
			gb:NM_006644.1 /DEF=Homo sapiens heat shock 105kD (HSP105B), mRNA. /FEA=mRNA /GEN=HSP105B		
			/PROD=heat shock 105kD /DB_XREF=gi:5729878		
•		ANA OOGEAA	/UG=Hs.36927 heat shock 105kD /FL=gb:AB003333.1		
2009/0 s at		##0000 ININI	db:NM 018691.1 /DEF=Homo sapiens chromosome 5 open		
			/GEN=C5ORF3 /PROD=hypothetical protein		
			/DB_XREF=gi:8922068 /UG=Hs.166551 chromosome 5 open		
218588_s_at		NM_018691	reading frame 3 /FL=gb:NM 018691.1		
			gb:U46837.1 /DEF=Human RNA polymerase II holoenzyme		-
		-	component SRB7 (SRB7) mRNA, complete cds. /FEA=mRNA		
			/GEN=SKB/ /PKOD=SKB/ /DB_XKEF=g:119/662		
			/UG=Hs.286145 SRB7 (suppressor of RNA polymerase B,		
20000		1146037	yeast) homolog /FL=gb:U46837.1 gb:U52960.1		
209303 s at		040037	gb:nw _004264.		

MM_002475 KEO4 AL568449 MM_003096 MM_016127 MM_016127 MM_0003398	2				
at NM 002475 KEO4 AL568449 NM 003096 NM 016127 BC003398 at BC003398				gb:NM_002475.1 /DEF=Homo sapiens myosin, light polypeptide 1, alkali; skeletal, fast (MYL1), mRNA.	
at NM 002475 KEO4 AL568449 NM 003096 NM 016127 BC003398			_	/FEA=mRNA /GEN=MYL1 /PROD=myosin, light polypeptide 1,	
at NM_002475 AL568449 at NM_003096 BC003398 at NM_000917				alkali; skeletal,fast /DB_XREF=gi:4505302 /UG=Hs.90318	
at NM_002475 KEO4 AL568449 NM_003096 NM_016127 BC003398 At BC003398					
HEO4 AL568449 at NM_003096 at NM_016127 at BC003398 at NM_000917	204173_at		-	/FL=gb:M31211.1 gb:NM_002475.1	
at NM_003096 at NM_016127 at BC003398 at NM_000917		KEO4	AL568449		Hs.285818
at NM_003096 at BC003398 at NM_00917				gb:NM_003096.1 /DEF=Homo sapiens small nuclear	
at NM_003096 at NM_016127 at BC003398 at NM_000917				ribonucleoprotein polypeptide G (SNRPG), mRNA.	
at NM_003096 at NM_016127 at BC003398 at NM_000917				/FEA=mRNA /GEN=SNRPG /PROD=small nuclear	
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at NM_003096 at NM_016127 at BC003398 at NM_000917				/UG=Hs.77496 small nuclear ribonucleoprotein polypeptide G	
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AUG=HS.279921 HSPC035 protein /FL=gb:AF100748.1 NM_016127 gb:BC003398.1 /DEF=Homo sapiens, hypothetical protein FLJ10788, clone MGC:4929, mRNA, complete cds. //FEA=mRNA /PROD=hypothetical protein FLJ10788 /DB_XREF=gi:13097287 /UG=Hs.196437 hypothetical protein FLJ10788 /FL=gb:AB016839.1 gb:BC003398.1 BC003398 gb:NM_018221.1 gb:NG003398.1 gb:NM_000917.1 /DEF=Homo sapiens procollagen-proline, oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide I (P4HA1), mRNA. /FEA=mRNA /GEN=P4HA1 /PROD=procollagen-proline, 2-oxoglutarate4-dioxygenase (proline 4-hydroxylase), alpha polypeptide I /DB_XREF=gi:4505564 /UG=Hs.76768 procollagen-proline, oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide I /FL=gb:MZ4486.1 gb:NM_000917.1				/PROD=HSPC035 protein /DB_XREF=gi:7706384	
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/FEA=mRNA /PROD=hypothetical protein FLJ10788 /DB_XREF=gi:13097287 /UG=Hs.196437 hypothetical proteing				FLJ10788, clone MGC:4929, mRNA, complete cds.	
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oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide I (P4HA1), mRNA. /FEA=mRNA /GEN=P4HA1 /PROD=procollagen-proline, 2-oxoglutarate4-dioxygenase (proline 4-hydroxylase), alpha polypeptide //DB_XREF=gi:4505564 /UG=Hs.76768 procollagen-proline, oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha alpha //FL=gb:M24486.1 gb:NM_000917.1					
polypeptide I (P4HA1), mRNA. /FEA=mRNA /GEN=P4HA1 /PROD=procollagen-proline, 2-oxoglutarate4-dioxygenase (proline 4-hydroxylase), alpha polypeptide1 //DB_XREF=gi:4505564 /UG=Hs.76768 procollagen-proline, oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha at NM_000917 polypeptide I /FL=gb:M24486.1 gb:NM_000917.1				oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha	
/PROD=procollagen-proline, 2-oxoglutarate4-dioxygenase (proline 4-hydroxylase), alpha polypeptidel /DB_XREF=gi:4505564 /UG=Hs.76768 procollagen-proline, oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha at NM_000917 polypeptide 1 /FL=gb:M24486.1 gb:NM_000917.1				polypeptide I (P4HA1), mRNA. /FEA=mRNA /GEN=P4HA1	
(proline 4-hydroxylase), alpha polypeptidel //DB_XREF=gi:4505564 /UG=Hs.76768 procollagen-proline, oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha at NM_000917 polypeptide 1 /FL=gb:M24486.1 gb:NM_000917.1				/PROD=procollagen-proline, 2-oxoglutarate4-dioxygenase	
/DB_XREF=gi:4505564 /UG=Hs.76768 procollagen-proline, oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha at NM_000917 polypeptide 1 /FL=gb:M24486.1 gb:NM_000917.1				(proline 4-hydroxylase), alpha polypeptidel	
at NM_000917					
_at					
	207543_s_at		_ iI		

21281	galorino contra.			
			gb:BC000305.1 /DEF=Homo sapiens, caspase 6, apoptosis- related cysteine protease, clone MGC:8388, mRNA, complete	
			cds. /FEA=mRNA /PROD=caspase 6, apoptosis-related	
		_	cysteine protease /Ub_AREF=gl.12000070 /UG=ns.0200	
			// / / / / / / / / / / / / / / / / / /	
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			Consensus includes gb:AL050040.1 /DEF=Homo sapiens	
			mRNA; cDNA DKFZp566K0524 (from clone	
			DKFZp566K0524); partial cds. /FEA=mRNA	
			/GEN=DKFZp566K0524 /PROD=hypothetical protein	
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215172_at		AL050040	protein	
213365_at	KIAA1504	N64622	KIAA1504 protein	Hs.157426
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			gb:NM_003010.1 /DEF=Homo sapiens mitogen-activated	
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			/GEN=MAP2K4 /PROD=mitogen-activated protein kinase	
			kinase 4 /DB_XREF=gi:4506888 /UG=Hs.75217 mitogen-	
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			gb:NM_022154.1 /DEF=Homo sapiens up-regulated by BCG-	
			CWS (LOC64116), mRNA. /FEA=mRNA /GEN=LOC64116	
			/PROD=up-regulated by BCG-CWS /DB_XREF=gi:11545899	
			/UG=Hs.284205 up-regulated by BCG-CWS	
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			gb:NM_002414.1 /DEF=Homo sapiens antigen identified by	
			monoclonal antibodies 12E7, F21 and O13 (MIC2), mRNA.	
			/FEA=mRNA /GEN=MIC2 /PROD=antigen identified by	
			monoclonal antibodies12E7, F21 and O13	
			/DB_XREF=gi:4505182 /UG=Hs.177543 antigen identified by	
			monoclonal antibodies 12E7, F21 and O13	
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201029_s_at		NM 0024 14		

21861	igaic / D Colleg.			
			gb:NM_006070.1 /DEF=Homo sapiens TRK-fused gene (TFG), mRNA. /FEA=mRNA /GEN=TFG /PROD=TRK-fused	
217839_at		NM_006070		
			gb:NM_005765.1 /DEF=Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) membrane	
-			sector associated protein M8-9 (APT6M8-9), mRNA.	
			/FEA=mRNA /GEN=APT6M8-9 /PROD=ATPase, H+	
			transporting, lysosomal (vacuolarproton pump) membrane	
			sector associated protein M8-9 /DB_XREF=gi:5031590	
			/UG=Hs.183434 ATPase, H+ transporting, lysosomal	
		,	(vacuolar proton pump) membrane sector associated protein	
201444 s_at		NM_005765		
			gb:NM_021813.1 /DEF=Homo sapiens BTB and CNC	
			homology 1, basic leucine zipper transcription factor 2	
			(BACH2), mRNA. /FEA=mRNA /GEN=BACH2 /PROD=BTB	
			and CNC homology 1, basic leucine zippertranscription factor	
221234_s_at		NM_021813	2 /DB_XREF=gi:13540489 /FL=gb:NM_021813.1	
45633_at F	FLJ13912	AI421812	hypothetical protein FLJ13912	Hs.404434
213937_s_at F	FTSJ1	AV723177	FtsJ homolog 1 (E. coli)	Hs.23170
			gb.AF191492.1 /DEF=Homo sapiens nasopharyngeal	
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			complete cds. /FEA=mRNA /GEN=NAG8	
			/PROD=nasopharyngeal carcinoma associated geneprotein-8	
			/DB_XREF=gi:11065903 /UG=Hs.26937 brain and	
			nasopharyngeal carcinoma susceptibility protein	
210109_at		AF191492	/FL=gb:AF191492.1	
			gb:NM_003927.2 /DEF=Homo sapiens methyl-CpG binding	,
			domain protein 2 (MBD2), transcript variant 1, mRNA.	
			/FEA=mRNA /GEN=MBD2 /PROD=methyl-CpG binding	
			domain protein 2, isoform 1 /DB_XREF=gi:7710146	
7000		700000	/UG=Hs.25674 methyl-CpG binding domain protein 2	-
202485_S_at		ININ_003927	//FL=gb:Aru/zz4z:1 gb:nivi	

_		_	_				_		_			_						_	_		_	_			_	_					_
			-																				Hs.12773								Hs. 78202
	gb:BC003633.1 /DEF=Homo sapiens, translocase of outer mitochondrial membrane 70 (yeast) homolog A, clone	MGC:3766, mRNA, complete cds. /FEA=mRNA	/PROD=translocase of outer mitochondrial membrane	70(yeast) homolog A /DB_XREF=gi:13177705 /UG=Hs.21198	translocase of outer mitochondrial membrane 70 (yeast)	homolog A /FL=gb:BC003633.1 gb:AB018262.1	gb:NM_014820.1	gb:NM_003332.1 /DEF=Homo sapiens TYRO protein tyrosine	kinase binding protein (TYROBP), mRNA. /FEA=mRNA	/GEN=TYROBP /PROD=TYRO protein tyrosine kinase binding	protein /DB_XREF=gi:4507754 /UG=Hs.9963 TYRO protein	tyrosine kinase binding protein /FL=gb:AF019562.1		Consensus includes gb:AB014608.1 /DEF=Homo sapiens	mRNA for KIAA0708 protein, partial cds. /FEA=mRNA	/GEN=KIAA0708 /PROD=KIAA0708 protein	/DB_XREF=gi:3327229 /UG=Hs.117177 KIAA0708 protein	gb:BC004191.1 /DEF=Homo sapiens, dynactin 4, clone	MGC:3248, mRNA, complete cds. /FEA=mRNA	//PROD=dynactin 4 /DB_XREF=gi:13278857 /UG=Hs.111429	Homo sapiens, dynactin 4, clone MGC:3248, mRNA,	complete cds /FL=gb:BC004191.1	acyl-Coenzyme A oxidase 3, pristanoyl	gb:AB026730.1 /DEF=Homo sapiens B3GALT4 mRNA for	beta-1,3-galactosyltransferase-4, complete cds. /FEA=mRNA	//GEN=B3GALT4 /PROD=beta-1,3-galactosyltransferase-4	/DB_XREF=gi:6683013 /UG=Hs.21495 UDP-Gal:betaGlcNAc	beta 1,3-galactosyltransferase, polypeptide 4	/FL=gb:AF063595.1 gb:NM_003782.1 gb:AB026730.1	SWI/SNF related, matrix associated, actin dependent regulator of	chromatin, subfamily a, member 4
							BC003633						NM_003332				AB014608					BC004191	BF055171						AB026730		Al831675
riguie / D Corit a.																							ACOX3								SMARCA4
Ligure							201512_s_at						204122_at				213204_at					209232_s_at	204241_at						210205 at		213720_s_at

_				_			
				Hs.808			
						-	
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	NM_000178	NM 020958	e1 i	A1591354	NM_003202	NM_002198	NM_007064
igaic 12 contra:				HNRPF			
Sing.	201415 at	220672 at	218040_at	201376_s_at	205255_x_at	202531_at	206078 at

							$\overline{}$		- 1				
										Hs.23263			
gb:AF180527.1 /DEF=Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds. /FEA=mRNA /GEN=DOKDEL	/PROD=p22Dokdel /DB_XREF=gi:6606314 /UG=Hs.103854 docking protein 1, 62kD (downstream of tyrosine kinase 1) /FL=ab:AF180527.1	gb:NM_030968.1 /DEF=Homo sapiens G protein coupled receptor interacting protein, complement-c1q tumor necrosis	factor-related (ZSIG37), mRNA. /FEA=mRNA /GEN=ZSIG37 /PROD=G protein coupled receptor interacting protein complement-c1a tumor necrosis factor-related	030968 //DB_XREF=gi:13569943 /FL=gb:NM_030968.1	gb:NM_007046.1 /DEF=Homo sapiens elastin microfibril interface located protein (EMILIN), mRNA. /FEA=mRNA			gb:NM_025013.1 /DEF=Homo sapiens KIAA1031 protein (KIAA1031), mRNA. /FEA=mRNA /GEN=KIAA1031 /PROD=hypothetical protein FLJ13787 /DB_XREF=gi:13430879	/UG=Hs.25347 KIAA1031 protein /FL=gb:NM_025013.1	KIAA0350 protein	gb:NM_001965.1 /DEF=Homo sapiens early growth response 4 (EGR4), mRNA. /FEA=mRNA /GEN=EGR4 /PROD=early growth response 4 /DB_XREF=gi:4503494 /UG=Hs.3052 early growth response 4 /FL=gb:NM_001965.1		/GEN=DKFZp434H0350 /PROD=nypotnetical protein //DB XREF=qi:5912039 /UG=Hs.173571 KIAA1053 protein
	AF180527			NM_030968		97 OZ OZ OZ OZ OZ OZ OZ OZ OZ OZ OZ OZ OZ	NIVI 007040		NM_025013	AA731693	NM 001965	II.	AL117523
										KIAA0350			
	211121 s at	\		220975_s_at		2.00	2041b3_at		206169_x_at	212786_at	207767 s at	}	215495 s at

ainfil	riguie / D Colling.		
			gb:NM_000308.1 /DEF=Homo sapiens protective protein for
			Deta-galactosidase (galactosialidosis) (PPGD), IIIRNA. /FEA=mRNA /GEN=PPGB /PROD=protective protein for beta-
			galactosidase /DB_XREF=gi:4505988 /UG=Hs.118126
70000			protective protein for beta-galactosidase (galactosialidosis)
Z00001_at		NINI DODOSOO	JUUSUS I/FL=gp:BCUUUS97.1 gp:WIZZ96U.1 gp:NM_UUUSUS.1
			Beta (RARR) mRNA /FFA=mRNA /GEN=RARR
			//PROD=retinoic acid receptor. beta /DB XREF=ai:4506420
			//UG=Hs.171495 retinoic acid receptor, beta
205080_at		NM_000965	000965 /FL=gb:NM_000965.1
			gb:NM_004878.1 /DEF=Homo sapiens prostaglandin E
			synthase (PTGES), mRNA. /FEA=mRNA /GEN=PTGES
			/PROD=prostaglandin E synthase /DB_XREF=gi:4758909
			/UG=Hs.146688 prostaglandin E synthase /FL=gb:AF027740.1
207388_s_at		NM_004878	
			gb:NM 016418.1 /DEF=Homo sapiens clone FLB5214
			(LOC51219), mRNA. /FEA=mRNA /GEN=LOC51219
			/PROD=clone FLB5214 /DB_XREF=gi:9994194 /UG=Hs.5486
218915 at		NM 016418	clone FLB5214 /FL=gb:AF113694.1 gb:NM_016418.1
		J	gb:AF262032.1 /DEF=Homo sapiens MAB21L2 protein
			/GEN=MAB21L2 /PROD=MAB21L2 protein
			/DB_XREF=gi:9964006 /UG=Hs.251390 mab-21 (C. elegans)-
210302_s_at		AF262032	like 2 /FL=gb:NM_006439.2 gb:AF262032.1
			gb:NM_025165.1 /DEF=Homo sapiens hypothetical protein
			FLJ22637 (FLJ22637), mRNA. /FEA=mRNA /GEN=FLJ22637
			/PROD=hypothetical protein FLJ22637 /DB_XREF=gi:13376767
			/UG=Hs.296178 hypothetical protein FLJ22637
219518_s_at		NM_025165	/FL=gb:NM_025165.1
			gb:NM_000096.1 /DEF=Homo sapiens ceruloplasmin
			(ferroxidase) (CP), mRNA. /FEA=mRNA /GEN=CP
			/PROD=ceruloplasmin (ferroxidase) /DB_XREF=gi:4557484
,		1	/UG=Hs.296634 ceruloplasmin (ferroxidase) /FL=gb:M13699.1
204846_at		NM_000096	NM_000096 gb:NM_000096.1

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218986_s_at		NM_017631	gb:NM_017631.1 /DEF=Homo sapiens hypothetical protein FLJ20035 (FLJ20035), mRNA. /FEA=mRNA /GEN=FLJ20035 /PROD=hypothetical protein FLJ20035 /DB_XREF=gi:8923037 /UG=Hs.109309 hypothetical protein FLJ20035	
219697_at		NM_006043	gb:NM_006043.1 /DEF=Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 2 (HS3ST2), mRNA. /FEA=mRNA /GEN=HS3ST2 /PROD=heparan sulfate D-glucosaminyl3-O-sulfotransferase 2 /DB_XREF=gi:5174462 /UG=Hs.115830 heparan sulfate (glucosamine) 3-O-sulfotransferase 2 /FL=gb:AF105374.1 gb:AF105375.1	
211795_s_at		AF198052	gb:AF198052.1 /DEF=Homo sapiens EVH1 domain binding protein mRNA, complete cds. /FEA=CDS /PROD=EVH1 domain binding protein /DB_XREF=gi:7416992 /UG=Hs.58435 FYN-binding protein (FYB-120130) /FL=gb:AF198052.1	
205111_s_at		NM_016341	gb:NM_016341.1 /DEF=Homo sapiens pancreas-enriched phospholipase C (LOC51196), mRNA. /FEA=mRNA /GEN=LOC51196 /PROD=pancreas-enriched phospholipase C /DB_XREF=gi:7705940 /UG=Hs.6733 pancreas-enriched phospholipase C /FL=gb:AF190642.2 gb:AF117948.1 gb:NM_016341.1	
208124 s. at		NM_004263	gb:NM_004263.1 /DEF=Homo sapiens sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4F (SEMA4F), mRNA. /FEA=mRNA /GEN=SEMA4F /PROD=semaphorin W /DB_XREF=gi:4759093 /UG=Hs.25887 sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4F /FL=gb:AB022317.1 gb:NM_004263.1	
220422 <u>a</u> t	-	NM_017481	gb:NM_017481.1 /DEF=Homo sapiens ubiquilin 3 (UBQLN3), mRNA. /FEA=mRNA /GEN=UBQLN3 /PROD=ubiquilin 3 /DB_XREF=gi:8567417 /UG=Hs.189184 ubiquilin 3 017481 /FL=gb:AF230481.1 gb:NM_017481.1	

Figure	rigure / b Cont a.				
			gb:NM_024988.1 /DEF=Homo sapiens hypothetical protein FLJ12355 (FLJ12355) mRNA /FEA=mRNA /GEN=FLJ12355		
, , , , , , , , , , , , , , , , , , ,		0000	/PROD=hypothetical protein FLJ12355 /DB_XREF=gi:13376491 /UG=Hs.287521 hypothetical protein FLJ12355		
220465_at		NIVI_024988	/FL=gb:NM_024988.1		
			gb:NM_004265.1 /DEF=Homo sapiens delta-6 fatty acid desaturase (FADSD6), mRNA. /FEA=mRNA /GEN=FADSD6		
			/PROD=delta-6 fatty acid desaturase /DB_XREF=gi:4758333		
202218 s at		NM 004265	/UG=Hs.184641 fatty acid desaturase 2 /FL=gb:AF084559.1 gb:AF126799.1 gb:NM_004265.1		
			gb:NM_014226.1 /DEF=Homo sapiens renal tumor antigen		
			(RAGE), mRNA. /FEA=mRNA /GEN=RAGE /PROD=renal		
			tumor antigen /DB_XREF=gi:7657497 /UG=Hs.104119 renal		
205130_at		NM_014226	014226 tumor antigen /FL=gb:AB022694.1 gb:NM_014226.1		
			gb:NM_022774.1 /DEF=Homo sapiens hypothetical protein		
			FLJ21144 (FLJ21144), mRNA. /FEA=mRNA /GEN=FLJ21144		
			/PROD=hypothetical protein FLJ21144 /DB_XREF=gi:12232456		
219567_s_at		NM_022774	/FL=gb:NM_022774.1		
at	23	AW136988	KIAA0923 protein		Hs.22587
at	ESPL1	D79987	extra spindle poles like 1 (S. cerevisiae)	NM_012291	Hs.153479
)t		AI862454	PAP-1 binding protein		Hs.404884
			gb:NM_001640.2 /DEF=Homo sapiens N-acylaminoacyl-		
			peptide hydrolase (APEH), mRNA. /FEA=mRNA /GEN=APEH		
			/PROD=N-acylaminoacyl-peptide hydrolase		
			/DB_XREF=gi:9951916 /UG=Hs.78223 N-acylaminoacyl-peptide		
			hydrolase /FL=gb:BC000362.1 gb:BC001826.1 gb:J03068.1		
201284_s_at		NM_001640			
			gb:NM_018256.1 /DEF=Homo sapiens hypothetical protein		
			FLJ10881 (FLJ10881), mRNA. /FEA=mRNA /GEN=FLJ10881		
	_		/PROD=hypothetical protein FLJ10881 /DB_XREF=gi:8922736		
			/UG=Hs.73291 hypothetical protein FLJ10881		
218512_at		NM_018256	/FL=gb:AF242546.1 gb:NM_018256.1		

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			gb:NM_012430.1 /DEF=Homo sapiens sec22 homolog	
-			(SEC22A), mKNA. /FEA=mKNA /GEN=SEC22A	
			//PKUD=sec22_nomolog_/DB_XREF=gl:691264/ ///C=uc_182666_cec/2_homolog_/E1_ak:8E100746_1	
218703 at		NM_012430	12430 gb:NM 012430.1	
			Consensus includes gb:BE964689 /FEA=EST	
			/DB_XREF=gi:11768267	
			/CLONE=IMAGE:3885630 /UG=Hs.108104 ubiquitin-conjugating	
200683_s_at		NM_003347	enzyme E2L 3 /FL=gb:NM_003347.1	
			gb:NM_017742.1 /DEF=Homo sapiens hypothetical protein	
			FLJ20281 (FLJ20281), mRNA. /FEA=mRNA /GEN=FLJ20281	
			/PROD=hypothetical protein FLJ20281 /DB_XREF=gi:8923259	
			/UG=Hs.18800 hypothetical protein FLJ20281	
219062_s_at		NM_017742	_	
			gb:M73069.1 /DEF=Human androgen receptor mutant gene,	
-			mRNA, complete cds. /FEA=mRNA /GEN=AR	
			/PROD=androgen receptor /DB_XREF=gi:178655	
211621_at		M73069	/FL=gb:M73069.1	
			gb:NM_016605.1 /DEF=Homo sapiens putative nuclear	
			protein (LOC51307), mRNA. /FEA=mRNA /GEN=LOC51307	
			/PROD=putative_nuclear_protein /DB_XREF=gi:7706138	
			/UG=Hs.102469 putative nuclear protein /FL=gb:AF251040.1	
218023_s_at		NM_016605	_	
			gb:NM_017948.1 /DEF=Homo sapiens hypothetical protein	
			FLJ20736 (FLJ20736), mRNA. /FEA=mRNA /GEN=FLJ20736	
			/PROD=hypothetical protein FLJ20736 /DB_XREF=gi:8923662	
			/UG=Hs.48712 hypothetical protein FLJ20736	_
218244_at		NM_017948		
			gb:NM_016245.1 /DEF=Homo sapiens retinal short-chain	
			dehydrogenasereductase retSDR2 (LOC51170), mRNA.	
			/FEA=mRNA /GEN=LOC51170 /PROD=retinal short-chain	
			dehydrogenasereductaseretSDR2 /DB_XREF=gi:7705904	
			/UG=Hs.12150 retinal short-chain dehydrogenasereductase	
217989_at		NM_016245	NM_016245 retSDR2 /FL=gb:AF126780.1 gb:NM_016245.1	
211982_x_at KIAA0370	KIAA0370	AL546600		Hs.392793

rigure	rigure / a Cont a.				
			gb:NM_018135.1 /DEF=Homo sapiens hypothetical protein FLJ10548 (FLJ10548), mRNA. /FEA=mRNA /GEN=FLJ10548 /PROD=hypothetical protein FLJ10548 /DB_XREF=gi:8922510		- · · · · · · · · · · · · · · · · · · ·
218385 at		NM_018135	/UG=Hs.9622 hypothetical protein FLJ10548 /FL=gb:NM_018135.1		
			gb:NM_018234.1 /DEF=Homo sapiens hypothetical protein	!	
			FLJ10829 (FLJ10829), mRNA.		
			/UG=Hs.57655 hypothetical protein FLJ10829		
218424_s_at		NM_018234	/FL=gb:NM_018234.1		
74694_s_at	FLJ23282		hypothetical protein FLJ23282		Hs. 170253
			gb:NM_000801.1 /DEF=Homo sapiens FK506-binding protein		
			1A (12kD) (FKBP1A), mRNA. /FEA=mRNA /GEN=FKBP1A		
			/PROD=FK506-binding protein 1A (12kD)	-	
			/DB_XREF=gi:4503724 /UG=Hs.752 FK506-binding protein 1A		
200709 at		NM 000801	(12kD) /FL=gb:BC001925.1 gb:M34539.1 gb:NM_000801.1		
221898 at	T1A-2	BF337209	lung type-I cell membrane-associated glycoprotein		Hs.135150
			gb:NM_000484.1 /DEF=Homo sapiens amyloid beta (A4)	_	
			precursor protein (protease nexin-II, Alzheimer disease)		
			(APP), mRNA. /FEA=mRNA /GEN=APP /PROD=amyloid beta	-	
			(A4) precursor protein (proteasenexin-II, Alzheimer disease)		
			/DB_XREF=gi:4502166 /UG=Hs.177486 amyloid beta (A4)		
			precursor protein (protease nexin-II, Alzheimer disease)		
200602_at		NM_000484	/FL=gb:NM_000484.1		
37232 at	TIMM9	AB011158	translocase of inner mitochondrial membrane 9 homolog (yeast) NM_0	NM_014749	Hs.77724
at	85	A1858000	hypothetical protein FLJ10385		Hs.30922
			gb:BC006337.1 /DEF=Homo sapiens, clone MGC:12798, mRNA_complete_cds_/FEA=mRNA_/PROD=Unknown (protein)		
211047 × at		BC006337	for MGC:12798) /DB_XREF=gi:13623468 /FL=gb:BC006337.1		
			gb:NM_024322.1 /DEF=Homo sapiens hypothetical protein		
			MGC11266 (MGC11266), MRNA. /FEA=MRNA /OENI=MGC11266 /DBOD=bysothetical protein MGC11266		
			// VEEX = INCO / FIXOD-11/Pourerical Protein INCO / IZOO /		
219472 at		NM 024322	MGC11266 /FL=gb:BC002870.1 gb:NM_024322.1		

Lignie	rigule / D Colit a.			
			gb:NM_030798.1 /DEF=Homo sapiens hypothetical protein DKFZp434D0421 (DKFZP434D0421), mRNA. /FEA=mRNA	
			/GEN=DKFZP434D0421 /PROD=hypothetical protein DKFZp434D0421 /DR_XRFF=qi:13540581	-
221247 s at		NM_030798		
			gb:BC002356.1 /DEF=Homo sapiens, nucleobindin 1, clone	
			MGC:8479, mRNA, complete cds. /FEA=mRNA	_
	-		/PROD=nucleobindin 1 /DB_XREF=gi:12803104	
			/UG=Hs.172609 nucleobindin 1 /FL=gb:BC002356.1	
200649_at		BC002356	gb:M96824.1 gb:NM_006184.1	
59631_at		AI247566	thioredoxin reductase 2	Hs.20030
213306 at	MPDZ	AA917899	multiple PDZ domain protein	Hs.169378
213754 s at	PAIP1	AW613203	polyadenylate binding protein-interacting protein 1	Hs.109643
			Consensus includes gb:NM_006211.1 /DEF=Homo sapiens	
			proenkephalin (PENK), mRNA. /FEA=CDS /GEN=PENK	
			/PROD=proenkephalin /DB_XREF=gi:5453875 /UG=Hs.93557	
213791_at		NM_006211	proenkephalin /FL=gb:NM_006211.1	
			Consensus includes gb:AL050199.1 /DEF=Homo sapiens	
			mRNA; cDNA DKFZp586D0923 (from clone	
			DKFZp586D0923). /FEA=mRNA /DB_XREF=gi:4884438	
			/UG=Hs.62669 Homo sapiens mRNA; cDNA	
213853_at		AL050199	DKFZp586D0923 (from clone DKFZp586D0923)	
213246_at	DKFZP564F1123	AI346504	DKFZP564F1123 protein	Hs.275352
×at	DJ328E19.C1.1	BE299495	hypothetical protein DJ328E19.C1.1	Hs.323463
213729_at	FNBP3	Z78308	formin binding protein 3	Hs.107213
			Consensus includes gb:AI749193 /FEA=EST	
			/DB_XREF=gi:5127457 /DB_XREF=est:at40e04.x1	
			/CLONE=IMAGE:2374494 /UG=Hs.17639 Homo sapiens	_
212403_at		AL096740	ubiquitin protein ligase (UBE3B) mRNA, partial cds	
			ESTs, Highly similar to putative human HLA class II associated	
			protein I; cerebellar leucine rich acidic nuclear protein [Homo	
201038_s_at		BE560202	sapiens] [H.sapiens]	Hs.356089
217901_at	DSG2	BF031829	desmoglein 2	Hs.359784

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221688_s_at		AL136913	gb:AL136913.1 /DEF=Homo sapiens mRNA; cDNA DKFZp586L0118 (from clone DKFZp586L0118); complete cds. /FEA=mRNA /GEN=DKFZp586L0118 /PROD=hypothetical protein /DB_XREF=gi:12053320 /UG=Hs.6118 hypothetical protein FLJ10968 /FL=gb:AL136913.1	
216092_s_at		AL365347	Consensus includes gb:AL365347.1 /DEF=Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 298948. /FEA=mRNA /DB_XREF=gi:9187134 /UG=Hs.22891 solute carrier family 7 (cationic amino acid transporter, y+ system), member 8	
214293_at	FLJ10849	AI539361	hypothetical protein FLJ10849	Hs.8768
212093_s_at		AL096842	Consensus includes gb:Al695017 /FEA=EST /DB_XREF=gi:4982917 /DB_XREF=est:we45d07.x1 /CLONE=IMAGE:2344045 /UG=Hs.7946 KIAA1288 protein	
214722_at		AW516297	ESTs, Weakly similar to hypothetical protein FLJ20378 [Homo sapiens] [H.sapiens]	Hs.408543
214109_at	LRBA	AI659561	LPS-responsive vesicle trafficking, beach and anchor containing	Hs.62354
214499_s_at		AF249273	Consensus includes gb:AF249273.1 /DEF=Homo sapiens Bcl- 2-associated transcription factor short form mRNA, complete cds. /FEA=CDS /PROD=Bcl-2-associated transcription factor shortform /DB_XREF=gi:7582385 /UG=Hs.80338 KIAA0164 gene product /FL=gb:AF249273.1	
209387_s_at		M90657	gb:M90657.1 /DEF=Human tumor antigen (L6) mRNA, complete cds. /FEA=mRNA /GEN=L6 /DB_XREF=gi:186803 /UG=Hs.3337 transmembrane 4 superfamily member 1 /FL=gb:M90657.1	
			gb:NM_017450.1 /DEF=Homo sapiens BAI1-associated protein 2 (BAIAP2), transcript variant 1, mRNA. /FEA=mRNA /GEN=BAIAP2 /PROD=BAI1-associated protein 2, isoform 1 /DB_XREF=gi:9257196 /UG=Hs.7936 BAI1-associated protein 2 /FL=ab:AB015019.1 ab:AB017120.1 ab:NM 017450.1	
205294_at		NM 01/450		

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			gb:NM_014905.1 /DEF=Homo sapiens glutaminase (GLS),	
			MRNA /FEA=mRNA /GEN=GLS /PROD=glutaminase C	
			/DB_XREF=gi:7662327 /UG=Hs.239189 glutaminase	
203159_at		NM_014905		
			Consensus includes gb:Al922509 /FEA=EST	
			/DB_XREF=gi:5658473 /DB_XREF=est:wh13g11.x1	
		·	/CLONE=IMAGE:2380676 /UG=Hs.23440 KIAA1105 protein	
209284 s at		AF180425	/FL=gb:AF180425.2	
			gb:NM_005872.1 /DEF=Homo sapiens breast carcinoma	
			amplified sequence 2 (BCAS2), mRNA. /FEA=mRNA	
			/GEN=BCAS2 /PROD=breast carcinoma amplified sequence 2	
			/DB_XREF=gi:5031652 /UG=Hs.22960 breast carcinoma	
			amplified sequence 2 /FL=gb:BC005285.1 gb:AF081788.1	
203053_at		NM_005872	gb:AB020623.1 gb:NM 005872.1	
			gb:NM 000125.1 /DEF=Homo sapiens estrogen receptor 1	
			(ESR1), mRNA /FEA=mRNA /GEN=ESR1 /PROD=estrogen	
			receptor 1 /DB_XREF=gi:4503602 /UG=Hs.1657 estrogen	
205225 at		NM_000125		
209838_at		AA496247		Hs.380120
			sequence from clone RP5-976O13 on chromosome 1p21.2-	
			22.2 Contains part of the gene for CGI-100 protein, 3	
			isoforms of the gene for M96 protein, ESTs, STSs, GSSs	
			and a CpG Island /FEA=mRNA_1 /DB_XREF=gi:6822199	
			/UG=Hs.296155 CGI-100 protein /FL=gb.AF151858.1	
202194_at		AL117354	gb:NM_016040.1	
			gb:NM_003689.1 /DEF=Homo sapiens aldo-keto reductase	
			family 7, member A2 (aflatoxin aldehyde reductase)	
-			(AKR7A2), mRNA. /FEA=mRNA /GEN=AKR7A2 /PROD=aldo-	
			keto reductase family 7, member A2(aflatoxin aldehyde	-
			reductase) /DB_XREF=gi:4502020 /UG=Hs.6980 aldo-keto	
			reductase family 7, member A2 (aflatoxin aldehyde	
			reductase) /FL=gb:BC004111.1 gb:AF026947.1	
202139_at		NM_003689	NM_003689 gb:NM_003689.1	

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209778 at		AF007217	gb:AF007217.1 /DEF=Homo sapiens Trip230 mRNA, complete cds. /FEA=mRNA /GEN=Trip230 /PROD=Trip230 /DB_XREF=gi:2253416 /UG=Hs.85092 thyroid hormone receptor interactor 11 /FL=gb:NM_004239.1 gb:AF007217.1
202557_at	STCH	AI718418	stress 70 protein chaperone, microsome-associated, 60kDa
			gb:NM_004124.1 /DEF=Homo sapiens glia maturation factor, beta (GMFB), mRNA. /FEA=mRNA /GEN=GMFB /PROD=glia
			maturation factor, beta /DB_XREF=gi:4758441
			/UG=Hs.151413 glia maturation factor, beta
202544_at		NM_004124	gb:NM_004124.1
			gb:NM_005191.1 /DEF=Homo sapiens CD80 antigen (CD28 antigen ligand 1, B7-1 antigen (CD80), mRNA /FEA=mRNA /GEN=CD80 /PROD=CD80 antigen (CD28 antigen ligand 1,
207176 s at		NM_005191	B7-1antigen) /DB_XREF=gi:4885122 /UG=Hs.838 CD80 antigen (CD28 antigen ligand 1, B7-1 antigen) /FL=gb:NM_005191.1
			gb:AF153330.1 /DEF=Homo sapiens thiamine carrier 1 (TC1) mRNA, complete cds. /FEA=mRNA /GEN=TC1
			/PROD=thiamine carrier 1 /DB_XREF=gi:5453325 /UG=Hs.30246 solute carrier family 19 (thiamine transporter), member 2 /FL=ab:AF153330.1 ab:AF135488.1 ab:AF160812.1
209681_at		AF153330	
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		NW 00428	gb:NM_004135.1 /DEF=Homo sapiens isocitrate dehydrogenase 3 (NAD+) gamma (IDH3G), mRNA. //FEA=mRNA /GEN=IDH3G /PROD=isocitrate dehydrogenase 3 (NAD+) gamma /DB_XREF=gi:4758581 /UG=Hs.75253 //FL=gb:BC001902.1 gb:BC000933.2 gb:U40272.1
4		I	gb:NM_005502.1 /DEF=Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 1 (ABCA1), mRNA. /FEA=mRNA /GEN=ABCA1 /PROD=ATP-binding cassette, sub
203504_s_at		NM_005502	ATP-binding cassette, sub-family A (ABC1), member 1 /FL=gb:AF165281.1 gb:NM_005502.1 gb:AF285167.1

Lidare	ridare / b conta.			
			Consensus includes gb:AL031714 / DEF=Human DNA sequence from clone 1.416-358B7 on chromosome 16	
			Contains the UBE21 gene for ubiquitin-conjugating enzyme	
			E2I (homologous to yeast UBC9), and an RPS20 (40S	
			Ribosomal protein S20) pseudogene. Contains ES1s, S1Ss.	
			GSSs and a putative CpG is /FEA=mRNA	
			/DB_XREF=gi:4775608 /UG=Hs.84285 ubiquitin-conjugating	
			enzyme E2I (homologous to yeast UBC9) /FL=gb:U45328.1	
			gb:U31933.1 gb:BC000427.1 gb:BC004429.1 gb:U31882.1	
			gb:U66818.1 gb:U66867.1 gb:U38785.1 gb:NM_003345.1	
208760_at		NM_003345	_	
			gb:NM_005873.1 /DEF=Homo sapiens regulator of G-protein	
			signalling 19 (RGS19), mRNA. /FEA=mRNA /GEN=RGS19	
			/PROD=G protein signalling regulator 19	
			/DB XREF=gi:5031704 /UG=Hs.22698 regulator of G-protein	
204336 s at		NM 005873	_	
1			_	
			complete cds. /FEA=mRNA /GEN=TCF3	
			/DB_XREF=gi:339477 /UG=Hs.101047 transcription factor 3	
			(E2A immunoglobulin enhancer binding factors E12E47)	
209153 s at		M31523	/FL=gb:M31523.1	
			e 4D, cAMP-specific (phosphodiesterase E3	
204491 at	PDE4D	R40917		Hs.172081
			gb:M62898.1 /DEF=Human lipocortin (LIP) 2 pseudogene	
			mRNA, complete cds-like region. /FEA=mRNA	
			/DB_XREF=gi:187147 /UG=Hs.217493 annexin A2	
208816 x at		M62898	/FL=gb:M62898.1	
			gb:NM_005066.1 /DEF=Homo sapiens splicing factor	
			prolineglutamine rich (polypyrimidine tract-binding protein-	
			associated) (SFPQ), mRNA /FEA=mRNA /GEN=SFPQ	
			/PROD=splicing factor prolineglutamine rich(polypyrimidine	
			tract-binding protein-associated) /DB_XREF=gi:4826997	
			/UG=Hs.180610 splicing factor prolineglutamine rich	
201586_s_at		NM_005066	/FL=gb:NM_005066.1	

Figure	Figure /b Conta.			
			gb:NM_002395.2 /DEF=Homo sapiens malic enzyme 1,	
			NADP(+)-dependent, cytosolic (ME1), mRNA. /FEA=mRNA ///////////////////////////////////	
			/DB_XREF=gi:13435400 /UG=Hs.14732 malic enzyme 1	
204059_s_at		NM_002395	002395 NADP(+)-dependent, cytosolic /FL=gb:NM_002395.2	
			gb:NM_018693.1 /DEF=Homo sapiens vitiligo-associated	
			protein VIT-1 (VIT1), mRNA. /FEA=mRNA /GEN=VIT1	
			/PROD=vitiligo-associated protein VIT-1	
L				
203255_at		NM_018693	protein VII-1 /FL=gb:NM_018693.1 gb:AF264/14.1	
			gb:M23114.1 /DEF=Homo sapiens calcium-ATPase (HK1)	
			mRNA, complete cds. /FEA=mRNA /GEN=HK1	
			/DB_XREF=gi:184100 /UG=Hs.1526 ATPase, Ca++	
209186 at		M23114	transporting, cardiac muscle, slow twitch 2 /FL=gb:M23114.1	
204671_s_at	ANKRD6	BE677131	ankyrin repeat domain 6	Hs.30991
			gb:NM 005151.1 /DEF=Homo sapiens ubiquitin specific	
			protease 14 (tRNA-guanine transglycosylase) (USP14),	
			mRNA. /FEA=mRNA /GEN=USP14 /PROD=ubiquitin specific	
			protease 14 (tRNA-guaninetransglycosylase)	
			/DB_XREF=gi:4827049 /UG=Hs.75981 ubiquitin specific	
			protease 14 (tRNA-guanine transglycosylase)	
201672_s_at		NM_005151	005151 /FL=gb:BC003556.1 gb:NM_005151.1 gb:U30888.1	
201836_s_at	STAF65(gamma)	AU154740	SPTF-associated factor 65 gamma	Hs.6232
			gb:NM_001551.1 /DEF=Homo sapiens immunoglobulin	
			(CD/9A) binding protein 1 (IGBP1), mKNA. /FEA=mKNA	
			/GEN=IGBP1 /PROD=immunoglobulin-binding protein 1	
			/DB_XREF=gi:4557662 /UG=Hs.3631 immunoglobulin (CD/9A)	
202105_at		NM_001551	binding protein 1 /FL=gb:BC004137.1 gb:NM_001551.1	
			gb:NM_005296.1 /DEF=Homo sapiens G protein-coupled	
			receptor 23 (GPR23), mRNA. /FEA=mRNA /GEN=GPR23	
			/PROD=G protein-coupled receptor 23 /DB_XREF=gi:4885310	
4			/UG=Hs.27812 G protein-coupled receptor 23	
206960_at		NM_005296 /	/FL=gb:U90322.1 gb:NM_005296.1	

rigure	rigule / b cont a.			
			gb:NM_012286.1 /DEF=Homo sapiens MORF-related gene X	
			(KIAA0026), mRNA. /FEA=mRNA /GEN=KIAA0026	
			/PROD=MORF-related gene X /DB_XREF=gi:691244/	
2000		00000	/UG=Hs.173714 MORF-related gene X /FL=gb:D14812.1	
201994_at		NIM 012286	gb:AF100620.1 gb:NM_012286.1 gb:AF16/1/4.1	
			gb:NM_006809.1 /DEF=Homo sapiens translocase of outer	
			mitochondrial membrane 34 (TOM34), mRNA. /FEA=mRNA	
			/GEN=TOM34 /PROD=translocase of outer mitochondrial	
			membrane 34 /DB_XREF=gi:5803204 /UG=Hs.76927	
			translocase of outer mitochondrial membrane 34	
201870_at		008900 WN		
			gb:NM_021975.1 /DEF=Homo sapiens v-rel avian	
-			reticuloendotheliosis viral oncogene homolog A (nuclear	
			factor of kappa light polypeptide gene enhancer in B-cells 3	
			(p65)) (RELA), mRNA. /FEA=mRNA /GEN=RELA /PROD=v-	
			rel avian reticuloendotheliosis viral oncogenehomolog A	
			(nuclear factor of kappa light polypeptide geneenhancer in B-	
			cells 3 (p65)) /DB_XREF=gi:11496238 /UG=Hs.75569 v-rel	
			avian reticuloendotheliosis viral oncogene homolog A (nuclear	
			factor of kappa light polypeptide gene enhancer in B-cells 3	
201783 s at		NM 021975	(p65)) /FL=gb:NM_021975.1 gb:L19067.1	
I I		ł	ESTs, Highly similar to SM3D_HUMAN Semaphorin 3D precursor	
215643_at		AU145680	[H.sapiens]	Hs.306613
			gb:NM_006702.1 /DEF=Homo sapiens neuropathy target	
			esterase (NTE), mRNA. /FEA=mRNA /GEN=NTE	
			/PROD=neuropathy target esterase /DB_XREF=gi:5729950	
			/UG=Hs.5038 neuropathy target esterase	
203718_at		NM_006702	/FL=gb:NM_006702.1	
			Consensus includes gb:AW139131 /FEA=EST	
			/DB_XREF=gi:6143449 /DB_XREF=est:UI-H-BI1-aet-a-12-0-	
			UI.ST /CLONE=IMAGE:Z/Z0183 /UG=HS:154Z94 discs, large	
202514_at		NM_004087	(Drosophila) homolog 1 /FL=gb:NM_00408/.1 gb:U13896.1	

ainfil	I Iguie / D Colina.				
			gb:NM_013344.1 /DEF=Homo sapiens leucine zipper-like		
			protein (LZLP), mKNA. /FEA=mKNA /GEN=LZLP /PROD=leveine zigner-like protein /DR XRFF=qi-7106350		
			//UG=Hs.278952 leucine zipper-like protein /FL=gb:AFT59055.1		
208238_x_at		NM_013344	013344 gb:NM_013344.1		
			gb:BC002600.1 /DEF=Homo sapiens, mature T-cell		•
			proliferation 1, clone MGC:2069, mRNA, complete cds.		
			/FEA=mRNA /PROD=mature T-cell proliferation 1		
			/DB_XREF=gi:12803540 /UG=Hs.3548 mature T-cell		
210212_x_at		BC002600	proliferation 1 /FL=gb:BC002600.1		
			gb:NM_018204.1 /DEF=Homo sapiens cytoskeleton		
			associated protein 2 (CKAP2), mRNA. /FEA=mRNA		
			/GEN=CKAP2 /PROD=cytoskeleton associated protein 2		
			/DB_XREF=gi:8922641 /UG=Hs.24641 cytoskeleton associated		
218252_at		NM_018204	018204 protein 2 /FL=gb:AL136848.1 gb:NM 018204.1		
47550_at	LZTS1	N21184	leucine zipper, putative turnor suppressor 1		Hs.93605
at	SYN47	BE550452	Homer, neuronal immediate early gene, 1B		Hs.337737
			Consensus includes gb:AK024185.1 /DEF=Homo sapiens		
•			CDNA FLJ14123 fis, clone MAMMA1002155. /FEA=mRNA		
			/DB_XREF=gi:10436502 /UG=Hs.269314 Homo sapiens cDNA		
215545_at		AK024185	FLJ14123 fis, clone MAMMA1002155		}
			even-pass G-type receptor 2 (flamingo		
36499_at	CELSR2	D87469	homolog, Drosophila)	NM_001408	Hs.57652
			thyroid hormone receptor, alpha (erythroblastic leukemia viral (v-		,
35846_at	THRA	M24899		NM_003250	Hs.724
216561_x_at	80X29	AF032454	Homo sapiens SOX-29 protein (SOX29) gene, partial cds.		
-			gb:BC005254.1 /DEF=Homo sapiens, Similar to C-type		
			(calcium dependent, carbohydrate-recognition domain) lectin,		-
			superfamily member 2 (activation-induced), clone		
			MGC:12289, mRNA, complete cds. /FEA=mRNA		
			/PROD=Similar to C-type (calcium dependent,carbohydrate-		
			recognition domain) lectin, superfamilymember 2 (activation-		
			induced) /DB_XREF=gi:13528920 /UG=Hs.85201 C-type		
			(calcium dependent, carbohydrate-recognition domain) lectin,		
\$6 657006		BCOOKSKA	Superfamily member 2 (activation-induced)		
203132 at		BC0002534	SD. IN		

Ligare	rigure / D Colit a.			
			gb:NM_017590.1 /DEF=Homo sapiens hypothetical protein DKFZp434K0920 (DKFZp434K0920), mRNA. /FEA=mRNA	
			/GEN=DKFZp434K0920 /PROD=hypothetical protein	
•		047500		
Z030// S at		080 / 10 IMINI	ab: NM 004079 1 /DEF=Homo sapiens cathebsin S (CTSS).	
			mRNA. /FEA=mRNA /GEN=CTSS /PROD=cathepsin S	
			/DB_XREF=gi:4758097 /UG=Hs.181301 cathepsin S	
			/FL=gb:BC002642.1 gb:M86553.1 gb:NM_004079.1	
202902_s_at		NM_004079	gb:M90696.1	
			gb:BC002630.1 /DEF=Homo sapiens, Similar to integrin, beta	
			8, clone MGC:3946, mRNA, complete cds. /FEA=mRNA	
			/PROD=Similar to integrin, beta 8 /DB_XREF=gi:12803590	
211488 s at		BC002630	/UG=Hs.52620 integrin, beta 8 /FL=gb:BC002630.1	
213696_s_at	MED8	AA421957	mediator of RNA polymerase II transcription subunit MED8	Hs.301756
			Consensus includes gb:AB023179.1 /DEF=Homo sapiens	
			mRNA for KIAA0962 protein, partial cds. /FEA=mRNA	
			/GEN=KIAA0962 /PROD=KIAA0962 protein	
212911_at		AB023179	/DB_XREF=gi:4589567 /UG=Hs.9059 KIAA0962 protein	
			gb:U85430.1 /DEF=Human transcription factor NFATx4	
			mRNA, complete cds. /FEA=mRNA /PROD=transcription	
			factor NFATx4 /DB_XREF=gi:1835590 /UG=Hs.172674	
			nuclear factor of activated T-cells, cytoplasmic, calcineurin-	
210556_at		U85430	dependent 3 /FL=gb:U85430.1	
			gb:NM_001216.1 /DEF=Homo sapiens carbonic anhydrase IX	
			(CA9), mRNA. /FEA=mRNA /GEN=CA9 /PROD=carbonic	
			anhydrase IX precursor /DB_XREF=gi:9955947 /UG=Hs.63287	
205199_at		NM_001216	carbonic anhydrase IX /FL=gb:NM_001216.1	
			aldo-keto reductase family 1, member C1 (dihydrodiol	
			dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid	
217626_at	AKR1C1	BF508244	dehydrogenase)	Hs.306098

Lignie	riguie / D Colita.			
			gb:NM_018182.1 /DEF=Homo sapiens hypothetical protein FLJ10700 (FLJ10700), mRNA. /FEA=mRNA /GEN=FLJ10700	
			/PROD=hypothetical protein FLJ10700 /DB_XREF=gi:8922595	
218464 s at		NM_018182	/UG=Hs.295909 hypothetical protein FLJ10/00 NM 018182 /FL=qb:NM 018182.1	
			gb:AB004903.1 /DEF=Homo sapiens mRNA for STAT	
			induced STAT inhibitor-2, complete cds. /FEA=mRNA	
			/PROD=STAT induced STAT inhibitor-2	
			/DB_XREF=gi:2443360 /UG=Hs.110776 STAT induced STAT	
			inhibitor-2 /FL=gb:AB004903.1 gb:AB006966.1 gb:AF037989.1	
203372_s_at		AB004903	gb:AF020590.1 gb:NM_003877.1	
			gb:BC005253.1 /DEF=Homo sapiens, Similar to Kelch motif	
			containing protein, clone MGC:12288, mRNA, complete cds.	
			/FEA=mRNA /PROD=Similar to Kelch motif containing protein	
			/DB_XREF=gi:13528917 /UG=Hs.106290 Kelch motif	
210635 s at		BC005253	containing protein /FL=gb:BC005253.1	
			gb:NM_006682.1 /DEF=Homo sapiens fibrinogen-like 2	
			(FGL2), mRNA. /FEA=mRNA /GEN=FGL2 /PROD=fibrinogen-	
			like 2 /DB_XREF=gi:5730074 /UG=Hs.2659 fibrinogen-like 2	
204834_at		NM_006682	/FL=gb:NM_006682.1	-
			Consensus includes gb:AF070596.1 /DEF=Homo sapiens	
	_		clone 24796 mRNA sequence. /FEA=mRNA	
			/DB_XREF=gi:3387973 /UG=Hs.27191 hypothetical protein	_
213272_s_at		AF070596	from clone 24796	
			gb:U89358.1 /DEF=Human I(3)mbt protein homolog mRNA,	_
-			complete cds. /FEA=mRNA /PROD=I(3)mbt protein homolog	
			/DB_XREF=gi:3811110 /UG=Hs.300863 lethal (3) malignant	
			brain tumor I(3)mbt protein (Drosophila) homolog	
210306_at		U89358	/FL=gb:U89358.1	
			gb:NM_006185.1 /DEF=Homo sapiens nuclear mitotic	
			apparatus protein 1 (NUMA1), mRNA. /FEA=mRNA	
			/GEN=NUMA1 /PROD=nuclear mitotic apparatus protein 1	· · · · · · · · · · · · · · · · ·
			/DB_XREF=gi:5453819 /UG=Hs.301512 nuclear mitotic	
200747_s_at		NM_006185	NM_006185 apparatus protein 1 /FL=gb:NM_006185.1	
36545_s_at	KIAA0542	AB011114		Hs.62209
213409_s_at RHEB2	RHEB2	BF593727		Hs.355976

			Ab.NIM ORESER 2 JDEE-Home conjugat conjugation appropriate	
			go.nwcoccoc.z /Dcr_filonic sapiens requient, apoptosis	
			/GEN=REQ /PROD=requiem /DB_XREF=gi:10862706	
		1	/UG=Hs.13495 requiem, apoptosis response zinc finger gene	-
202116_at		NM_006268 /	/FL=gb:NM_006268.2_gb:U94585.1_gb:AF001433.1	
213823_at		H94842	ESTs	Hs.17882
59375_at	MYO15B	AI825877	myosin XVB, pseudogene	Hs.286035
			gb:NM_018263.1 /DEF=Homo sapiens hypothetical protein	
			FLJ10898 (FLJ10898), mRNA. /FEA=mRNA /GEN=FLJ10898	
			/PROD=hypothetical protein FLJ10898 /DB_XREF=gi:8922749	
218659_at		NM_018263	/UG=Hs.13801 KIAA1685 protein /FL=gb:NM_018263.1	
			gb:NM_001909.1 /DEF=Homo sapiens cathepsin D	
			(lysosomal aspartyl protease) (CTSD), mRNA. /FEA=mRNA	
			/GEN=CTSD /PROD=cathepsin D (lysosomal aspartyl	
			protease) /DB_XREF=gi:4503142 /UG=Hs.79572 cathepsin D	
			(lysosomal aspartyl protease) /FL=gb:M11233.1	
200766_at		NM_001909		
			gb:AF130054.1 /DEF=Homo sapiens clone FLB4816	
			PRO1252 mRNA, complete cds. /FEA=mRNA	
			/PROD=PRO1252 /DB_XREF=gi:11493414 /UG=Hs.326159	
			leucine rich repeat (in FLII) interacting protein 1	
211452_x_at		AF130054	/FL=gb:AF130054.1	
			gb:BC000687.1 /DEF=Homo sapiens, translocating chain-	
		-	associating membrane protein, clone MGC:784, mRNA,	
			complete cds. /FEA=mRNA /PROD=translocating chain-	
			associating membraneprotein /DB_XREF=gi:12653796	
			/UG=Hs.4147 translocating chain-associating membrane	
201398_s_at		BC000687		
200849_s_at	FCGR2B	AA479488	Fc fragment of IgG, low affinity IIb, receptor for (CD32)	Hs.82316

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			gb:NM_000430.2 /DEF=Homo sapiens platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit (45kD)	
			/PROD=platelet-activating factor acetylhydrolase,isoform lb, alpha subunit (45kD) /DB XREF=gi:6031206 /UG=Hs.77318	
			platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit (45kD) /FL=qb:L13385.1 qb:L13386.1	
200816_s_at		NM_000430	gb:NM_000430.2	
			gb:NM_001071.1 /DEF=Homo sapiens thymidylate synthetase	-
		·	(TYMS), MKNA. /FEA=MKNA /GEN=TYMS /PROD=thymidylate synthetase /DB XREF=gi:4507750	
			/UG=Hs.82962 thymidylate synthetase /FL=gb:BC002567.1	
		NM_001071	gb:NM_001071.1	
201964_at	KIAA0625	N64643	KIAA0625 protein Hs. *	Hs.154919
	PURA	BF739943	purine-rich element binding protein A	Hs.29117
			Consensus includes gb:AL049646 /DEF=Human DNA	- 1-
			sequence from clone RP4-568F9 on chromosome 20	
			Contains the ZNF133 (zinc finger protein 133 (clone pHZ-	
			13)) gene, part of a gene for a novel protein, ESTs, STSs,	
			GSSs and CpG Islands /FEA=mKNA_Z	-
216960 s at		AI 049646	/DB_XREF=gi:11121205 /UG=Hs./8434 zinc tinger protein 133 (close pHZ-13)	
2 10300 S at		ALU43040		
			Consensus includes gb:AL035669 /DEF=Human DNA	
			sequence from clone RP5-885L7 on chromosome 20q13.2-	
			13.33 Contains ESTs, STSs, GSSs and eight CpG islands.	
			Contains the 3 end of the NTSR1 gene for high affinity	
			neurotensin receptor 1, a putative novel gene, a novel gene	
			similar to a f /FEA=mRNA_3 /DB_XREF=gi:8979786	
213213_at		AL035669	/UG=Hs.155313 death associated transcription factor 1	
			gb:NM_024656.1 /DEF=Homo sapiens hypothetical protein	
			FLJ22329 (FLJ22329), mRNA. /FEA=mRNA /GEN=FLJ22329	
			/PROD=hypothetical protein FLJ22329 /DB_XREF=gi:13375904	
			/UG=Hs.61478 hypothetical protein FLJ22329	
218473_s_at		NM_024656	/FL=gb:NM_024656.1	

	55			
			gb:NM_U04648.1 /UEF=Homo sapiens protein tyrosine	
			pnosphatase, non-receptor type substrate 1 (PTPNST), mRNA /FFA=mRNA /GFN=PTPNS1 /PROD=protein typosine	
			phosphatase, non-receptor typesubstrate 1	
			/DB_XREF=gi:4758977 /UG=Hs.156114 protein tyrosine	
			phosphatase, non-receptor type substrate 1 /FL=gb:D86043.1	
202896_s_at		NM_004648		
			gb:BC005299.1 /DEF=Homo sapiens, cytochrome c, clone	-
			MGC:12367, mRNA, complete cds. /FEA=mRNA	
			/PROD=cytochrome c /DB_XREF=gi:13529022	
_			/UG=Hs.169248 cytochrome c /FL=gb:NM_018947.1	
208905_at		BC005299	gb:BC005299.1	
			splicing factor proline/glutamine rich (polypyrimidine tract binding	
201585_s_at	SFPQ	BG035151	protein associated) Hs.180	Hs.180610
			gb:NM_014721.1 /DEF=Homo sapiens KIAA0680 gene	
			product (KIAA0680), mRNA. /FEA=mRNA /GEN=KIAA0680	
			/PROD=KIAA0680 gene product /DB_XREF=gi:7662247	
			/UG=Hs.102471 KIAA0680 gene product /FL=gb:AB014580.1	
204049_s_at		NM_014721	NM_014721 gb:NM_014721.1	
			gb:NM_000176.1 /DEF=Homo sapiens nuclear receptor	
			subfamily 3, group C, member 1 (NR3C1), mRNA.	
			/FEA=mRNA /GEN=NR3C1 /PROD=nuclear receptor	
			subfamily 3, group C, member 1 /DB_XREF=gi:4504132	
			/UG=Hs.75772 nuclear receptor subfamily 3, group C,	
201866_s_at		NM_000176		
213051 at	ZAP	AI133727		Hs.35254
			Consensus includes gb:AL050136.1 /DEF=Homo sapiens	
			mRNA; cDNA DKFZp586L141 (from clone DKFZp586L141).	_
			/FEA=mRNA /DB_XREF=gi:4884346 /UG=Hs.140945 Homo	_
			sapiens mRNA; cDNA DKFZp586L141 (from clone	
214948_s_at		AL050136	DKFZp586L141)	

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botholog SINGING Compliant Company to Company of the Company of th	go.niv_003003.1 / DEF-F0110 Sapiets SWISNE Telated, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SMARCA1), mRNA. /FEA=mRNA. /GEN=SMARCA1 /PROD=SWISNF related, matrix associated, actindependent regulator of chromatin, subfamily a, member 1 /DB_XREF=gi:4507066 /UG=Hs.152292 SWISNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 /FL=gb:M88163.1 gb:NM_003069.1	gb:NM_005245.1 /DEF=Homo sapiens FAT tumor suppressor (Drosophila) homolog (FAT), mRNA. /FEA=mRNA /GEN=FAT /PROD=FAT tumor suppressor precursor //DB_XREF=gi:4885228 /UG=Hs.166994 FAT tumor suppressor (Drosophila) homolog /FL=gb:NM_005245.1	gb:NM_002923.1 /DEF=Homo sapiens regulator of G-protein signalling 2, 24kD (RGS2), mRNA. /FEA=mRNA /GEN=RGS2 /PROD=regulator of G-protein signalling 2, 24kD /DB_XREF=gi:4506516 /UG=Hs.78944 regulator of G-protein signalling 2, 24kD /FL=gb:L13463.1 gb:NM_002923.1	gb:NM_002023.2 /DEF=Homo sapiens fibromodulin (FMOD), mRNA. /FEA=mRNA /GEN=FMOD /PROD=fibromodulin precursor /DB_XREF=gi:5016093 /UG=Hs.230 fibromodulin /FL=gb:NM 002023.2	gb:NM_004499.1 /DEF=Homo sapiens heterogeneous nuclear ribonucleoprotein AB (HNRPAB), mRNA. /FEA=mRNA /GEN=HNRPAB /PROD=heterogeneous nuclear ribonucleoprotein AB /DB_XREF=gi:4758541 /UG=Hs.81361 heterogeneous nuclear ribonucleoprotein AB /FL=gb:BC002625.1 gb:BC004561.1 gb:M65028.1 gb:NM 004499.1	
	690E00_MN	NM_005245	NM_002923	NM_002023	NM 004499	
,	203874_s_at	201579_at	202388 at	202709 at	201277 s at	် ပ

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			gb:NM_020199.1 /DEF=Homo sapiens HTGN29 protein (HTGN29), mRNA. /FEA=mRNA /GEN=HTGN29 // PROD=HTGN29 protein /DB_XREF=gi:9910277	
203024_s_at		NM_020199		
			gb:AF225981.1 /DEF=Homo sapiens calcium transport	
			ATPase ATP2C1 (ATP2C1) mRNA, complete cds.	
			//FEA=mRNA /GEN=ATP2C1 /PROD=calcium transport	
			ATPase ATP2C1 /DB_XREF=gi:7021496 /UG=Hs.106778	
			ATPase, Ca++ transporting, type 2C, member 1	
209934_s_at		AF225981	/FL=gb:AF225981.1	
212539_at	FLJ22530	AI422099	hypothetical protein FLJ22530	Hs.14570
32091_at	KIAA0446	AB007915	KIAA0446 gene product	Hs.158286
			Consensus includes gb:AB033080.1 /DEF=Homo sapiens	
			mRNA for KIAA1254 protein, partial cds. /FEA=mRNA	
			/GEN=KIAA1254 /PROD=KIAA1254 protein	
			/DB_XREF=gi:6330892 /UG=Hs.82506 KIAA1254 protein	
221511_x_at		AB033080	/FL=gb:AF212228.1	
215754 at		AU148040	AU148040 MAMMA1 Homo sapiens cDNA clone MAMMA1002428 3', mRNA sequence.	
			000 minter and a contract of the contract of t	
			gb:Nivi_ouse/4.1 /DEF=nomio_sapiens_zinc_iniger_protein_zss /ZNF239_mRNA_/FFA=mRNA_/GFN=ZNF39_/PROD=zinc_	
			finaer protein 239 /DB XREF=ai:5032244 /UG=Hs.25040 zinc	
206261 at		NM 005674	finger protein 239 /FL=gb:NM_005674.1	
202126_at	PRPF4B	AA156948	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	Hs.198891
			gb:NM_006588.1 /DEF=Homo sapiens sulfotransferase family,	
			cytosolic, 1C, member 2 (SULT1C2), mRNA. /FEA=mRNA	
			/GEN=SULT1C2 /PROD=SULT1C sulfotransferase	
			/DB_XREF=gi:5730070 /UG=Hs.312644 sulfotransferase	
			family, cytosolic, 1C, member 2 /FL=gb:AF055584.1	
205812_s_at		NM_006588		
214085_x_at	GLIPR	AI912583	glioma pathogenesis-related protein	Hs.154762

207128_s_at		NM_013361	gb:NM_013361.1 /DEF=Homo sapiens zinc finger protein 223 (ZNF223), mRNA. /FEA=mRNA /GEN=ZNF223 /PROD=zinc finger protein 223 /DB_XREF=gi:7019588 /UG=Hs.279782 zinc finger protein 223 /FL=gb:AF187989.1 gb:NM_013361.1	
207163 s at		NM 005163	gb:NM_005163.1 /DEF=Homo sapiens v-akt murine thymoma viral oncogene homolog 1 (AKT1), mRNA. /FEA=mRNA /GEN=AKT1 /PROD=serinethreonine protein kinase /DB_XREF=gi:4885060 /UG=Hs.71816 v-akt murine thymoma viral oncogene homolog 1 /FL=gb:M63167.1 gb:NM_005163.1	
ਗ	TAZ	AA081084	transcriptional co-activator with PDZ-binding motif (TAZ)	Hs.408434
209883_at		AF288389	gb:AF288389.1 /DEF=Homo sapiens C1orf17 mRNA, complete cds. /FEA=mRNA /PROD=C1orf17 /DB_XREF=gi:12620187 /UG=Hs.106794 KIAA0584 protein /FL=gb:AF288389.1	
210312 s at		BC002640	gb:BC002640.1 /DEF=Homo sapiens, Similar to uterine protein, clone MGC:4279, mRNA, complete cds. /FEA=mRNA /PROD=Similar to uterine protein /DB_XREF=gi:12803610 /UG=Hs.4187 hypothetical protein 24636 /FL=gb:BC002640.1	
၂ ဟ	TRIM22	AA083478	tripartite motif-containing 22	Hs.318501
208745_at		AA917672	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit g	Hs.107476
205141 at		NM 001145		
218001_at			gb:NM_016034.1 /DEF=Homo sapiens CGI-91 protein (LOC51116), mRNA. /FEA=mRNA /GEN=LOC51116 // PROD=CGI-91 protein /DB_XREF=gi:7705804 /UG=Hs.20776 CGI-91 protein /FL=gb:AF151849.1 gb:NM_016034.1	

208812 x at		BC004489	gb:BC004489.1 /DEF=Homo sapiens, major histocompatibility complex, class 1, C, clone MGC:11039, mRNA, complete cds. /FEA=mRNA /PROD=major histocompatibility complex, class 1, C /DB_XREF=gi:13325360 /UG=Hs.277477 major histocompatibility complex, class 1, C /FL=gb:NM_002117.1 gb:M99388.1 gb:U06487.1 gb:BC002463.1 gb:BC004489.1 gb:M84174.1 gb:M84171.1 gb:M84172.1 gb:M84173.1 gb:M84174.1 gb:M26429.1 gb:D50852.1 gb:D50853.1 gb:U41420.1 gb:U41386.1 gb:D50852.1 gb:D50853.1 gb:D50854.1 gb:D83031.1 gb:U57028.1 gb:U06695.1 gb:D8695.1 gb:U6696.1 gb:M99389.1 gb:M99380.1 gb:M28160.1 gb:U09853.1 gb:AF168611.1 gb:L38251.1 gb:D31817.1	
206929 s at 212151 at 210092 at	PSMB5	NM_005597 BF967998	gb:NM_005597.1 /DEF=Homo sapiens nuclear factor IC (CCAAT-binding transcription factor) (NFIC), mRNA. /FEA=mRNA /GEN=NFIC /PROD=nuclear factor IC (CCAAT-binding transcriptionfactor) /DB_XREF=gi:10835080 /UG=Hs.184771 nuclear factor IC (CCAAT-binding transcription factor) /FL=gb:NM_005597.1 005597 transcription factor) /FL=gb:NM_005597.1 gb:AF067173.1 /DEF=Homo sapiens Mago homolog mRNA, complete cds. /FEA=mRNA /PROD=Mago homolog /DB_XREF=gi:4894379 /UG=Hs.57904 mago-nashi (Drosophila) homolog, proliferation-associated (Drosophila) thomolog, proliferation-associated /FL=gb:AF035940.1 gb:AF067173.1 gb:NM_002370.2	Hs.78596
212372_at		AK026977	Consensus includes gb:AK026977.1 /DEF=Homo sapiens cDNA: FLJ23324 fis, clone HEP12482, highly similar to HUMMYOHCB Human nonmuscle myosin heavy chain-B (MYH10) mRNA. /FEA=mRNA /DB_XREF=gi:10439970 /UG=Hs.296842 Homo sapiens, clone IMAGE:3357927, mRNA, partial cds	

	:			
	<u>-</u>		gb:NM_015180.1 /DEF=Homo sapiens synaptic nuclei	
-			expressed gene 2; KIAA1011 protein (KIAA1011), mRNA.	
			/FEA=mRNA /GEN=KIAA1011 /PROD=KIAA1011 protein	
			/DB_XREF=gi:11056019 /UG=Hs.57749 synaptic nuclei	
			expressed gene 2; KIAA1011 protein /FL=gb:NM_015180.1	
202761_s_at	Z	NM_015180	gb:AL080133.1	
			gb:NM_024613.1 /DEF=Homo sapiens hypothetical protein	
			FLJ13187 (FLJ13187), mRNA. /FEA=mRNA /GEN=FLJ13187	
		•	/PROD=hypothetical protein FLJ13187 /DB_XREF=gi:13375826	
	,		/UG=Hs.29724 hypothetical protein FLJ13187	
218640_s_at	Z	NM_024613	/FL=gb:NM_024613.1	
			gb:NM_016640.1 /DEF=Homo sapiens programmed cell death	
			9 (PDCD9), mRNA. /FEA=mRNA /GEN=PDCD9	
			/PROD=(HSA)PAP protein /DB_XREF=gi:7706187	
			/UG=Hs.28555 programmed cell death 9 /FL=gb:AL136706.1	
-			gb:BC002460.1 gb:AF146192.2 gb:AF217523.1	
218398_at	Z	NM_016640	gb:NM 016640.1	
			gb:AF180519.1 /DEF=Homo sapiens GABA-A receptor-	
			associated protein mRNA, complete cds. /FEA=mRNA	
			/PROD=GABA-A receptor-associated protein	
		_	/DB_XREF=gi:13241283 /UG=Hs.326776 Homo sapiens	
			GABA-A receptor-associated protein mRNA, complete cds	
211458_s_at	₹	AF180519	/FL=gb:AF180519.1	
	-		gb:NM_023039.1 /DEF=Homo sapiens ankyrin repeat, family	
	-		A (RFXANK-like), 2 (ANKRA2), mRNA. /FEA=mRNA	
			/GEN=ANKRA2 /PROD=ankyrin repeat, family A (RFXANK-	
			like), 2 /DB_XREF=gi:12746411 /UG=Hs.239154 ankyrin	
			repeat, family A (RFXANK-like), 2 /FL=gb:AF314032.1	
218769_s_at	Z	M_023039	gb:NM_023039.1	
203438_at STC2	Ā	AI435828	stanniocalcin 2	Hs.155223
			gb:NM_003126.1 /DEF=Homo sapiens spectrin, alpha,	
			erythrocytic 1 (elliptocytosis 2) (SPTA1), mKNA. /FEA=mKNA	
			/GEN=SPTA1 /PROD=spectrin, alpha, erythrocytic 1	
			(elliptocytosis2) /DB_XREF=gi:4507188 /UG=Hs.1985 spectrin,	
			alpha, erythrocytic 1 (elliptocytosis 2) /FL=gb:M61877.1	
		NM_003126	gb:NM_003126.1	
215948_x_at ZNF237		1522311	zinc finger protein 237	Hs.278985

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217919_s_at MRPL42	MRPL42	BE782148	mitochondrial ribosomal protein L42	HS.112110
			gb:NM_020150.1 /DEF=Homo sapiens SAR1 protein (SAR1), mRNA. /FEA=mRNA /GEN=SAR1 /PROD=SAR1 protein	
			/DB_XREF=gi:9910541 /UG=Hs.110796 SAR1 protein	
201543 s at		NM 020150	/FL=gb:AT008z68:1 gb:AL136/24:1 gb:AF261/1/:1 gb:NM 020150.1	
⊢	PEX10	BF339133	BF339133 peroxisome biogenesis factor 10	Hs.247220
			gb:NM_007182.2 /DEF=Homo sapiens Ras association	
			(RalGDSAF-6) domain family 1 (RASSF1), mRNA.	
			/FEA=mRNA /GEN=RASSF1 /PROD=Ras association	
			(RalGDSAF-6) domain family 1 /DB_XREF=gi:9256633	
			/UG=Hs.26931 Ras association (RalGDSAF-6) domain family	
			1 /FL=gb:AF061836.1 gb:AF132676.1 gb:AF040703.2	
204346_s_at		NM_007182	NM_007182 gb:NM_007182.2	
			gb:NM_007344.1 /DEF=Homo sapiens transcription	
			termination factor, RNA polymerase I (TTF1), mRNA.	
			/FEA=mRNA /GEN=TTF1 /PROD=transcription termination	
			factor, RNA polymerasel /DB_XREF=gi:6678454	
			/UG=Hs.54780 transcription termination factor, RNA	
204772_s_at		NM 007344	7344 polymerase 1 /FL=gb:NM_007344.1	
			gb:NM_003503.2 /DEF=Homo sapiens CDC7 (cell division	
			cycle 7, S. cerevisiae, homolog)-like 1 (CDC7L1), mRNA.	
			/FEA=mRNA /GEN=CDC7L1 /PROD=CDC7-like 1	
			/DB_XREF=gi:11038647 /UG=Hs.28853 CDC7 (cell division	
			cycle 7, S. cerevisiae, homolog)-like 1 /FL=gb:NM_003503.2	
204510 at		NM 003503	gb:AB003698.1 gb:AF005209.1 gb:AF015592.1	
1			gb:NM_000046.1 /DEF=Homo sapiens arylsulfatase B	
			(ARSB), mRNA. /FEA=mRNA /GEN=ARSB	
			/PROD=arylsulfatase B precursor /DB_XREF=gi:4557332	
			/UG=Hs.1256 arylsulfatase B /FL=gb:J05225.1	
206129_s_at		NM_000046		
			Consensus includes gb:AF035594.1 /DEF=Homo sapiens	-
			protein kinase C-alpha mRNA, partial 3 UTR. /FEA=mRNA	
		1	/DB_XREF=gi:3168857 /UG=Hs.279856 Homo sapiens protein	
215195_at		AF035584	Kinase C-aipna mknA, partial 3 OTR	

ainfil	rigule / D Collica.				
			gb:NM_018241.1 /DEF=Homo sapiens hypothetical protein FLJ10846 (FLJ10846), mRNA. /FEA=mRNA /GEN=FLJ10846		
219074 at		NM 018241	/PROD=hypothetical protein FLJ10846 /DB_XREF=gi:8922706 /UG=Hs.32271 hypothetical protein FLJ10846 /D18241 /FI = ab:NM 018241.1		
		·.i	gb:NM_004795.1 /DEF=Homo sapiens klotho (KL), mRNA.		
205978 at		NM 004795	// EA=mknA /GEN=KL /PKUD=klotno /DB_AKEF=gt.4/30033 // UG=Hs.94592 klotho /FL=gb:AB005142.1 gb:NM_004795.1		
			gb:NM_006842.1 /DEF=Homo sapiens splicing factor 3b, subunit 2, 145kD (SF3B2), mRNA, /FEA=mRNA		
			/GEN=SF3B2 /PROD=splicing factor 3b, subunit 2, 145kD		-
200640 24		CERADO MIN	/DB_XREF=gi:5803154 /UG=Hs.75916 splicing factor 3b,	, , ,	
2000 19 at		ì	aubullit 2, 143kD // E-98.0419/ 111 92.188 octobrilike		
			factor 1 (CRLF1), mRNA. /FEA=mRNA /GEN=CRLF1		
			/PROD=cytokine_receptor-like_factor 1 /DB_XREF=gi:4758061		
			/UG=Hs.114948 cytokine receptor-like factor 1		
			/FL=gb:AF059293.1 gb:NM_004750.1 gb:AF073515.1		
206315_at		NM_004750	gb:AF178684.1		
37005_at	NBL1	D28124		NM_005380 Hs.76307	Hs.76307
			gb:NM_020987.1 /DEF=Homo sapiens ankyrin 3, node of		
			Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA.		
			/FEA=mRNA /GEN=ANK3 /PROD=ankyrin 3, isoform 1		
			/DB_XREF=gi:10947055 /UG=Hs.75893 ankyrin 3, node of		
206385_s_at		NM_020987	Ranvier (ankyrin G) /FL=gb:NM_020987.1 gb:U13616.1		
			gb:NM_021188.1 /DEF=Homo sapiens clones 23667 and		
			23775 zinc finger protein (LOC57862), mRNA. /FEA=mRNA		
			//GEN=LOC57862 /PROD=clones 23667 and 23775 zinc		
			finger protein /DB_XREF=gi:10863994 /UG=Hs.7137 clones		
			23667 and 23775 zinc finger protein /FL=gb:NM_021188.1		
202010_s_at		NM_021188	-		
			gb:NM_004390.1 /DEF=Homo sapiens cathepsin H (CTSH),		
			mRNA. /FEA=mRNA /GEN=CTSH /PROD=cathepsin H		
			/DB_XREF=gi:4758095 /UG=Hs.288181 cathepsin H		
202295_s_at		NM_004390	004390 /FL=gb:BC002479.1 gb:NM_004390.1		

			gb:D29805.1 /DEF=Human mRNA for beta-1,4-	
			galactosyltransferase, complete cds. /FEA=mRNA	
			/PROD=beta-1,4-galactosyltransferase /DB_XREF=gi:474986	
			/UG=Hs.198248 UDP-Gal:betaGlcNAc beta 1,4-	
			galactosyltransferase, polypeptide 1 /FL=gb:NM_001497.1	
201883_s_at		D29805	gb:D29805.1	
	-		gb:NM_001393.1 /DEF=Homo sapiens extracellular matrix	
			protein 2, female organ and adipocyte specific (ECM2),	
			mRNA. /FEA=mRNA /GEN=ECM2 /PROD=extracellular matrix	
			protein 2 /DB_XREF=gi:4557542 /UG=Hs.35094 extracellular	
			matrix protein 2, female organ and adipocyte specific	
206101_at		NM 001393	001393 /FL=gb:AB011792.1 gb:NM_001393.1	
			gb:NM_004962.2 /DEF=Homo sapiens growth differentiation	
	_		factor 10 (GDF10), mRNA. /FEA=mRNA /GEN=GDF10	
			/PROD=growth differentiation factor 10 precursor	
			/DB XREF=gi:11641417 /UG=Hs.2171 growth differentiation	
206159 at		NM 004962	004962 factor 10 /FL=gb:NM 004962.2	
203625_x_at SKP2	2	BG105365	S-phase kinase-associated protein 2 (p45)	Hs.23348
			gb:NM_000129.2 /DEF=Homo sapiens coagulation factor XIII,	
		- · · · -	A1 polypeptide (F13A1), mRNA. /FEA=mRNA /GEN=F13A1	
			/PROD=coagulation factor XIII A1 subunit precursor	
			/DB_XREF=gi:9961355 /UG=Hs.80424 coagulation factor XIII,	
203305 at		NM 000129	A1 polypeptide /FL=gb:M14354.1 gb:NM_000129.2	
			gb:NM_016072.1 /DEF=Homo sapiens CGI-141 protein	
			(LOC51026), mRNA. /FEA=mRNA /GEN=LOC51026	
			/PROD=CGI-141 protein /DB_XREF=gi:7705635	
			/UG=Hs.62275 CGI-141 protein /FL=gb:AF151899.1	
218193_s_at		NM_016072	gb:AL136571.1 gb:NM_016072.1	
			Consensus includes gb:AB002390.1 /DEF=Human mRNA for	
			KIAA0392 gene, partial cds. /FEA=mRNA /GEN=KIAA0392	
			/DB_XREF=gi:2280487 /UG=Hs.201377 apyrase, lysosomal	
204076_at		AB002390	/FL=gb:AF016032.1 gb:NM_004901.1	

בולמוע	בלכוני בי סבוני.			
			gb:U16307.1 /DEF=Human glioma pathogenesis-related protein (GliPR) mRNA, complete cds. /FEA=mRNA	
			/GEN=GliPR /PROD=glioma pathogenesis-related protein	
		1	/DB_XREF=gi:1100927 /UG=Hs.64639 glioma pathogenesis-	
204221_x_at		U16307		
			gb:NM_014863.1 /DEF=Homo sapiens B cell RAG associated	
			protein (BRAG), mRNA. /FEA=mRNA /GEN=BRAG	
			/PROD=KIAA0598 gene product /DB_XREF=gi:7662195	
			/UG=Hs.6079 B cell RAG associated protein	
			/FL=gb:AB011170.1 gb:AF026477.1 gb:NM_014863.1	
203066_at		NM_014863	014863 gb:NM_015892.1	
			gb:NM_004577.1 /DEF=Homo sapiens phosphoserine	
			phosphatase (PSPH), mRNA. /FEA=mRNA /GEN=PSPH	
			/PROD=phosphoserine phosphatase /DB_XREF=gi:4758971	
			/UG=Hs.56407 phosphoserine phosphatase	
205194_at		NM_004577		
			gb:NM_024633.1 /DEF=Homo sapiens hypothetical protein	
			FLJ21276 (FLJ21276), mRNA. /FEA=mRNA /GEN=FLJ21276	
			/PROD=hypothetical protein FLJ21276 /DB_XREF=gi:13375863	
			/UG=Hs.41502 hypothetical protein FLJ21276	
219563_at		NM_024633	024633 /FL=gb:NM_024633.1	
			qb:AF306510.1 /DEF=Homo sapiens RANBPM mRNA,	
			complete cds. /FEA=mRNA /PROD=RANBPM	
			/DB XREF=gi:13194575 /UG=Hs.279886 RAN binding protein	
202582 s at		AF306510	9 /FL=gb:AF306510.1 gb:AB008515.1 gb:NM_005493.1	
			gb:BC003566.1 /DEF=Homo sapiens, zinc finger protein 24	
			(KOX 17), clone MGC:2057, mRNA, complete cds.	
			//FEA=mRNA /PROD=zinc finger protein 24 (KOX 17)	
			//DB_XREF=gi:13097725 /UG=Hs.183593 zinc finger protein	
			24 (KOX 17) /FL=gb:BC003566.1 gb:U68536.1	
203247_s_at		BC003566	gb:AF038964.1 gb:NM 006965.1	

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203232 s at		NM 000332	gb:NM_000332.1 /DEF=Homo sapiens spinocerebellar ataxia 1 (olivopontocerebellar ataxia 1, autosomal dominant, ataxin 1) (SCA1), mRNA. /FEA=mRNA /GEN=SCA1 /PROD=ataxin 1 /DB_XREF=gi:4506792 /UG=Hs.74520 spinocerebellar ataxia 1 (olivopontocerebellar ataxia 1, autosomal dominant, ataxin 1) /FL=gb:NM_000332.1	
ν		∥ ⊼	gb:U29586.1 /DEF=Human beta-sarcoglycan dystrophin-associated glycoprotein mRNA, complete cds. /FEA=mRNA /PROD=dystrophin-associated glycoprotein /DB_XREF=gi:1794188 /UG=Hs.77501 sarcoglycan, beta (43kD dystrophin-associated glycoprotein) /FL=gb:U31116.1 gb:U29586.1 gb:NM_000232.1	
֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓		AI672541	ESTs, Weakly similar to S41161 keratin 9, cytoskeletal - human [H.sapiens]	Hs.409252
209122 at		BC005127	gb:BC005127.1 /DEF=Homo sapiens, adipose differentiation-related protein, clone MGC:10598, mRNA, complete cds. /FEA=mRNA /PROD=adipose differentiation-related protein /DB_XREF=gi:13477306 /UG=Hs.3416 adipose differentiation-related protein /FL=gb:BC005127.1 gb:NM 001122.1	
×	NPR2	AA565715	natriuretic peptide receptor B/guanylate cyclase B (atrionatriuretic peptide receptor B)	Hs.78518
		NM_004513	Consensus includes gb:NM_004513.1 /DEF=Homo sapiens interleukin 16 (lymphocyte chemoattractant factor) (IL16), mRNA. /FEA=CDS /GEN=IL16 /PROD=interleukin 16 //DB_XREF=gi:4758595 /UG=Hs.82127 interleukin 16 (lymphocyte chemoattractant factor) /FL=gb:S81601.1 gb:U82972.1 gb:AF053412.1 gb:M90391.1 gb:NM_004513.1	
208415 x at		NM 005537	gb:NM_005537.1 /DEF=Homo sapiens inhibitor of growth 1 family, member 1 (ING1), mRNA. /FEA=mRNA /GEN=ING1 /PROD=inhibitor of growth 1 family, member 1 /DB_XREF=gi:5031792 /UG=Hs.46700 inhibitor of growth 1 family, member 1 /FL=gb:AF001954.1 gb:NM_005537.1	
212572_at		AB023182	Consensus includes gb:AW779556 /FEA=EST /DB_XREF=gi:7794159 /DB_XREF=est:hn81f05.x1 /CLONE=IMAGE:3034305 /UG=Hs.184523 KIAA0965 protein	
208632_at	RNF10	AL578551	ring finger protein 10	Hs.5094

1010330 at 10	at ITEND4	Pensee	francorintion factor Do 1	He 70353
1	-	2000	וומוזכן ומנוסו ושבינו חלים	113.1
		•	Consensus includes gb:NM_005221.3 /DEF=Homo sapiens	
			distal-less homeo box 5 (DLX5), mRNA. /FEA=CDS	
			//GEN=DLX5 /PROD=distal-less homeo box 5	
			/DB_XREF=gi:6224974 /UG=Hs.99348 distal-less homeo box	
213707_s_at		NM_005221	5 /FL=gb:NM_005221.3	
			gb.AF112222.1 /DEF=Homo sapiens nuclear protein SDK3	
			mRNA, complete cds. /FEA=mRNA /PROD=nuclear protein	
			SDK3 /DB XREF=qi:6563229 /UG=Hs.44499 pinin,	,
210183 x at		AF112222	desmosome associated protein /FL=qb:AF112222.1	
			gb:U85430.1 /DEF=Human transcription factor NFATx4	
			mRNA, complete cds. /FEA=mRNA /PROD=transcription	
			factor NFATx4 /DB_XREF=gi:1835590 /UG=Hs.172674	
			nuclear factor of activated T-cells, cytoplasmic, calcineurin-	
210555_s_at		U85430	dependent 3 /FL=gb:U85430.1	
			gb:M14333.1 /DEF=Homo sapiens c-syn protooncogene	
			mRNA, complete cds. /FEA=mRNA /DB_XREF=gi:181171	
			/UG=Hs.169370 FYN oncogene related to SRC, FGR, YES	
210105_s_at		M14333	/FL=gb:M14333.1 gb:M14676.1 gb:NM_002037.1	
	FBXL7	AU145127	F-box and leucine-rich repeat protein 7	Hs.76798
213134_x_at	втсз	AI765445	BTG family, member 3	Hs.77311
			gb:NM_002485.2 /DEF=Homo sapiens Nijmegen breakage	
			syndrome 1 (nibrin) (NBS1), mRNA. /FEA=mRNA	
			/GEN=NBS1 /PROD=nibrin /DB_XREF=gi:6996019	
			/UG=Hs.25812 Nijmegen breakage syndrome 1 (nibrin)	
202907_s_at		NM_002485	/FL=gb:AF058696.1 gb:AF051334.1 gb:NM_002485.2	
ä	MGC40413	AI692203	hypothetical protein MGC40413	Hs.372549
			gb:AF113129.1 /DEF=Homo sapiens vacuolar ATPase	
			isoform VA68 mRNA, complete cds. /FEA=mRNA	
			/PROD=vacuolar ATPase isoform VA68	
		-	/DB_XREF=gi:6523820 /UG=Hs.281866 ATPase, H+	
			transporting, lysosomal (vacuolar proton pump), alpha	
201072 24		VE442420	polypeptide, 70kD, isoform 1 /FL=gb:L09235.1	
2013/2 at		AF 113123	JUD. 14 W. O. 1 G. O. 1 J. C. 3 1 1 1 1 1 1 1 1 1	

rigure	rigure / b Conta.			
			gb:BC000419.1 /DEF=Homo sapiens, catechol-O-	
			methyltransferase, clone MGC:8663, mRNA, complete cds.	
		_	/FEA=mRNA /PROD=catechol-O-methyltransferase	
			/DB_XREF=gi:12653300 /UG=Hs.240013 catechol-O-	
			methyltransferase /FL=gb:BC000419.1 gb:M58525.1	-
208817_at		BC000419	gb:M65212.1 gb:NM_007310.1 gb:NM_000754.2	
			gb:NM_014666.1 /DEF=Homo sapiens KIAA0171 gene	
			product (KIAA0171), mRNA. /FEA=mRNA /GEN=KIAA0171	
			/PROD=KIAA0171 gene product /DB_XREF=gi:7661967	
			/UG=Hs.155623 KIAA0171 gene product /FL=gb:D79993.1	
201769_at		NM_014666	gb:BC004467.1 gb:NM_014666.1	
			gb:NM_004481.2 /DEF=Homo sapiens UDP-N-acetyl-alpha-D-	
			galactosamine:polypeptide N-acetylgalactosaminyltransferase 2	
			(GaINAc-T2) (GALNT2), mRNA. /FEA=mRNA /GEN=GALNT2	
			/PROD=polypeptide N-acetylgalactosaminyltransferase 2	
			/DB_XREF=gi:9945385_/UG=Hs.130181_UDP-N-acetyl-alpha-D-	
			galactosamine:polypeptide N-acetylgalactosaminyltransferase 2	
217788 s at		NM 004481	(GaINAc-T2) /FL=gb:NM_004481.2	
<u>ب</u> ـ ال		AL049370	EST	Hs.13350
			Consensus includes qb:AK024252.1 /DEF=Homo sapiens	
			CDNA FLJ14190 fis. clone NT2RP2006534. moderately	
			similar to 5-AMP-ACTIVATED PROTEIN KINASE	-
			CATALYTIC ALDHA-1 CHAIN (FIC 271-) /FEA=mRNA	
			O(1)	
			/U.D. ARET-gi. 10450301 /U.GIIS. 200340 IIOIIIO Sapielis CDINA	
			FLJ14190 fis, clone NT2RP2006534, moderately similar to 5-	
			AMP-ACTIVATED PROTEIN KINASE, CATALYTIC ALPHA-1	
214917_at		AK024252	CHAIN (EC 2.7.1)	
218486_at	TIEG2	AA149594	TGFB inducible early growth response 2	Hs.12229
			gb:U15174.1 /DEF=Homo sapiens BCL2adenovirus E1B 19kD	
			interacting protein 3 (BNIP3) mRNA, complete cds.	
			/FEA=mRNA /GEN=BNIP3 /PROD=BCL2adenovirus E1B	
		•	19kD-interacting protein 3 /DB XREF=gi:558845	
			/UG=Hs.79428 BCL2adenovirus E1B 19kD-interacting protein	
201848_s_at		U15174	3 /FL=gb:AF002697.1 gb:U15174.1 gb:NM 004052.2	
89948_at	C20orf67	AI743331	chromosome 20 open reading frame 67	Hs.272814

- Figure	rigure / b Cont a.			
			Consensus includes gb:AK021569.1 /DEF=Homo sapiens	
216107 2		AK021569	/DB_XREF=gi:10432775 /UG=Hs.314347 Homo sapiens cDNA	
		2001 20017	ab:NM 000575.1 /DEF=Homo sapiens interleukin 1, alpha	
			(IL1A), mRNA /FEA=mRNA /GEN=IL1A /PROD=interleukin 1,	
			alpha /DB_XREF=gi:13236493 /UG=Hs.1722 interleukin 1,	
208200_at		NM_000575	alpha /FL=gb:NM_000575.1_gb:M28983.1	
			Consensus includes gb:BF215996 /FEA=EST	
			/DB_XREF=gi:11109582 /DB_XREF=est:601881549F1	
			/CLONE=IMAGE:4093740 /UG=Hs.121576 Homo sapiens	
			cDNA FLJ20153 fis, clone COL08656, highly similar to	
			AJ001381 Homo sapiens incomplete cDNA for a mutated	
212365_at		AK000160	allele	
			gb:NM_017939.1 /DEF=Homo sapiens hypothetical protein	
			FLJ20718 (FLJ20718), mRNA. /FEA=mRNA /GEN=FLJ20718	
			/PROD=hypothetical protein FLJ20718 /DB_XREF=gi:8923644	
			/UG=Hs.50579 hypothetical protein FLJ20718	
219289_at		NM_017939	/FL=gb:NM_017939.1	
			gb:NM_022840.1 /DEF=Homo sapiens hypothetical protein	
			FLJ23017 (FLJ23017), mRNA. /FEA=mRNA /GEN=FLJ23017	
			/PROD=hypothetical protein FLJ23017 /DB_XREF=gi:12383089	
			/UG=Hs.122546 hypothetical protein FLJ23017	
219698_s_at		NM_022840		
			ESTs, Moderately similar to Z254_HUMAN Zinc finger protein	
			ooietic cell	1
212608_s_at		W85912		Hs.409038
			gb:NM_006886.1 /DEF=Homo sapiens ATP synthase, H+	
			transporting, mitochondrial F1 complex, epsilon subunit	
			(ATP5E), mRNA. /FEA=mRNA /GEN=ATP5E /PROD=ATP	
			synthase, H+ transporting, mitochondrial F1complex, epsilon	
			subunit /DB_XREF=gi:5901895 /UG=Hs.177530 ATP	
			synthase, H+ transporting, mitochondrial F1 complex, epsilon	
		•	subunit /FL=gb:BC001690.1 gb:BC003671.1 gb:AF077045.1	
217801_at		NM_006886	gb:NM_006886.1_gb:AF052955.1	

Deciding 10 Deciding Decidi	rigure /	rigare / D Corita.			
at NM_018458 AF118652 AW451236 NM_024638 at NM_021941 M31159 at NAPK1 AA195999				gb:NM_018458.1 /DEF=Homo sapiens uncharacterized bone	
at NM 018458 AF118652 AW451236 NM 024638 AW45126 AW45126 AW451299 AM4195999				marrow protein BM042 (BM042), mRNA. /FEA=mRNA	
at NM 018458 AF118652 AW451236 NM 021941 M31159 at NM 000791 MAPK1 AA195999				/GEN=BM042 /PROD=uncharacterized bone marrow protein	
at NM_018458 AF118652 AW451236 NM_024638 at M31159 at MAPK1 AA195999				BM042 /DB_XREF=gi:8922101 /UG=Hs.324136	
at				uncharacterized bone marrow protein BM042	
at AF118652 AW451236 NM_024638 NM_021941 at M31159 at MAPK1 AA195999	υ¦		NM_018458	/FL=gb:AF217518.1_gb:NM_018458.1	
at AW451236 AW451236 NM_024638 at NM_021941 M31159 at MAPK1 AA195999				PKCq-interacting	
at AF118652 AW451236 NM_024638 at NM_021941 M31159 at MAPK1 AA195999				PICOT (PICOT) mRNA, complete cds. /FEA=mRNA	
at AF118652 AW451236 NM_024638 at M31159 at M31159 at MAPK1 AA195999				/GEN=PICOT /PROD=PKCq-interacting protein PICOT	
at AF118652 AW451236 NM_024638 at M31159 at M31159 at MAPK1 AA195999				/DB XREF=gi:6840952 /UG=Hs.42644 thioredoxin-like	
at NM_021941 M31159 MAPK1 MAPK1 MA195999			AF118652	/FL=gb:BC005289.1 gb:AF118649.1 gb:AF118652.1	
at NM_024638 NM_021941 M31159 at MAPK1 AA195999				ESTs, Highly similar to FINC_HUMAN Fibronectin precursor (FN)	
at NM_024638 MM_021941 M31159 at M31159 A4195999	213604_at		AW451236		Hs.409286
at NM_024638 MM_021941 M31159 at M31159 A4195999				gb:NM_024638.1 /DEF=Homo sapiens hypothetical protein	
at NM_024638 MM_021941 M31159 at M31159 MM_000791 MAPK1 AA195999				FLJ12960 (FLJ12960), mRNA. /FEA=mRNA /GEN=FLJ12960	
at NM_024638 M31159 M31159 MM_000791 MAPK1 AA195999				/PROD=hypothetical protein FLJ12960 /DB_XREF=gi:13375871	
at NM_024638 MM_021941 M31159 at M31159 MAPK1 AA195999				/UG=Hs.45005 hypothetical protein FLJ12960	
at NM_021941 M31159 at M31159 MM_000791 MAPK1 AA195999	219178_at		NM_024638	/FL=gb:NM_024638.1	
at NM_021941 M31159 at M31159 M31159 A4195999				gb:NM_021941.1 /DEF=Homo sapiens hypothetical protein	
at M31159 M31159 at MAPK1 MAPK1 AA195999				FLJ21324 (FLJ21324), mRNA. /FEA=mRNA /GEN=FLJ21324	
at M31159 M31159 at MAPK1 AA195999				/PROD=hypothetical protein FLJ21324 /DB_XREF=gi:11345479	
at NM_021941 M31159 at MAPK1 AA195999				/UG=Hs.4746 hypothetical protein FLJ21324	
at M31159 at MAPK1 A4195999	ဟ		NM_021941	/FL=gb:NM_021941.1_gb:BC003651.1	
at M31159 M31159 MM 000791 MAPK1 AA195999				gb:M31159.1 /DEF=Human growth hormone-dependent insulin-	
at MAPK1 AA195999				a	
at MAPK1 AA195999				/FEA=mRNA /GEN=IGFBP1 /DB_XREF=gi:183115	
at M31159 M31159 M31159				/UG=Hs.77326 insulin-like growth factor binding protein 3	
at NA 000791 NA 000791			M31159	/FL=gb:BC000013.1 gb:M31159.1	
at NM 000791 NA 04195999				gb:NM_000791.2 /DEF=Homo sapiens dihydrofolate reductase	
at NM 000791 AA195999				(DHFR), mRNA. /FEA=mRNA /GEN=DHFR	
at NM 000791 AA195999				/PROD=dihydrofolate reductase /DB_XREF=gi:7262376	
MAPK1 AA195999				/UG=Hs.83765 dihydrofolate reductase /FL=gb:BC000192.1	
MAPK1 AA195999	at		NM_000791		
			AA195999	mitogen-activated protein kinase 1	Hs.324473

aingi i	igale i o collea.			
			gb:D50579.1 /DEF=Homo sapiens mRNA for	
_			carboxylesterase, complete cds. /FEA=mRNA	
		1	/UG=Hs.282975 carboxylesterase 2 (intestine, liver)	
209668_x_at		D50579	/FL=gb:U60553.1 gb:D50579.1 gb:NM 003869.2	
			gb:BC003561.1 /DEF=Homo sapiens, Similar to adaptor-	
			related protein complex 1, sigma 1 subunit, clone	
			MGC:1929, mRNA, complete cds. /FEA=mRNA	
			/PROD=Similar to adaptor-related protein complex 1, sigma 1	
			subunit /DB_XREF=gi:13097710 /UG=Hs.57600 adaptor-	
			related protein complex 1, sigma 1 subunit	
209635_at		BC003561	/FL=gb:BC003561.1	
221751_at	TMSB10	AL565516	thymosin, beta 10	Hs.76293
			gb:AF274950.1 /DEF=Homo sapiens PNAS-25 mRNA,	
			complete cds. /FEA=mRNA /PROD=PNAS-25	
			/DB_XREF=gi:12751064 /UG=Hs.22595 hypothetical protein	
221652_s_at		AF274950	FLJ10637 /FL=gb:AF274950.1	
222371_at		AI732802	ESTs	Hs.292679
			gb:NM_002668.1 /DEF=Homo sapiens proteolipid protein 2	
			(colonic epithelium-enriched) (PLP2), mRNA. /FEA=mRNA	
			/GEN=PLP2 /PROD=proteolipid protein 2 (colonicepithelium-	
			enriched) /DB XREF=ai:4505892 /UG=Hs.77422 proteolipid	
			protein 2 (colonic epithelium-enriched) /FL=ab:L09604.1	
201136_at		NM_002668		
			gb:NM_019847.2 /DEF=Homo sapiens ankylosis, progressive	
			(mouse) homolog (ANKH), mRNA. /FEA=mRNA /GEN=ANKH	
			/PROD=homolog of mouse Ank /DB_XREF=gi:10947057	
			/UG=Hs.168640 ankylosis, progressive (mouse) homolog	
220076_at		NM_019847	/FL=gb:NM_019847.2	
			gb:J02639.1 /DEF=Human plasma serine protease (protein	
			C) inhibitor mRNA, complete cds. /FEA=mRNA	
			/DB_XREF=gi:180549 /UG=Hs.76353 serine (or cysteine)	
			proteinase inhibitor, clade A (alpha-1 antiproteinase,	
			antitrypsin), member 5 /FL=gb:NM_000624.1 gb:U35464.1	
209443_at		J02639	gb:J02639.1 gb:S58545.1	
			ESTs, Moderately similar to hypothetical protein FLJ20378	
217540_at		AA721025	[Homo sapiens] [H.sapiens]	Hs.293253

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201690_s_at TPD52	rPD52	BE974098	tumor protein D52	Hs.2384
213905_x_at E	BGN	AA845258	biglycan	Hs.821
000000		PROSOC WIN	gb:NM_006851.1 /DEF=Homo sapiens glioma pathogenesis- related protein (RTVP1), mRNA. /FEA=mRNA /GEN=RTVP1 /PROD=glioma pathogenesis-related protein /DB_XREF=gi:5803150 /UG=Hs.64639 glioma pathogenesis-	
204222			Consensus includes gb:AL132773 /DEF=Human DNA sequence from clone RP4-741H3 on chromosome 20 Contains parts of isoform 1 and isoform 2 (KIAA0548) of the ATRN (attractin (with dipentidylneptidase IV activity))	
212517_at		AL132773	gene, ESTs, STSs and GSSs /FEA=mRNA_1 /DB_XREF=gi:7159777 /UG=Hs.194019 attractin	
202141 s at		BC003090	gb:BC003090.1 /DEF=Homo sapiens, COP9 homolog, clone MGC:1297, mRNA, complete cds. /FEA=mRNA /PROD=COP9 homolog /DB_XREF=gi:13111846 /UG=Hs.75193 COP9 homolog /FL=gb:BC003090.1 gb:U51205.1 gb:NM_006710.1	
203932 at		NM 002118		
212612_at		D31888	Consensus includes gb:D31888.1 /DEF=Human mRNA for KIAA0071 gene, partial cds. /FEA=mRNA /GEN=KIAA0071 /DB_XREF=gi:506340 /UG=Hs.78398 KIAA0071 protein /FL=gb:AF155595.1 gb:NM_015156.1	
÷ 0 0000		BC004233	gb:BC001233.1 /DEF=Homo sapiens, Similar to KIAA0092 gene product, clone MGC:4896, mRNA, complete cds. /FEA=mRNA /PROD=Similar to KIAA0092 gene product /DB_XREF=gi:12654780 /UG=Hs.134158 Homo sapiens, Similar to KIAA0092 gene product, clone MGC:4896, mRNA, complete cds /Ei = ch-BC001233.1	
203002 2 al		00001233	colliplete cus /re-gb:bcool233:1	

ainfi i	igaic / D Colleg.			
212914_at		AV648364	ESTs, Highly similar to potassium voltage-gated channel, Isk-related subfamily, gene 4; potassium voltage-gated channel-like protein, Isk-related subfamily [Homo sapiens] [H.sapiens]	Hs.356416
212249_at		M61906	Consensus includes gb:Al934473 /FEA=EST /DB_XREF=gi:5673433 /DB_XREF=est:wp58d05.x1 /CLONE=IMAGE:2465961 /UG=Hs.6241 phosphoinositide-3-kinase, regulatory subunit, polypeptide 1 (p85 alpha)	
204806_x_at		NM_018950		
205726_at		NM_006729	gb:NM_006729.1 /DEF=Homo sapiens diaphanous (Drosophila, homolog) 2 (DIAPH2), transcript variant 156, mRNA. /FEA=mRNA /GEN=DIAPH2 /PROD=diaphanous 2 isoform 156 /DB_XREF=gi:5803002 /UG=Hs.226483 NM_006729 diaphanous (Drosophila, homolog) 2 /FL=gb:NM_006729.1	
201036_s_at		NM_005327	gb:NM_005327.1 /DEF=Homo sapiens L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain (HADHSC), mRNA. /FEA=mRNA /GEN=HADHSC /PROD=L-3-hydroxyacyl-Coenzyme A dehydrogenase, shortchain /DB_XREF=gi:4885386 /UG=Hs.8110 L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain /FL=gb:BC000306.1 gb:NM_005327.1	
211263_s_at		D87994	gb:D87994.1 /DEF=Homo sapiens mRNA for PACE4E-II, complete cds. /FEA=mRNA /PROD=PACE4E-II /DB_XREF=gi:2330550 /UG=Hs.170414 paired basic amino acid cleaving system 4 /FL=gb:D87994.1	
217667_at		AV761014	SEC14-like protein 1	Hs.291972
at at	PART1	AI770098	drogen-regulated transcript 1	Hs.96744
47105_at F	FLJ20399	AA886893	hypothetical protein FLJ20399	Hs.8575

2136				
			gb:NM_015583.1 /DEF=Homo sapiens DKFZP586M0622	
	•		protein (DKFZP586M0622), mRNA. /FEA=mRNA	·
-			//GEN=DKFZP586M0622 /PROD=DKFZP586M0622 protein	
			/DB_XREF=gi:7661687 /UG=Hs.241544 DKFZP586M0622	
208015_at		NM_015583	_	
			gb:NM_004563.1 /DEF=Homo sapiens phosphoenolpyruvate	
			carboxykinase 2 (mitochondrial) (PCK2), mRNA. /FEA=mRNA	
			//GEN=PCK2_/PROD=phosphoenolpyruvate_carboxykinase_	
	•		2(mitochondrial) /DB_XREF=gi:4758885 /UG=Hs.75812	
	•		phosphoenolpyruvate carboxykinase 2 (mitochondrial)	
202847_at	;	NM_004563	/FL=gb:BC001454.1 gb:NM_004563.1	
- Series			gb:NM_024937.1 /DEF=Homo sapiens hypothetical protein	
			FLJ12929 (FLJ12929), mRNA. /FEA=mRNA /GEN=FLJ12929	
			/PROD=hypothetical protein FLJ12929 /DB_XREF=gi:13376412	
	٠		/UG=Hs.278956 hypothetical protein FLJ12929	
219631_at		NM_024937		
			ESTs, Highly similar to SRA4_HUMAN CTD-binding SR-like	
222311_s_at	٠	AA648521	protein RA4 [H.sapiens]	Hs.390734
			gb:NM_012091.2 /DEF≂Homo sapiens adenosine deaminase,	
			tRNA-specific 1 (ADAT1), mRNA. /FEA=mRNA /GEN=ADAT1	
			/PROD=adenosine deaminase, tRNA-specific 1	
			/DB_XREF=gi:7382475 /UG=Hs.188661 adenosine deaminase,	
			tRNA-specific 1 /FL=gb:BC002758.1 gb:AF125188.1	
219384_s_at		NM_012091	_	
203224_at	FLJ11149	BF340123	hypothetical protein FLJ11149	Hs.37558
			Consensus includes gb:AL110158.1 /DEF=Homo sapiens	
			mRNA; cDNA DKFZp586F0424 (from clone	
	•		DKFZp586F0424); partial cds. /FEA=mRNA	
			/GEN=DKFZp586F0424 /PROD=hypothetical protein	:
217196_s_at		AL110158	/DB_XREF=gi:5817061 /UG=Hs.23585 KIAA1078 protein	
			gb:NM_004516.1 /DEF=Homo sapiens interleukin enhancer	
			binding factor 3, 90kD (ILF3), mRNA. /FEA=mRNA	
			/GEN=ILF3 /PROD=interleukin enhancer binding factor 3,	
			90kD /DB_XREF=gi:4758603 /UG=Hs.256583 interleukin	
			enhancer binding factor 3, 90kD /FL=gb:BC003086.1	
0			gb:NM_004516.1 gb:U10324.1 gb:AF167570.1	
21/805_at		NM 004516	NM_004516 [gb:NM_012218.1	

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			gb:NM_000365.1 /DEF=Homo sapiens triosephosphate isomerase 1 (TPI1), mRNA. /FEA=mRNA /GEN=TPI1		
			/PROD=triosephosphate isomerase 1 /DB_XREF=gi:4507644		
1					
200822_x_at		NM_000365			
			Consensus includes gb:AL080080.1 /DEF=Homo sapiens		
			mRNA; cDNA DKFZp564E1962 (from clone		
			DKFZp564E1962); partial cds. /FEA=mRNA		
			/GEN=DKFZp564E1962 /PROD=hypothetical protein		
			/DB_XREF=gi:5262491 /UG=Hs.24766 thioredoxin-related		
209476_at		AL080080	transmembrane protein /FL=gb:AB048246.1		
			ESTs, Weakly similar to 2109260A B cell growth factor [Homo		
215314_at		AU146646	sapiens] [H.sapiens]		Hs.179752
				NM_001854;	
			collagen, type XI, alpha 1	NM_080629;	
37892_at	COL11A1	J04177		NM_080630	Hs.82772
55662_at	FLJ13114	H27225	hypothetical protein FLJ13114		Hs.9444
91816_f_at		C18318	Homo sapiens mRNA for OK/SW-CL.4, complete cds		Hs.123469
			gb:NM 005095.1 /DEF=Homo sapiens zinc finger protein 262		
			(ZNF262), mRNA. /FEA=mRNA /GEN=ZNF262 /PROD=zinc		
			finger protein 262 /DB_XREF=gi:4827068 /UG=Hs.150390		
202051 s at		NM 005095			
			gb:NM_030802.1 /DEF=Homo sapiens CEBP-induced protein		
			(LOC81558), mRNA. /FEA=mRNA /GEN=LOC81558		
			/PROD=CEBP-induced protein /DB_XREF=gi:13540589		
221249_s_at		NM_030802)30802 /FL=gb:NM_030802.1		
			gb:NM_021643.1 /DEF=Homo sapiens GS3955 protein		
			(GS3955), mRNA. /FEA=mRNA /GEN=GS3955		
			/PROD=GS3955 protein /DB_XREF=gi:11056053		
			/UG=Hs.155418 GS3955 protein /FL=gb:NM_021643.1		
202478_at		NM_021643	gb:BC002637.1 gb:D87119.1		

Figure	Figure /b Cont'a.			
			gb:NM_017491.1 /DEF=Homo sapiens WD repeat domain 1	
			(WDR1), transcript variant 1, mRNA. /FEA=mRNA	
			/GEN=WDR1 /PROD=WD repeat-containing protein 1,	
			isoform 1 /DB_XREF=gi:9257256 /UG=Hs.85100 WD repeat	
			domain 1 /FL=gb:BC000201.1 gb:BC002489.1 gb:AF020056.1	
200609_s_at		NM_017491		
208842 s at	GORASP2	W93787		Hs.6880
			gb:NM_001854.1 /DEF=Homo sapiens collagen, type XI,	
			alpha 1 (COL11A1), mRNA. /FEA=mRNA /GEN=COL11A1	
			/PROD=collagen, type XI, alpha 1 /DB_XREF=gi:4502938	
			/UG=Hs.82772 collagen, type XI, alpha 1 /FL=gb:J04177.1	
204320 at		NM 001854	db:NM 001854.1	
			gb:NM_003730.2 /DEF=Homo sapiens ribonuclease 6	
			precursor (RNASE6PL), mRNA. /FEA=mRNA	
			/GEN=RNASE6PL /PROD=ribonuclease 6 precursor	
			/DB XREF=qi:5231227 /UG=Hs.8297 ribonuclease 6 precursor	-
			/FL=qb:BC001660.1 qb:BC001819.1 gb:U85625.2	_
217984 at		NM 003730		
			Consensus includes gb:AK000089.1 /DEF=Homo sapiens	
			cDNA FLJ20082 fis, clone COL03245. /FEA=mRNA	
			/DB_XREF=gi:7019950 /UG=Hs.323797 Homo sapiens cDNA	
215246_at		AK000089	FLJ20082 fis, clone COL03245	
221967 at	NXPH4	AI933199		Hs.120911
217921 at	MAN1A2	H97940	alpha, class 1A, member 2	Hs.367638
			ESTs, Weakly similar to hypothetical protein FLJ20489 [Homo	
213184_at		N48361		Hs.393053
			gb:NM_016940.1 /DEF=Homo sapiens chromosome 21 open	
			reading frame 6 (C21ORF6), mRNA. /FEA=mRNA	
			/GEN=C21ORF6 /PROD=chromosome 21 open reading frame	
			6 /DB_XREF=gi:8393017 /UG=Hs.34136 chromosome 21	-
218377 s at		NM 016940	open reading frame 6 /FL=gb:AF212232.1 gb:NM_016940.1	
l I		II.	Consensus includes gb:AF055024.1 /DEF=Homo sapiens	
			clone 24763 mRNA sequence. /FEA=mRNA	
			/DB_XREF=gi:3005752 /UG=Hs.153489 ASB-1 protein	
212818_s_at		AF055024	b:AF156777.1 gb:NM 016114.1	
222270_at		BG540048	ESTs	HS.389799

rigue	rigare / b conta.			
216012_at		U43604	Consensus includes gb:U43604.1 /DEF=Human unidentified mRNA, partial sequence. /FEA=mRNA /DB_XREF=gi:1171236 /UG=Hs.159901 Human unidentified mRNA, partial sequence	
208837 at		BC000027	gb:BC000027.1 /DEF=Homo sapiens, integral type I protein, clone MGC:1302, mRNA, complete cds. /FEA=mRNA /PROD=integral type I protein /DB_XREF=gi:12652570 /UG=Hs.179516 integral type I protein /FL=gb:BC000027.1 ob:NM 007364.1	
221827 at	C20orf18	Π	open reading frame 18	Hs.247280
			Consensus includes gb:AA515560 /FEA=EST /DB_XREF=gi:2255160 /DB_XREF=est:ni42c09.s1 /CLONE=IMAGE:979504 /UG=Hs.283473 hypothetical protein PRO2900	
< ¦			gb:NM_025195.1 /DEF=Homo sapiens phosphoprotein regulated by mitogenic pathways (C8FW), mRNA. /FEA=mRNA /GEN=C8FW /PROD=G-protein-coupled receptor induced protein /DB_XREF=gi:13399327 /UG=Hs.7837 phosphoprotein regulated by mitogenic pathways	
202241_at		NM_025195		
400000		MM 0007	gb:NM_000713.1 /DEF=Homo sapiens biliverdin reductase B (flavin reductase (NADPH)) (BLVRB), mRNA. /FEA=mRNA /GEN=BLVRB /PROD=biliverdin reductase B (flavin reductase(NADPH)) /DB_XREF=gi:4502418 /UG=Hs.76289 biliverdin reductase B (flavin reductase (NADPH))	
203745 at	HCCS	01013	holocytochrome c synthase (cytochrome c heme-lyase)	Hs.211571
201952 at		27	Consensus includes gb:AA156721 /FEA=EST // IDB_XREF=gi:1728335 /IDB_XREF=est:zl18b04.s1 // ICLONE=IMAGE:502255 // IUG=Hs.10247 activated leucocyte cell adhesion molecule /FL=qb:NM 001627.1 gb:L38608.1	
215034 s at	TM4SF1	39753	transmembrane 4 superfamily member 1	Hs.351316
		ì	gb:NM_000305.1 /DEF=Homo sapiens paraoxonase 2 (PON2), mRNA. /FEA=mRNA /GEN=PON2 /PROD=paraoxonase 2 /DB_XREF=gi:4505952 /UG=Hs.169857 paraoxonase 2 /FL=gb:L48513.1	
201876_at		NM_000305	000305 gb:AF001601.1 gb:NM_000305.1	

rigure	Figure / D Cont a.			
-			gb:M13436.1 /DEF=Human ovarian beta-A innibin mKNA, complete cds. /FEA=mRNA /GEN=INHBA /DB XREF=qi:186414 /UG=Hs.727 inhibin. beta A (activin A.	
210511_s_at		M13436	activin AB alpha polypeptide) /FL=gb:M13436.1	
			gb:NM_002999.1 /DEF=Homo sapiens syndecan 4 (amphiglycan, ryudocan) (SDC4), mRNA, /FEA=mRNA	
			/GEN=SDC4 /PROD=syndecan 4 (amphiglycan, ryudocan)	
_			/DB_XREF=gi:4506860 /UG=Hs.252189 syndecan 4	
2071_at		NM_002999	(amphiglycan, ryudocan) /FL=gb:NM_002999.1	
202050_s_at	ZNF262	AA521508	zinc finger protein 262	Hs.150390
			gb:NM_021070.1 /DEF=Homo sapiens latent transforming growth factor beta binding protein 3 (LTBP3), mRNA.	
			factor beta bindingprotein 3 /DB_XREF=gi:10835104	
219922_s_at		NM_021070	/UG=Hs.289019 latent transforming growth ractor beta 021070 binding protein 3 /FL=gb:NM_021070.1 gb:AF135960.2	
			gb:M95541.1 /DEF=Homo sapiens adenosine triphosphatase mRNA, complete cds. /FEA=mRNA /PROD=adenosine triphosphatase /DB_XREF=gi:184269 /UG=Hs.78546 ATPase, Ca++ transporting, plasma membrane 1 /FL=gb:M95541.1	
209281_s_at		M95541	gb:NM_001682.1 gb:J04027.1	
_			gb:NM_002901.1 /DEF=Homo sapiens reticulocalbin 1, EF- hand calcium binding domain (RCN1), mRNA. /FEA=mRNA	
			/DB_XREF=gi:4506454 /UG=Hs.167791 reticulocalbin 1, EF-	
201063 at		NM 002901	hand calcium binding domain /FL=gb:D42073.1	
		ri 💮	Consensus includes gb:BG251175 /FEA=EST	
			/DB_XREF=gi:12760991 /DB_XREF=est:602364982F1	
202515_at		NM_004087	(Drosophila) homolog 1 /FL=gb:NM_004087.1 gb:U13896.1	
			gb:BC002416.1 /DEF=Homo sapiens, biglycan, clone	-
			MGC:2298, MKNA, complete cds. /FEA=MKNA /PROD=biglycan /DB_XREF=gi:12803216 /UG=Hs.821 biglycan	
;		000046	/FL=gb:BC002416.1 gb:BC004244.1 gb:J04599.1	
201261_x_at		BC002416	JOD:NM JOUT/11:1	

200647 x at	NM_003752	gb:NM_003752.2 /DEF=Homo sapiens eukaryotic translation initiation factor 3, subunit 8 (110kD) (EIF3S8), mRNA. //FEA=mRNA /GEN=EIF3S8 /PROD=eukaryotic translation initiation factor 3,subunit 8 (110kD) /DB_XREF=gi:5579457 //UG=Hs.4835 eukaryotic translation initiation factor 3, subunit 8 (110kD) /FL=gb:NM_003752.2	
218730_s_at	NM_014057	gb:NM_014057.1 /DEF=Homo sapiens osteoglycin (osteoinductive factor, mimecan) (OGN), mRNA. /FEA=mRNA /GEN=OGN /PROD=osteoglycin /DB_XREF=gi:7661703 /UG=Hs.109439 osteoglycin (osteoinductive factor, mimecan) /FL=gb:NM_024416.1 gb:AF100758.1 gb:AL110267.1 gb:NF_014057 gb:NM_014057.1	